

Attorney Docket No. 2750-1096P

Table 1

Client Docket No. 80142.004

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Maximum Length Sequence corresponding to clone ID 101665

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1
- Ceres seq_id 1481332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2
- Ceres seq_id 1481333
- Location of start within SEQ ID NO 1: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 107900

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 3
- Ceres seq_id 1481342

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4
- Ceres seq_id 1481343
- Location of start within SEQ ID NO 3: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 5
- Ceres seq_id 1481344
- Location of start within SEQ ID NO 3: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 6
- Ceres seq_id 1481345
- Location of start within SEQ ID NO 3: at 518 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 108514

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 7
- Ceres seq_id 1481346

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 8
- Ceres seq_id 1481347
- Location of start within SEQ ID NO 7: at 629 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 9

- Ceres seq_id 1481348
- Location of start within SEQ ID NO 7: at 779 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 10
- Ceres seq_id 1481349
- Location of start within SEQ ID NO 7: at 828 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 109446

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 11
- Ceres seq_id 1481357

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 12
- Ceres seq_id 1481358
- Location of start within SEQ ID NO 11: at 342 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 13
- Ceres seq_id 1481359
- Location of start within SEQ ID NO 11: at 387 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 14
- Ceres seq_id 1481360
- Location of start within SEQ ID NO 11: at 396 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 113536

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 15
- Ceres seq_id 1481372

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 16
- Ceres seq_id 1481373
- Location of start within SEQ ID NO 15: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 17
- Ceres seq_id 1481374
- Location of start within SEQ ID NO 15: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 18
- Ceres seq_id 1481375
- Location of start within SEQ ID NO 15: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 115279

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 19
- Ceres seq_id 1481388

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 20
- Ceres seq_id 1481389
- Location of start within SEQ ID NO 19: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 21
- Ceres seq_id 1481390
- Location of start within SEQ ID NO 19: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 22
- Ceres seq_id 1481391
- Location of start within SEQ ID NO 19: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 118207

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 23
- Ceres seq_id 1481423

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 24
- Ceres seq_id 1481424
- Location of start within SEQ ID NO 23: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 25
- Ceres seq_id 1481425
- Location of start within SEQ ID NO 23: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 125028

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 26
- Ceres seq_id 1481471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 27
- Ceres seq_id 1481472
- Location of start within SEQ ID NO 26: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 28
- Ceres seq_id 1481473
- Location of start within SEQ ID NO 26: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 29
- Ceres seq_id 1481474
- Location of start within SEQ ID NO 26: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 126108

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 30
- Ceres seq_id 1481479

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 31
- Ceres seq_id 1481480
- Location of start within SEQ ID NO 30: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 32

- Ceres seq_id 1481481
- Location of start within SEQ ID NO 30: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 33
- Ceres seq_id 1481482
- Location of start within SEQ ID NO 30: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 12613

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 34
- Ceres seq_id 1481483

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 35
- Ceres seq_id 1481484
- Location of start within SEQ ID NO 34: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 36
- Ceres seq_id 1481485
- Location of start within SEQ ID NO 34: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 37
- Ceres seq_id 1481486
- Location of start within SEQ ID NO 34: at 283 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 13607

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 38
- Ceres seq_id 1481487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 39
- Ceres seq_id 1481488
- Location of start within SEQ ID NO 38: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 40
 - Ceres seq_id 1481489
 - Location of start within SEQ ID NO 38: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 41
 - Ceres seq_id 1481490
 - Location of start within SEQ ID NO 38: at 145 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 1367

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 42
 - Ceres seq_id 1481491
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 43
 - Ceres seq_id 1481492
 - Location of start within SEQ ID NO 42: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 14568

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 44
 - Ceres seq_id 1481504
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 45
 - Ceres seq_id 1481505
 - Location of start within SEQ ID NO 44: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 46
 - Ceres seq_id 1481506
 - Location of start within SEQ ID NO 44: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 47
 - Ceres seq_id 1481507
 - Location of start within SEQ ID NO 44: at 41 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 147980

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 48
- Ceres seq_id 1481516

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 49
- Ceres seq_id 1481517
- Location of start within SEQ ID NO 48: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 50
- Ceres seq_id 1481518
- Location of start within SEQ ID NO 48: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 51
- Ceres seq_id 1481519
- Location of start within SEQ ID NO 48: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 147983

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 52
- Ceres seq_id 1481520

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 53
- Ceres seq_id 1481521
- Location of start within SEQ ID NO 52: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 54
- Ceres seq_id 1481522
- Location of start within SEQ ID NO 52: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 55

- Ceres seq_id 1481523
- Location of start within SEQ ID NO 52: at 170 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148070

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 56
 - Ceres seq_id 1481524
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 57
 - Ceres seq_id 1481525
 - Location of start within SEQ ID NO 56: at 448 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 58
 - Ceres seq_id 1481526
 - Location of start within SEQ ID NO 56: at 1241 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 59
 - Ceres seq_id 1481527
 - Location of start within SEQ ID NO 56: at 1403 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148232

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 60
 - Ceres seq_id 1481532
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 61
 - Ceres seq_id 1481533
 - Location of start within SEQ ID NO 60: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 62
 - Ceres seq_id 1481534
 - Location of start within SEQ ID NO 60: at 108 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 63
 - Ceres seq_id 1481535
 - Location of start within SEQ ID NO 60: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148887

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 64
- Ceres seq_id 1481540

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 65
- Ceres seq_id 1481541
- Location of start within SEQ ID NO 64: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 66
- Ceres seq_id 1481542
- Location of start within SEQ ID NO 64: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 67
- Ceres seq_id 1481543
- Location of start within SEQ ID NO 64: at 238 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 149204

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 68
- Ceres seq_id 1481544

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 69
- Ceres seq_id 1481545
- Location of start within SEQ ID NO 68: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 70
- Ceres seq_id 1481546
- Location of start within SEQ ID NO 68: at 178 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 71
- Ceres seq_id 1481547
- Location of start within SEQ ID NO 68: at 280 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 150293

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 72
- Ceres seq_id 1481564

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 73
- Ceres seq_id 1481565
- Location of start within SEQ ID NO 72: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 74
- Ceres seq_id 1481566
- Location of start within SEQ ID NO 72: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 75
- Ceres seq_id 1481567
- Location of start within SEQ ID NO 72: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 150540

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 76
- Ceres seq_id 1481580

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 77
- Ceres seq_id 1481581
- Location of start within SEQ ID NO 76: at 594 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 78

- Ceres seq_id 1481582
- Location of start within SEQ ID NO 76: at 630 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 79
- Ceres seq_id 1481583
- Location of start within SEQ ID NO 76: at 768 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 151413

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 80
- Ceres seq_id 1481596

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 81
- Ceres seq_id 1481597
- Location of start within SEQ ID NO 80: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 82
- Ceres seq_id 1481598
- Location of start within SEQ ID NO 80: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 83
- Ceres seq_id 1481599
- Location of start within SEQ ID NO 80: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 152305

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 84
- Ceres seq_id 1481613

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 85
- Ceres seq_id 1481614
- Location of start within SEQ ID NO 84: at 403 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 86
 - Ceres seq_id 1481615
 - Location of start within SEQ ID NO 84: at 562 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 87
 - Ceres seq_id 1481616
 - Location of start within SEQ ID NO 84: at 616 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 153154

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 88
 - Ceres seq_id 1481621
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 89
 - Ceres seq_id 1481622
 - Location of start within SEQ ID NO 88: at 180 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 90
 - Ceres seq_id 1481623
 - Location of start within SEQ ID NO 88: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 91
 - Ceres seq_id 1481624
 - Location of start within SEQ ID NO 88: at 345 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 153808

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 92
 - Ceres seq_id 1481625
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 93
 - Ceres seq_id 1481626
 - Location of start within SEQ ID NO 92: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 94
- Ceres seq_id 1481627
- Location of start within SEQ ID NO 92: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 95
- Ceres seq_id 1481628
- Location of start within SEQ ID NO 92: at 499 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155661

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 96
- Ceres seq_id 1481632

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 97
- Ceres seq_id 1481633
- Location of start within SEQ ID NO 96: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 98
- Ceres seq_id 1481634
- Location of start within SEQ ID NO 96: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155696

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 99
- Ceres seq_id 1481635

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 100
- Ceres seq_id 1481636
- Location of start within SEQ ID NO 99: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 101

- Ceres seq_id 1481637
- Location of start within SEQ ID NO 99: at 409 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 102
- Ceres seq_id 1481638
- Location of start within SEQ ID NO 99: at 457 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155707

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 103
- Ceres seq_id 1481639

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 104
- Ceres seq_id 1481640
- Location of start within SEQ ID NO 103: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 105
- Ceres seq_id 1481641
- Location of start within SEQ ID NO 103: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 106
- Ceres seq_id 1481642
- Location of start within SEQ ID NO 103: at 712 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 156573

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 107
- Ceres seq_id 1481647

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 108
- Ceres seq_id 1481648
- Location of start within SEQ ID NO 107: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 109
- Ceres seq_id 1481649
- Location of start within SEQ ID NO 107: at 243 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 110
- Ceres seq_id 1481650
- Location of start within SEQ ID NO 107: at 429 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 1939

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 111
- Ceres seq_id 1481668

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 112
- Ceres seq_id 1481669
- Location of start within SEQ ID NO 111: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 113
- Ceres seq_id 1481670
- Location of start within SEQ ID NO 111: at 405 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 20783

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 114
- Ceres seq_id 1481681

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 115
- Ceres seq_id 1481682
- Location of start within SEQ ID NO 114: at 239 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 116
- Ceres seq_id 1481683
- Location of start within SEQ ID NO 114: at 398 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 218721

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 117
- Ceres seq_id 1481700

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 118
- Ceres seq_id 1481701
- Location of start within SEQ ID NO 117: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 119
- Ceres seq_id 1481702
- Location of start within SEQ ID NO 117: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 120
- Ceres seq_id 1481703
- Location of start within SEQ ID NO 117: at 292 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 218758

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 121
- Ceres seq_id 1481704

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 122
- Ceres seq_id 1481705
- Location of start within SEQ ID NO 121: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 123
- Ceres seq_id 1481706
- Location of start within SEQ ID NO 121: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 124

- Ceres seq_id 1481707
- Location of start within SEQ ID NO 121: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 125
- Ceres seq_id 1481716

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 126
- Ceres seq_id 1481717
- Location of start within SEQ ID NO 125: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 127
- Ceres seq_id 1481718
- Location of start within SEQ ID NO 125: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 128
- Ceres seq_id 1481719
- Location of start within SEQ ID NO 125: at 395 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 129
- Ceres seq_id 1481728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 130
- Ceres seq_id 1481729
- Location of start within SEQ ID NO 129: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 131
- Ceres seq_id 1481730
- Location of start within SEQ ID NO 129: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 132
 - Ceres seq_id 1481731
 - Location of start within SEQ ID NO 129: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220829

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 133
 - Ceres seq_id 1481732
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 134
 - Ceres seq_id 1481733
 - Location of start within SEQ ID NO 133: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 135
 - Ceres seq_id 1481734
 - Location of start within SEQ ID NO 133: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 136
 - Ceres seq_id 1481735
 - Location of start within SEQ ID NO 133: at 405 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220846

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 137
 - Ceres seq_id 1481740
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 138
 - Ceres seq_id 1481741
 - Location of start within SEQ ID NO 137: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 139
 - Ceres seq_id 1481742
 - Location of start within SEQ ID NO 137: at 10 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 140
- Ceres seq_id 1481743
- Location of start within SEQ ID NO 137: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220852

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 141
- Ceres seq_id 1481744

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 142
- Ceres seq_id 1481745
- Location of start within SEQ ID NO 141: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 143
- Ceres seq_id 1481746
- Location of start within SEQ ID NO 141: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 144
- Ceres seq_id 1481747

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 145
- Ceres seq_id 1481748
- Location of start within SEQ ID NO 144: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 146
- Ceres seq_id 1481749
- Location of start within SEQ ID NO 144: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 147

- Ceres seq_id 1481750

- Location of start within SEQ ID NO 144: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220915

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 148

- Ceres seq_id 1481755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 149

- Ceres seq_id 1481756

- Location of start within SEQ ID NO 148: at 178 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220934

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 150

- Ceres seq_id 1481764

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 151

- Ceres seq_id 1481765

- Location of start within SEQ ID NO 150: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 152

- Ceres seq_id 1481766

- Location of start within SEQ ID NO 150: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220944

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 153

- Ceres seq_id 1481770

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 154

- Ceres seq_id 1481771

- Location of start within SEQ ID NO 153: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 155

- Ceres seq_id 1481772

- Location of start within SEQ ID NO 153: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226475

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 156
- Ceres seq_id 1481775

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 157
- Ceres seq_id 1481776
- Location of start within SEQ ID NO 156: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 158
- Ceres seq_id 1481777
- Location of start within SEQ ID NO 156: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 159
- Ceres seq_id 1481778
- Location of start within SEQ ID NO 156: at 255 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 160
- Ceres seq_id 1481779

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 161
- Ceres seq_id 1481780
- Location of start within SEQ ID NO 160: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226501

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 162
- Ceres seq_id 1481789

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 163
- Ceres seq_id 1481790
- Location of start within SEQ ID NO 162: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 164
- Ceres seq_id 1481791
- Location of start within SEQ ID NO 162: at 229 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226516

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 165
- Ceres seq_id 1481792

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 166
- Ceres seq_id 1481793
- Location of start within SEQ ID NO 165: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 167
- Ceres seq_id 1481794
- Location of start within SEQ ID NO 165: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 168
- Ceres seq_id 1481795
- Location of start within SEQ ID NO 165: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227154

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 169
- Ceres seq_id 1481796

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 170
- Ceres seq_id 1481797
- Location of start within SEQ ID NO 169: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 171

- Ceres seq_id 1481798
- Location of start within SEQ ID NO 169: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227202

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 172
- Ceres seq_id 1481799

Maximum Length Sequence corresponding to clone ID 227468

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 173
- Ceres seq_id 1481800

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 174
- Ceres seq_id 1481801
- Location of start within SEQ ID NO 173: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 175
- Ceres seq_id 1481802
- Location of start within SEQ ID NO 173: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 176
- Ceres seq_id 1481803
- Location of start within SEQ ID NO 173: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227480

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 177
- Ceres seq_id 1481808

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 178
- Ceres seq_id 1481809
- Location of start within SEQ ID NO 177: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 179
- Ceres seq_id 1481810
- Location of start within SEQ ID NO 177: at 15 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 180
- Ceres seq_id 1481811
- Location of start within SEQ ID NO 177: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227719

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 181
- Ceres seq_id 1481815

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 182
- Ceres seq_id 1481816
- Location of start within SEQ ID NO 181: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 183
- Ceres seq_id 1481817
- Location of start within SEQ ID NO 181: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 184
- Ceres seq_id 1481818
- Location of start within SEQ ID NO 181: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227812

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 185
- Ceres seq_id 1481819

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 186
- Ceres seq_id 1481820
- Location of start within SEQ ID NO 185: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 187
- Ceres seq_id 1481821
- Location of start within SEQ ID NO 185: at 57 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 188
- Ceres seq_id 1481822
- Location of start within SEQ ID NO 185: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227814

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 189
- Ceres seq_id 1481823

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 190
- Ceres seq_id 1481824
- Location of start within SEQ ID NO 189: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 191
- Ceres seq_id 1481825
- Location of start within SEQ ID NO 189: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 192
- Ceres seq_id 1481826
- Location of start within SEQ ID NO 189: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 193
- Ceres seq_id 1481827

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 194
- Ceres seq_id 1481828
- Location of start within SEQ ID NO 193: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 195
- Ceres seq_id 1481829
- Location of start within SEQ ID NO 193: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 196
- Ceres seq_id 1481830
- Location of start within SEQ ID NO 193: at 215 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 229883

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 197
- Ceres seq_id 1481831

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 198
- Ceres seq_id 1481832
- Location of start within SEQ ID NO 197: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 199
- Ceres seq_id 1481833
- Location of start within SEQ ID NO 197: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 200
- Ceres seq_id 1481834
- Location of start within SEQ ID NO 197: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 201
- Ceres seq_id 1481839

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 202
- Ceres seq_id 1481840
- Location of start within SEQ ID NO 201: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 203
- Ceres seq_id 1481841
- Location of start within SEQ ID NO 201: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 204
- Ceres seq_id 1481842
- Location of start within SEQ ID NO 201: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232410

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 205
- Ceres seq_id 1481847

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 206
- Ceres seq_id 1481848
- Location of start within SEQ ID NO 205: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 207
- Ceres seq_id 1481849
- Location of start within SEQ ID NO 205: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 208
- Ceres seq_id 1481850
- Location of start within SEQ ID NO 205: at 128 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232492

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 209
- Ceres seq_id 1481851

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 210
- Ceres seq_id 1481852
- Location of start within SEQ ID NO 209: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 211
- Ceres seq_id 1481853
- Location of start within SEQ ID NO 209: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 212
- Ceres seq_id 1481854
- Location of start within SEQ ID NO 209: at 122 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 237301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 213
- Ceres seq_id 1481859

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 214
- Ceres seq_id 1481860
- Location of start within SEQ ID NO 213: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 215
- Ceres seq_id 1481861
- Location of start within SEQ ID NO 213: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 216
- Ceres seq_id 1481862
- Location of start within SEQ ID NO 213: at 5 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 237328

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 217

- Ceres seq_id 1481863

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 218

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- Ceres seq_id 1481864
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- Location of start within SEQ ID NO 217: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 219

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- Ceres seq_id 1481865
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- Location of start within SEQ ID NO 217: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246496

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 220

- Ceres seq_id 1481873

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 221

- Ceres seq id 1481874

- Location of start within SEQ ID NO 220: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 222

- Ceres seq id 1481875

- Location of start within SEQ ID NO 220: at 379 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246936

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 223

```
- Ceres seq id 1481885
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 224

- Ceres seq id 1481886

- Location of start within SEQ ID NO 223: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 225

- Ceres seq id 1481887

- Location of start within SEQ ID NO 223: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 226
- Ceres seq_id 1481888
- Location of start within SEQ ID NO 223: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247196

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 227
- Ceres seq_id 1481893

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 228
- Ceres seq_id 1481894
- Location of start within SEQ ID NO 227: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 229
- Ceres seq_id 1481895
- Location of start within SEQ ID NO 227: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 230
- Ceres seq_id 1481896
- Location of start within SEQ ID NO 227: at 271 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247299

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 231
- Ceres seq_id 1481897

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 232
- Ceres seq_id 1481898
- Location of start within SEQ ID NO 231: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 233
- Ceres seq_id 1481899
- Location of start within SEQ ID NO 231: at 37 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 234
- Ceres seq_id 1481900
- Location of start within SEQ ID NO 231: at 70 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250561

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 235
- Ceres seq id 1481901

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 236
- Ceres seq_id 1481902
- Location of start within SEQ ID NO 235: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250647

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 237
- Ceres seq id 1481903

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 238
- Ceres seq_id 1481904
- Location of start within SEQ ID NO 237: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 239
- Ceres seq_id 1481905
- Location of start within SEQ ID NO 237: at 68 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 240
- Ceres seq\_id 1481906
- Location of start within SEQ ID NO 237: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

Maximum Length Sequence corresponding to clone ID 250663

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 241
- Ceres seq\_id 1481907

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 242
- Ceres seq\_id 1481908
- Location of start within SEQ ID NO 241: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250775

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 243
- Ceres seq\_id 1481913

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 244
- Ceres seq\_id 1481914
- Location of start within SEQ ID NO 243: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 245
- Ceres seq\_id 1481915
- Location of start within SEQ ID NO 243: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251921

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 246
- Ceres seq\_id 1481916

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 247
- Ceres seq\_id 1481917
- Location of start within SEQ ID NO 246: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 248
- Ceres seq\_id 1481918
- Location of start within SEQ ID NO 246: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

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Maximum Length Sequence corresponding to clone ID 252000

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 249
- Ceres seq\_id 1481919

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 250
- Ceres seq\_id 1481920
- Location of start within SEQ ID NO 249: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 251
- Ceres seq\_id 1481921
- Location of start within SEQ ID NO 249: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 252
- Ceres seq\_id 1481922
- Location of start within SEQ ID NO 249: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 252002

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 253
- Ceres seq\_id 1481923

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 254
- Ceres seq\_id 1481924
- Location of start within SEQ ID NO 253: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 255
- Ceres seq\_id 1481925
- Location of start within SEQ ID NO 253: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257043

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 256
- Ceres seq\_id 1481941

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 257

- Ceres seq\_id 1481942
- Location of start within SEQ ID NO 256: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 258
- Ceres seq\_id 1481943
- Location of start within SEQ ID NO 256: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 259
- Ceres seq\_id 1481944
- Location of start within SEQ ID NO 256: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257207

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 260
- Ceres seq\_id 1481949

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 261
- Ceres seq\_id 1481950
- Location of start within SEQ ID NO 260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 262
- Ceres seq\_id 1481951
- Location of start within SEQ ID NO 260: at 276 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 263
- Ceres seq\_id 1481952
- Location of start within SEQ ID NO 260: at 454 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 265955

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 264

- Ceres seq\_id 1481965
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 265
  - Ceres seq\_id 1481966
  - Location of start within SEQ ID NO 264: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 266
  - Ceres seq\_id 1481967
  - Location of start within SEQ ID NO 264: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 267
  - Ceres seq\_id 1481968
  - Location of start within SEQ ID NO 264: at 327 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266374

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 268
  - Ceres seq\_id 1481973
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 269
  - Ceres seq\_id 1481974
  - Location of start within SEQ ID NO 268: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 270
  - Ceres seq\_id 1481975
  - Location of start within SEQ ID NO 268: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266934

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 271
  - Ceres seq\_id 1481976
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 272
  - Ceres seq\_id 1481977
  - Location of start within SEQ ID NO 271: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 273
- Ceres seq\_id 1481978
- Location of start within SEQ ID NO 271: at 5 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 274
- Ceres seq\_id 1481979
- Location of start within SEQ ID NO 271: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266951

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 275
- Ceres seq\_id 1481980

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 276
- Ceres seq\_id 1481981
- Location of start within SEQ ID NO 275: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 277
- Ceres seq\_id 1481982
- Location of start within SEQ ID NO 275: at 307 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267031

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 278
- Ceres seq\_id 1481983

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 279
- Ceres seq\_id 1481984
- Location of start within SEQ ID NO 278: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 280



- Ceres seq\_id 1481985
- Location of start within SEQ ID NO 278: at 31 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267032

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 281
- Ceres seq\_id 1481986

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 282
- Ceres seq\_id 1481987
- Location of start within SEQ ID NO 281: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 283
- Ceres seq\_id 1481988
- Location of start within SEQ ID NO 281: at 38 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 284
- Ceres seq\_id 1481989
- Location of start within SEQ ID NO 281: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267296

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 285
- Ceres seq\_id 1481990

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 286
- Ceres seq\_id 1481991
- Location of start within SEQ ID NO 285: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 287
- Ceres seq\_id 1481992
- Location of start within SEQ ID NO 285: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 288
  - Ceres seq\_id 1481993
  - Location of start within SEQ ID NO 285: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267626

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 289
- Ceres seq\_id 1481994

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 290
- Ceres seq\_id 1481995
- Location of start within SEQ ID NO 289: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 291
- Ceres seq\_id 1481996
- Location of start within SEQ ID NO 289: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 292
- Ceres seq\_id 1481997
- Location of start within SEQ ID NO 289: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268353

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 293
- Ceres seq\_id 1482009

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 294
- Ceres seq\_id 1482010
- Location of start within SEQ ID NO 293: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 295
- Ceres seq\_id 1482011
- Location of start within SEQ ID NO 293: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 296
- Ceres seq\_id 1482012
- Location of start within SEQ ID NO 293: at 321 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268652

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 297
- Ceres seq\_id 1482013

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 298
- Ceres seq\_id 1482014
- Location of start within SEQ ID NO 297: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 299
- Ceres seq\_id 1482015
- Location of start within SEQ ID NO 297: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268680

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 300
- Ceres seq\_id 1482016

Maximum Length Sequence corresponding to clone ID 269248

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 301
- Ceres seq\_id 1482021

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 302
- Ceres seq\_id 1482022
- Location of start within SEQ ID NO 301: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 303
- Ceres seq\_id 1482023
- Location of start within SEQ ID NO 301: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 304
  - Ceres seq\_id 1482024
  - Location of start within SEQ ID NO 301: at 262 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270513

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 305
  - Ceres seq\_id 1482029
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 306
  - Ceres seq\_id 1482030
  - Location of start within SEQ ID NO 305: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 307
  - Ceres seq\_id 1482031
  - Location of start within SEQ ID NO 305: at 194 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 308
  - Ceres seq\_id 1482032
  - Location of start within SEQ ID NO 305: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270518

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 309
  - Ceres seq\_id 1482033
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 310
  - Ceres seq\_id 1482034
  - Location of start within SEQ ID NO 309: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 311
  - Ceres seq\_id 1482035
  - Location of start within SEQ ID NO 309: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 312
  - Ceres seq\_id 1482036
  - Location of start within SEQ ID NO 309: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271717

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 313
  - Ceres seq\_id 1482041
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 314
  - Ceres seq\_id 1482042
  - Location of start within SEQ ID NO 313: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 315
  - Ceres seq\_id 1482043
  - Location of start within SEQ ID NO 313: at 491 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 316
  - Ceres seq\_id 1482044
  - Location of start within SEQ ID NO 313: at 518 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271756

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 317
  - Ceres seq\_id 1482045
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 318
  - Ceres seq\_id 1482046
  - Location of start within SEQ ID NO 317: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 319
- Ceres seq\_id 1482047
- Location of start within SEQ ID NO 317: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 320
- Ceres seq\_id 1482048
- Location of start within SEQ ID NO 317: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271765

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 321
- Ceres seq\_id 1482049

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 322
- Ceres seq\_id 1482050
- Location of start within SEQ ID NO 321: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 323
- Ceres seq\_id 1482051
- Location of start within SEQ ID NO 321: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 324
- Ceres seq\_id 1482052
- Location of start within SEQ ID NO 321: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271936

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 325
- Ceres seq\_id 1482053

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 326
- Ceres seq\_id 1482054
- Location of start within SEQ ID NO 325: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272121

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 327  
- Ceres seq\_id 1482066

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 328
- Ceres seq_id 1482067
- Location of start within SEQ ID NO 327: at 2 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 329
- Ceres seq_id 1482068
- Location of start within SEQ ID NO 327: at 113 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

#### (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272124

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 330  
- Ceres seq id 1482069

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 331
- Ceres seq_id 1482070
- Location of start within SEQ ID NO 330: at 3 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 332
- Ceres seq_id 1482071
- Location of start within SEO ID NO 330: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 333
- Ceres seq_id 1482072
- Location of start within SEO ID NO 330: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272142

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 334
- Ceres seq id 1482073

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 335
- Ceres seq_id 1482074
- Location of start within SEQ ID NO 334: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 336
- Ceres seq_id 1482075
- Location of start within SEQ ID NO 334: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 337
- Ceres seq_id 1482076
- Location of start within SEQ ID NO 334: at 344 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272155

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 338
- Ceres seq_id 1482081

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 339
- Ceres seq_id 1482082
- Location of start within SEQ ID NO 338: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 340
- Ceres seq_id 1482083
- Location of start within SEQ ID NO 338: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 341
- Ceres seq_id 1482084
- Location of start within SEQ ID NO 338: at 178 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272156

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 342
 - Ceres seq_id 1482085
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 343
 - Ceres seq_id 1482086
 - Location of start within SEQ ID NO 342: at 302 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272162

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 344
 - Ceres seq_id 1482091
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 345
 - Ceres seq_id 1482092
 - Location of start within SEQ ID NO 344: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 346
 - Ceres seq_id 1482093
 - Location of start within SEQ ID NO 344: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 347
 - Ceres seq_id 1482094
 - Location of start within SEQ ID NO 344: at 102 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272166

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 348
 - Ceres seq_id 1482095
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 349
 - Ceres seq_id 1482096
 - Location of start within SEQ ID NO 348: at 229 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 350
 - Ceres seq_id 1482097

- Location of start within SEQ ID NO 348: at 322 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272200

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 351

- Ceres seq_id 1482102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 352

- Ceres seq_id 1482103

- Location of start within SEQ ID NO 351: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 353

- Ceres seq_id 1482104

- Location of start within SEQ ID NO 351: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 354

- Ceres seq_id 1482105

- Location of start within SEQ ID NO 351: at 366 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272214

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 355

- Ceres seq_id 1482106

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 356

- Ceres seq_id 1482107

- Location of start within SEQ ID NO 355: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 357

- Ceres seq_id 1482108

- Location of start within SEQ ID NO 355: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

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Maximum Length Sequence corresponding to clone ID 272239

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 358
- Ceres seq_id 1482113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 359
- Ceres seq_id 1482114
- Location of start within SEQ ID NO 358: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 360
- Ceres seq_id 1482115
- Location of start within SEQ ID NO 358: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 361
- Ceres seq_id 1482116
- Location of start within SEQ ID NO 358: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272250

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 362
- Ceres seq_id 1482117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 363
- Ceres seq_id 1482118
- Location of start within SEQ ID NO 362: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 364
- Ceres seq_id 1482119
- Location of start within SEQ ID NO 362: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 365
- Ceres seq_id 1482120
- Location of start within SEQ ID NO 362: at 264 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272258

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 366
- Ceres seq_id 1482121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 367
- Ceres seq_id 1482122
- Location of start within SEQ ID NO 366: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 368
- Ceres seq_id 1482127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 369
- Ceres seq_id 1482128
- Location of start within SEQ ID NO 368: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 370
- Ceres seq_id 1482129
- Location of start within SEQ ID NO 368: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 371
- Ceres seq_id 1482130
- Location of start within SEQ ID NO 368: at 529 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272312

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 372
- Ceres seq_id 1482131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 373
- Ceres seq_id 1482132
- Location of start within SEQ ID NO 372: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 374
 - Ceres seq_id 1482133
 - Location of start within SEQ ID NO 372: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 375
 - Ceres seq_id 1482134
 - Location of start within SEQ ID NO 372: at 168 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272389

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 376
 - Ceres seq_id 1482135
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 377
 - Ceres seq_id 1482136
 - Location of start within SEQ ID NO 376: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 378
 - Ceres seq_id 1482137
 - Location of start within SEQ ID NO 376: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272410

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 379
 - Ceres seq_id 1482142
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 380
 - Ceres seq_id 1482143
 - Location of start within SEQ ID NO 379: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 381
 - Ceres seq_id 1482144
 - Location of start within SEQ ID NO 379: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 382
- Ceres seq_id 1482145
- Location of start within SEQ ID NO 379: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272459

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 383
- Ceres seq_id 1482153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 384
- Ceres seq_id 1482154
- Location of start within SEQ ID NO 383: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 385
- Ceres seq_id 1482155
- Location of start within SEQ ID NO 383: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 386
- Ceres seq_id 1482156
- Location of start within SEQ ID NO 383: at 326 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272486

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 387
- Ceres seq_id 1482157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 388
- Ceres seq_id 1482158
- Location of start within SEQ ID NO 387: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 389
- Ceres seq_id 1482159
- Location of start within SEQ ID NO 387: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272506

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 390
- Ceres seq_id 1482164

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 391
- Ceres seq_id 1482165
- Location of start within SEQ ID NO 390: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 392
- Ceres seq_id 1482166
- Location of start within SEQ ID NO 390: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275387

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 393
- Ceres seq_id 1482167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 394
- Ceres seq_id 1482168
- Location of start within SEQ ID NO 393: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 395
- Ceres seq_id 1482169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 396
- Ceres seq_id 1482170
- Location of start within SEQ ID NO 395: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 397
- Ceres seq_id 1482171

- Location of start within SEQ ID NO 395: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 398
- Ceres seq_id 1482172
- Location of start within SEQ ID NO 395: at 360 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275778

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 399
- Ceres seq_id 1482177

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 400
- Ceres seq_id 1482178
- Location of start within SEQ ID NO 399: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 401
- Ceres seq_id 1482179
- Location of start within SEQ ID NO 399: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 402
- Ceres seq_id 1482180
- Location of start within SEQ ID NO 399: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275803

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 403
- Ceres seq_id 1482188

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 404
- Ceres seq_id 1482189
- Location of start within SEQ ID NO 403: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

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Maximum Length Sequence corresponding to clone ID 276193

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 405
- Ceres seq_id 1482193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 406
- Ceres seq_id 1482194
- Location of start within SEQ ID NO 405: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 294676

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 407
- Ceres seq_id 1482205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 408
- Ceres seq_id 1482206
- Location of start within SEQ ID NO 407: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296069

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 409
- Ceres seq_id 1482207

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 410
- Ceres seq_id 1482208
- Location of start within SEQ ID NO 409: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 411
- Ceres seq_id 1482209
- Location of start within SEQ ID NO 409: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 412
- Ceres seq_id 1482210
- Location of start within SEQ ID NO 409: at 271 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296091

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 413
- Ceres seq_id 1482217
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 414
 - Ceres seq_id 1482218
 - Location of start within SEQ ID NO 413: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296096

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 415
 - Ceres seq_id 1482219
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 416
 - Ceres seq_id 1482220
 - Location of start within SEQ ID NO 415: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 417
 - Ceres seq_id 1482221
 - Location of start within SEQ ID NO 415: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296205

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 418
 - Ceres seq_id 1482230
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 419
 - Ceres seq_id 1482231
 - Location of start within SEQ ID NO 418: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 420
 - Ceres seq_id 1482232
 - Location of start within SEQ ID NO 418: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 421
 - Ceres seq_id 1482233
 - Location of start within SEQ ID NO 418: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296209

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 422
- Ceres seq_id 1482234

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 423
- Ceres seq_id 1482235
- Location of start within SEQ ID NO 422: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 424
- Ceres seq_id 1482236
- Location of start within SEQ ID NO 422: at 221 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 425
- Ceres seq_id 1482237
- Location of start within SEQ ID NO 422: at 287 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296211

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 426
- Ceres seq_id 1482238

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 427
- Ceres seq_id 1482239
- Location of start within SEQ ID NO 426: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 428
- Ceres seq_id 1482240
- Location of start within SEQ ID NO 426: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 429
- Ceres seq_id 1482245

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 430
- Ceres seq_id 1482246
- Location of start within SEQ ID NO 429: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 431
- Ceres seq_id 1482247
- Location of start within SEQ ID NO 429: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296228

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 432
- Ceres seq_id 1482248

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 433
- Ceres seq_id 1482249
- Location of start within SEQ ID NO 432: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 434
- Ceres seq_id 1482250
- Location of start within SEQ ID NO 432: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 435
- Ceres seq_id 1482251
- Location of start within SEQ ID NO 432: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296237

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 436
- Ceres seq_id 1482254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 437
- Ceres seq_id 1482255

- Location of start within SEQ ID NO 436: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 438

- Ceres seq_id 1482256

- Location of start within SEQ ID NO 436: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296246

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 439

- Ceres seq_id 1482257

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 440

- Ceres seq_id 1482258

- Location of start within SEQ ID NO 439: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 441

- Ceres seq_id 1482259

- Location of start within SEQ ID NO 439: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 442

- Ceres seq_id 1482260

- Location of start within SEQ ID NO 439: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296620

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 443

- Ceres seq_id 1482261

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 444

- Ceres seq_id 1482262

- Location of start within SEQ ID NO 443: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 445
- Ceres seq_id 1482263
- Location of start within SEQ ID NO 443: at 313 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296648

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 446
- Ceres seq_id 1482264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 447
- Ceres seq_id 1482265
- Location of start within SEQ ID NO 446: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297691

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 448
- Ceres seq_id 1482270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 449
- Ceres seq_id 1482271
- Location of start within SEQ ID NO 448: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 450
- Ceres seq_id 1482272
- Location of start within SEQ ID NO 448: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 451
- Ceres seq_id 1482273
- Location of start within SEQ ID NO 448: at 199 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297711

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 452
- Ceres seq_id 1482274

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 453

- Ceres seq_id 1482275
- Location of start within SEQ ID NO 452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 454
- Ceres seq_id 1482276
- Location of start within SEQ ID NO 452: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 455
- Ceres seq_id 1482277
- Location of start within SEQ ID NO 452: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 299123

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 456
- Ceres seq_id 1482282

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 457
- Ceres seq_id 1482283
- Location of start within SEQ ID NO 456: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 458
- Ceres seq_id 1482284
- Location of start within SEQ ID NO 456: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 459
- Ceres seq_id 1482285
- Location of start within SEQ ID NO 456: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 299990

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 460

- Ceres seq_id 1482289

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 461

- Ceres seq_id 1482290

- Location of start within SEQ ID NO 460: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 462

- Ceres seq_id 1482291

- Location of start within SEQ ID NO 460: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 463

- Ceres seq_id 1482292

- Location of start within SEQ ID NO 460: at 123 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 299991

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 464

- Ceres seq_id 1482293

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 465

- Ceres seq_id 1482294

- Location of start within SEQ ID NO 464: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 466

- Ceres seq_id 1482295

- Location of start within SEQ ID NO 464: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 467

- Ceres seq_id 1482296

- Location of start within SEQ ID NO 464: at 349 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300985

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 468
- Ceres seq_id 1482297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 469
- Ceres seq_id 1482298
- Location of start within SEQ ID NO 468: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300986

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 470
- Ceres seq_id 1482299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 471
- Ceres seq_id 1482300
- Location of start within SEQ ID NO 470: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 472
- Ceres seq_id 1482301
- Location of start within SEQ ID NO 470: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300987

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 473
- Ceres seq_id 1482302

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 474
- Ceres seq_id 1482303
- Location of start within SEQ ID NO 473: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301009

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 475
- Ceres seq_id 1482307

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 476
- Ceres seq_id 1482308
- Location of start within SEQ ID NO 475: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 477
 - Ceres seq_id 1482309
 - Location of start within SEQ ID NO 475: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301084

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 478
 - Ceres seq_id 1482322
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 479
 - Ceres seq_id 1482323
 - Location of start within SEQ ID NO 478: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 480
 - Ceres seq_id 1482324
 - Location of start within SEQ ID NO 478: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 481
 - Ceres seq_id 1482325
 - Location of start within SEQ ID NO 478: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301128

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 482
 - Ceres seq_id 1482334
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 483
 - Ceres seq_id 1482335
 - Location of start within SEQ ID NO 482: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301143

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 484
 - Ceres seq_id 1482336

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 485
 - Ceres seq_id 1482337
 - Location of start within SEQ ID NO 484: at 1 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 486
 - Ceres seq_id 1482338
 - Location of start within SEQ ID NO 484: at 2 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301452

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 487
 - Ceres seq_id 1482339
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 488
 - Ceres seq_id 1482340
 - Location of start within SEQ ID NO 487: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 489
 - Ceres seq_id 1482341
 - Location of start within SEQ ID NO 487: at 96 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 490
 - Ceres seq_id 1482342
 - Location of start within SEQ ID NO 487: at 138 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301456

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 491
 - Ceres seq_id 1482346
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 492
 - Ceres seq_id 1482347
 - Location of start within SEQ ID NO 491: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 493
- Ceres seq_id 1482348
- Location of start within SEQ ID NO 491: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301464

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 494
- Ceres seq_id 1482349

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 495
- Ceres seq_id 1482350
- Location of start within SEQ ID NO 494: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 496
- Ceres seq_id 1482351
- Location of start within SEQ ID NO 494: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 497
- Ceres seq_id 1482352
- Location of start within SEQ ID NO 494: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301481

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 498
- Ceres seq_id 1482353

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 499
- Ceres seq_id 1482354
- Location of start within SEQ ID NO 498: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 500

- Ceres seq_id 1482355
- Location of start within SEQ ID NO 498: at 242 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 501
- Ceres seq_id 1482356

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 502
- Ceres seq_id 1482357
- Location of start within SEQ ID NO 501: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 503
- Ceres seq_id 1482358
- Location of start within SEQ ID NO 501: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301504

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 504
- Ceres seq_id 1482359

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 505
- Ceres seq_id 1482360
- Location of start within SEQ ID NO 504: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 506
- Ceres seq_id 1482361
- Location of start within SEQ ID NO 504: at 294 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 507
- Ceres seq_id 1482362
- Location of start within SEQ ID NO 504: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301535

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 508
- Ceres seq_id 1482363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 509
- Ceres seq_id 1482364
- Location of start within SEQ ID NO 508: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 510
- Ceres seq_id 1482365
- Location of start within SEQ ID NO 508: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 511
- Ceres seq_id 1482366
- Location of start within SEQ ID NO 508: at 205 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301541

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 512
- Ceres seq_id 1482371

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 513
- Ceres seq_id 1482372
- Location of start within SEQ ID NO 512: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 514
- Ceres seq_id 1482373
- Location of start within SEQ ID NO 512: at 206 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 515
- Ceres seq_id 1482374
- Location of start within SEQ ID NO 512: at 224 nt.

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(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301552

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 516
- Ceres seq_id 1482375

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 517
- Ceres seq_id 1482376
- Location of start within SEQ ID NO 516: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 518
- Ceres seq_id 1482377
- Location of start within SEQ ID NO 516: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301559

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 519
- Ceres seq_id 1482378

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 520
- Ceres seq_id 1482379
- Location of start within SEQ ID NO 519: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 521
- Ceres seq_id 1482380
- Location of start within SEQ ID NO 519: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 522
- Ceres seq_id 1482381
- Location of start within SEQ ID NO 519: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301584

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 523
- Ceres seq_id 1482382

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 524
- Ceres seq_id 1482383
- Location of start within SEQ ID NO 523: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 525
- Ceres seq_id 1482384
- Location of start within SEQ ID NO 523: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 526
- Ceres seq_id 1482385
- Location of start within SEQ ID NO 523: at 191 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301586

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 527
- Ceres seq_id 1482386

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 528
- Ceres seq_id 1482387
- Location of start within SEQ ID NO 527: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 529
- Ceres seq_id 1482388
- Location of start within SEQ ID NO 527: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 530
- Ceres seq_id 1482389
- Location of start within SEQ ID NO 527: at 437 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301930

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 531
- Ceres seq_id 1482398

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 532
- Ceres seq_id 1482399
- Location of start within SEQ ID NO 531: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 533
- Ceres seq_id 1482400
- Location of start within SEQ ID NO 531: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 534
- Ceres seq_id 1482401
- Location of start within SEQ ID NO 531: at 425 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301956

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 535
- Ceres seq_id 1482402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 536
- Ceres seq_id 1482403
- Location of start within SEQ ID NO 535: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301961

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 537
- Ceres seq_id 1482404

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 538
- Ceres seq_id 1482405
- Location of start within SEQ ID NO 537: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 539
- Ceres seq_id 1482406
- Location of start within SEQ ID NO 537: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 540
- Ceres seq_id 1482407
- Location of start within SEQ ID NO 537: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301981

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 541
- Ceres seq_id 1482408

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 542
- Ceres seq_id 1482409
- Location of start within SEQ ID NO 541: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 543
- Ceres seq_id 1482410
- Location of start within SEQ ID NO 541: at 442 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301994

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 544
- Ceres seq_id 1482411

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 545
- Ceres seq_id 1482412
- Location of start within SEQ ID NO 544: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 546
- Ceres seq_id 1482413
- Location of start within SEQ ID NO 544: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 547
- Ceres seq_id 1482414
- Location of start within SEQ ID NO 544: at 620 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302016

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 548
- Ceres seq_id 1482415

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 549
- Ceres seq_id 1482416
- Location of start within SEQ ID NO 548: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 550
- Ceres seq_id 1482417
- Location of start within SEQ ID NO 548: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 551
- Ceres seq_id 1482418

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 552
- Ceres seq_id 1482419
- Location of start within SEQ ID NO 551: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 553
- Ceres seq_id 1482420
- Location of start within SEQ ID NO 551: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 554
- Ceres seq_id 1482421
- Location of start within SEQ ID NO 551: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302415

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 555
 - Ceres seq_id 1482422
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 556
 - Ceres seq_id 1482423
 - Location of start within SEQ ID NO 555: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304700

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 557
 - Ceres seq_id 1482424
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 558
 - Ceres seq_id 1482425
 - Location of start within SEQ ID NO 557: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 559
 - Ceres seq_id 1482426
 - Location of start within SEQ ID NO 557: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 560
 - Ceres seq_id 1482427
 - Location of start within SEQ ID NO 557: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304743

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 561
 - Ceres seq_id 1482428
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 562
 - Ceres seq_id 1482429
 - Location of start within SEQ ID NO 561: at 206 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304764

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 563
- Ceres seq_id 1482430

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 564
- Ceres seq_id 1482431
- Location of start within SEQ ID NO 563: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 565
- Ceres seq_id 1482432
- Location of start within SEQ ID NO 563: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 566
- Ceres seq_id 1482433
- Location of start within SEQ ID NO 563: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304769

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 567
- Ceres seq_id 1482434

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 568
- Ceres seq_id 1482435
- Location of start within SEQ ID NO 567: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 569
- Ceres seq_id 1482436
- Location of start within SEQ ID NO 567: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 570

- Ceres seq_id 1482437
- Location of start within SEQ ID NO 567: at 18 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 305124

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 571
- Ceres seq_id 1482438

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 572
- Ceres seq_id 1482439
- Location of start within SEQ ID NO 571: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 30994

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 573
- Ceres seq_id 1482444

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 574
- Ceres seq_id 1482445
- Location of start within SEQ ID NO 573: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 575
- Ceres seq_id 1482446
- Location of start within SEQ ID NO 573: at 134 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 576
- Ceres seq_id 1482447
- Location of start within SEQ ID NO 573: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 33213

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 577
- Ceres seq_id 1482457

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 578
- Ceres seq_id 1482458
- Location of start within SEQ ID NO 577: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 579
 - Ceres seq_id 1482459
 - Location of start within SEQ ID NO 577: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 35310

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 580
 - Ceres seq_id 1482460

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 581
 - Ceres seq_id 1482461
 - Location of start within SEQ ID NO 580: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 582
 - Ceres seq_id 1482462
 - Location of start within SEQ ID NO 580: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 583
 - Ceres seq_id 1482463
 - Location of start within SEQ ID NO 580: at 470 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 37200

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 584
 - Ceres seq_id 1482481

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 585
 - Ceres seq_id 1482482
 - Location of start within SEQ ID NO 584: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 586
- Ceres seq_id 1482483
- Location of start within SEQ ID NO 584: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 587
- Ceres seq_id 1482484
- Location of start within SEQ ID NO 584: at 425 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 38293

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 588
- Ceres seq_id 1482490

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 589
- Ceres seq_id 1482491
- Location of start within SEQ ID NO 588: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 590
- Ceres seq_id 1482492
- Location of start within SEQ ID NO 588: at 138 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 591
- Ceres seq_id 1482493
- Location of start within SEQ ID NO 588: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 40190

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 592
- Ceres seq_id 1482504

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 593
- Ceres seq_id 1482505
- Location of start within SEQ ID NO 592: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 594
- Ceres seq_id 1482506
- Location of start within SEQ ID NO 592: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 595
- Ceres seq_id 1482507
- Location of start within SEQ ID NO 592: at 642 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 4026

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 596
- Ceres seq_id 1482508

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 597
- Ceres seq_id 1482509
- Location of start within SEQ ID NO 596: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 598
- Ceres seq_id 1482510
- Location of start within SEQ ID NO 596: at 475 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 40770

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 599
- Ceres seq_id 1482514

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 600
- Ceres seq_id 1482515
- Location of start within SEQ ID NO 599: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 601
- Ceres seq_id 1482516
- Location of start within SEQ ID NO 599: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 602
- Ceres seq_id 1482517
- Location of start within SEQ ID NO 599: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 6091

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 603
- Ceres seq_id 1482525

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 604
- Ceres seq_id 1482526
- Location of start within SEQ ID NO 603: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 9184

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 605
- Ceres seq_id 1482535

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 606
- Ceres seq_id 1482536
- Location of start within SEQ ID NO 605: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 607
- Ceres seq_id 1482537
- Location of start within SEQ ID NO 605: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 608
- Ceres seq_id 1482538
- Location of start within SEQ ID NO 605: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 92491

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 609
- Ceres seq_id 1482542
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 610
- Ceres seq_id 1482543
- Location of start within SEQ ID NO 609: at 2 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 611
- Ceres seq_id 1482544
- Location of start within SEQ ID NO 609: at 227 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 612
- Ceres seq_id 1482545
- Location of start within SEQ ID NO 609: at 275 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 93534

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 613
- Ceres seq_id 1482546
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 614
- Ceres seq_id 1482547
- Location of start within SEQ ID NO 613: at 218 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 615
- Ceres seq_id 1482548
- Location of start within SEQ ID NO 613: at 227 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 616
- Ceres seq_id 1482549
- Location of start within SEQ ID NO 613: at 260 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

[illegible]

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atccggtttcg	ccatttttgt	ttctcagtg	tctctgaaat	ggctctcttct	cttttttttg	60
tcgaatccaa	tctcaattat	gttggttatct	ttcttccatc	aatgggtaat	caaaacatag	120
aattgatg	gtaagactat	aaagggttag	tctttaacca	ttgtagattc	ctctgtctct	180
tgtgtatttg	attgatctgt	taatggataa	ccaaaaaggt	gctctctttc	ccgatgaggt	240
tattctccag	attcttgcta	gattacctgt	taaatctctc	ttcaggttca	aatccgtttg	300
caaatcatgg	tacagattac	cttctgacaa	atatttcaact	tccttggtca	atcaactctc	360
tgtaaaagag	caattgcttg	tggctcaagt	atcagattct	tctagtttga	tctgtgttga	420
taatctgaga	gggttttctg	agttatcatt	ggattttgtt	agagataggg	tgaggattag	480
ggtttcttct	aatgggttgt	tgtgtgttgc	aagcattcct	gaaaagggtg	tttactatgt	540
ttgtaatccg	tcgactagag	agtacaggaa	attgcctaag	agtcgagaaa	gaccgcgttac	600
tcgggttttat	cctgacggtg	aggctacact	tgttggtttg	gcttgtgatt	tgagtaggaa	660
caagtttaat	gtggtgttg	ctggttacca	taggtctttt	ggtcagagac	ctgatgggag	720
tttcatttgc	ttggtgttg	attctgagag	taacaaatgg	aggaagtttg	tttcggtggt	780
agaagaatgt	agtttcacac	acatgagtaa	gaaccaagtg	gtgtttgtta	atgggatgct	840
tcattgggtg	atgagtgttg	tgtgttatat	acttgcactt	gatgttgaac	atgatgtgtg	900
gagaaagatt	tctttgcctg	atgagattaa	aatcgggaat	gggtgtgtga	atcgggttta	960
tctcttgga	tccgatgggt	ttttgtcggt	gattcagtta	tcagatgtat	ggatgaagat	1020
ttggaagatg	agtgagtatg	agactgaaac	ttggagtgtt	gttgatagca	taagtttaag	1080
gtgcattaaa	ggattggtac	ctggaatctt	cccgatttgt	cagaccggtg	agtatgtttt	1140
cttggtact	cataaacagg	ttttggtgta	tcaaagacga	agtaagttat	ggaaagagat	1200
gttttctgta	aaaggaagct	cttctctgcc	tttgtgttgc	tctgctcacg	cctttcgcag	1260
caccatagta	ccctgtaatt	agcatgttta	tgtttccttc	tctactcttt	tatttttttg	1320
gtttatgttc	agctcttgga	tcttttaggg	cttatgaaaa	tttgttcaag	gttttataat	1380
ctttctggga	taacatcata	taaagtaatg	tacagttgat	ttcttctgtt	gcttttagta	1440
caaataagat	tttggttg					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Asn	Gln	Lys	Gly	Ala	Leu	Phe	Pro	Asp	Glu	Val	Ile	Leu	Gln
1			5				10				15				
Ile	Leu	Ala	Arg	Leu	Pro	Val	Lys	Ser	Leu	Phe	Arg	Phe	Lys	Ser	Val
			20				25				30				
Cys	Lys	Ser	Trp	Tyr	Arg	Leu	Pro	Ser	Asp	Lys	Tyr	Phe	Thr	Ser	Leu
			35				40				45				
Phe	Asn	Gln	Leu	Ser	Val	Lys	Glu	Gln	Leu	Leu	Val	Ala	Gln	Val	Ser
			50				55				60				
Asp	Ser	Ser	Ser	Leu	Ile	Cys	Val	Asp	Asn	Leu	Arg	Gly	Val	Ser	Glu
65				70						75					80

Leu Ser Leu Asp Phe Val Arg Asp Arg Val Arg Ile Arg Val Ser Ser
85 90 95
Asn Gly Leu Leu Cys Cys Ser Ser Ile Pro Glu Lys Gly Val Tyr Tyr
100 105 110
Val Cys Asn Pro Ser Thr Arg Glu Tyr Arg Lys Leu Pro Lys Ser Arg
115 120 125
Glu Arg Pro Val Thr Arg Phe Tyr Pro Asp Gly Glu Ala Thr Leu Val
130 135 140
Gly Leu Ala Cys Asp Leu Ser Arg Asn Lys Phe Asn Val Val Leu Ala
145 150 155 160
Gly Tyr His Arg Ser Phe Gly Gln Arg Pro Asp Gly Ser Phe Ile Cys
165 170 175
Leu Val Phe Asp Ser Glu Ser Asn Lys Trp Arg Lys Phe Val Ser Val
180 185 190
Leu Glu Glu Cys Ser Phe Thr His Met Ser Lys Asn Gln Val Val Phe
195 200 205
Val Asn Gly Met Leu His Trp Leu Met Ser Gly Leu Cys Tyr Ile Leu
210 215 220
Ala Leu Asp Val Glu His Asp Val Trp Arg Lys Ile Ser Leu Pro Asp
225 230 235 240
Glu Ile Lys Ile Gly Asn Gly Gly Gly Asn Arg Val Tyr Leu Leu Glu
245 250 255
Ser Asp Gly Phe Leu Ser Val Ile Gln Leu Ser Asp Val Trp Met Lys
260 265 270
Ile Trp Lys Met Ser Glu Tyr Glu Thr Glu Thr Trp Ser Val Val Asp
275 280 285
Ser Ile Ser Leu Arg Cys Ile Lys Gly Leu Val Pro Gly Ile Phe Pro
290 295 300
Ile Cys Gln Thr Gly Glu Tyr Val Phe Leu Ala Thr His Lys Gln Val
305 310 315 320
Leu Val Tyr Gln Arg Arg Ser Lys Leu Trp Lys Glu Met Phe Ser Val
325 330 335
Lys Gly Ser Ser Ser Leu Pro Leu Trp Phe Ser Ala His Ala Phe Arg
340 345 350
Ser Thr Ile Val Pro Cys Asn
355

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1353
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

casragamcc atwacywaga amcaycctaa tcgaaaaaac gccacaatca tggctttggt	60
cttatctcct aaaaccatca ctcttctctt cttctccctc tccctcgcac tctactgcag	120
catcgatcct ttccaccact gcgccatttc cgatttcccc aatttcgtct ctcacgaagt	180
tatctctcca cgtcccgacg aagttccatg ggagagagat tcacaaaatt cacttcagaa	240
atcaaagatt ctgtttttta accaaatcca aggtccagag agcgtcgcct ttgattctct	300
cggacgtggt ccgtacacag gcgttgctga tggtaggggt ttgttttggg atggagagaa	360
atggattgat ttcgcttata cttcgagtaa tcgatcggag atttgtgatc cgaagccttc	420
tgctttgagt tacttgagga atgaacatat atgtggtcgt cctttaggtc ttcgtttcga	480
taagagaacc ggagatttgt atatagctga tgcttatatg ggacttttga aagttgggtcc	540
tgaaggtggt ttagcaacgc cgcttgtaac tgaagctgaa ggtgtgccgt tgggggtttac	600
taatgatctt gacattgctg atgatggaac tgtttacttt acagatagca gcattagtta	660

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ccagaggagg aacttcttgc agctcgtttt ctctggagac aatactggga gggttctaaa 720
gtatgatcca gtagctaaga aagctgttgt tttgggtctca aatcttcagt ttccgaatgg 780
tgtctctatc agcagagacg gttctttctt tgtattctgc gaaggagata ttggaagcct 840
acgaagatac tgggtgaaag gcgagaaagc tggaacgaca gatgtgtttg cgtatttacc 900
agggcatcct gataacgtaa gaaccaacca aaagggtgaa ttttgggtag cgcttcattg 960
cagacgcaac tactactcat acttaatggc aagatatcct aagctgagga tgttcatact 1020
gagactgcca atcactgcga gaactcacta ctcgttccag ataggggtac ggccgcacgg 1080
gttgggtggtt aagtatagtc ctgaaggga gcttatgcat gttttggaag atagtgaagg 1140
gaaagtgtgt agatcagtaa gtgaagtgga agaaaaagat gggaagcttt ggatgggaag 1200
tgtgttgatg aactttgttg ctgtctatga cctctgatta cttgacctat acgtaaacca 1260
cttcactcag tttctagatt tagcaaattc tcaaaactgt taggtgtgta ctgaaaaaat 1320
caaacactta gcacaaacaa actcaatggtt att
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1481343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Xaa Arg Xaa Xaa Xaa Xaa Xaa Pro Asn Arg Lys Asn Ala Thr Ile
1      5      10      15
Met Ala Leu Phe Leu Ser Pro Lys Thr Ile Thr Leu Leu Phe Phe Ser
20      25      30
Leu Ser Leu Ala Leu Tyr Cys Ser Ile Asp Pro Phe His His Cys Ala
35      40      45
Ile Ser Asp Phe Pro Asn Phe Val Ser His Glu Val Ile Ser Pro Arg
50      55      60
Pro Asp Glu Val Pro Trp Glu Arg Asp Ser Gln Asn Ser Leu Gln Lys
65      70      75      80
Ser Lys Ile Leu Phe Phe Asn Gln Ile Gln Gly Pro Glu Ser Val Ala
85      90      95
Phe Asp Ser Leu Gly Arg Gly Pro Tyr Thr Gly Val Ala Asp Gly Arg
100     105     110
Val Leu Phe Trp Asp Gly Glu Lys Trp Ile Asp Phe Ala Tyr Thr Ser
115     120     125
Ser Asn Arg Ser Glu Ile Cys Asp Pro Lys Pro Ser Ala Leu Ser Tyr
130     135     140
Leu Arg Asn Glu His Ile Cys Gly Arg Pro Leu Gly Leu Arg Phe Asp
145     150     155     160
Lys Arg Thr Gly Asp Leu Tyr Ile Ala Asp Ala Tyr Met Gly Leu Leu
165     170     175
Lys Val Gly Pro Glu Gly Gly Leu Ala Thr Pro Leu Val Thr Glu Ala
180     185     190
Glu Gly Val Pro Leu Gly Phe Thr Asn Asp Leu Asp Ile Ala Asp Asp
195     200     205
Gly Thr Val Tyr Phe Thr Asp Ser Ser Ile Ser Tyr Gln Arg Arg Asn
210     215     220
Phe Leu Gln Leu Val Phe Ser Gly Asp Asn Thr Gly Arg Val Leu Lys
225     230     235     240
Tyr Asp Pro Val Ala Lys Lys Ala Val Val Leu Val Ser Asn Leu Gln
245     250     255
Phe Pro Asn Gly Val Ser Ile Ser Arg Asp Gly Ser Phe Phe Val Phe
260     265     270
Cys Glu Gly Asp Ile Gly Ser Leu Arg Arg Tyr Trp Leu Lys Gly Glu
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275	280	285
Lys Ala Gly Thr Thr Asp Val Phe Ala Tyr Leu Pro Gly His Pro Asp		
290	295	300
Asn Val Arg Thr Asn Gln Lys Gly Glu Phe Trp Val Ala Leu His Cys		
305	310	315
Arg Arg Asn Tyr Tyr Ser Tyr Leu Met Ala Arg Tyr Pro Lys Leu Arg		
	325	330
Met Phe Ile Leu Arg Leu Pro Ile Thr Ala Arg Thr His Tyr Ser Phe		
	340	345
Gln Ile Gly Leu Arg Pro His Gly Leu Val Val Lys Tyr Ser Pro Glu		
	355	360
Gly Lys Leu Met His Val Leu Glu Asp Ser Glu Gly Lys Val Val Arg		
	370	375
Ser Val Ser Glu Val Glu Glu Lys Asp Gly Lys Leu Trp Met Gly Ser		
385	390	395
Val Leu Met Asn Phe Val Ala Val Tyr Asp Leu		400
	405	410

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1481344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Thr	Ile	Thr	Leu	Leu	Phe	Phe	Ser
1				5				10						15	
Leu	Ser	Leu	Ala	Leu	Tyr	Cys	Ser	Ile	Asp	Pro	Phe	His	His	Cys	Ala
		20						25					30		
Ile	Ser	Asp	Phe	Pro	Asn	Phe	Val	Ser	His	Glu	Val	Ile	Ser	Pro	Arg
		35					40					45			
Pro	Asp	Glu	Val	Pro	Trp	Glu	Arg	Asp	Ser	Gln	Asn	Ser	Leu	Gln	Lys
		50				55				60					
Ser	Lys	Ile	Leu	Phe	Phe	Asn	Gln	Ile	Gln	Gly	Pro	Glu	Ser	Val	Ala
65				70					75					80	
Phe	Asp	Ser	Leu	Gly	Arg	Gly	Pro	Tyr	Thr	Gly	Val	Ala	Asp	Gly	Arg
			85					90					95		
Val	Leu	Phe	Trp	Asp	Gly	Glu	Lys	Trp	Ile	Asp	Phe	Ala	Tyr	Thr	Ser
		100						105					110		
Ser	Asn	Arg	Ser	Glu	Ile	Cys	Asp	Pro	Lys	Pro	Ser	Ala	Leu	Ser	Tyr
		115					120					125			
Leu	Arg	Asn	Glu	His	Ile	Cys	Gly	Arg	Pro	Leu	Gly	Leu	Arg	Phe	Asp
		130				135					140				
Lys	Arg	Thr	Gly	Asp	Leu	Tyr	Ile	Ala	Asp	Ala	Tyr	Met	Gly	Leu	Leu
145				150					155					160	
Lys	Val	Gly	Pro	Glu	Gly	Gly	Leu	Ala	Thr	Pro	Leu	Val	Thr	Glu	Ala
			165					170						175	
Glu	Gly	Val	Pro	Leu	Gly	Phe	Thr	Asn	Asp	Leu	Asp	Ile	Ala	Asp	Asp
		180					185						190		
Gly	Thr	Val	Tyr	Phe	Thr	Asp	Ser	Ser	Ile	Ser	Tyr	Gln	Arg	Arg	Asn
		195				200						205			
Phe	Leu	Gln	Leu	Val	Phe	Ser	Gly	Asp	Asn	Thr	Gly	Arg	Val	Leu	Lys
	210				215					220					
Tyr	Asp	Pro	Val	Ala	Lys	Lys	Ala	Val	Val	Leu	Val	Ser	Asn	Leu	Gln
225					230					235					240

Phe Pro Asn Gly Val Ser Ile Ser Arg Asp Gly Ser Phe Phe Val Phe
245 250 255
Cys Glu Gly Asp Ile Gly Ser Leu Arg Arg Tyr Trp Leu Lys Gly Glu
260 265 270
Lys Ala Gly Thr Thr Asp Val Phe Ala Tyr Leu Pro Gly His Pro Asp
275 280 285
Asn Val Arg Thr Asn Gln Lys Gly Glu Phe Trp Val Ala Leu His Cys
290 295 300
Arg Arg Asn Tyr Tyr Ser Tyr Leu Met Ala Arg Tyr Pro Lys Leu Arg
305 310 315 320
Met Phe Ile Leu Arg Leu Pro Ile Thr Ala Arg Thr His Tyr Ser Phe
325 330 335
Gln Ile Gly Leu Arg Pro His Gly Leu Val Val Lys Tyr Ser Pro Glu
340 345 350
Gly Lys Leu Met His Val Leu Glu Asp Ser Glu Gly Lys Val Val Arg
355 360 365
Ser Val Ser Glu Val Glu Glu Lys Asp Gly Lys Leu Trp Met Gly Ser
370 375 380
Val Leu Met Asn Phe Val Ala Val Tyr Asp Leu
385 390 395

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1481345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Leu Leu Lys Val Gly Pro Glu Gly Gly Leu Ala Thr Pro Leu
1 5 10 15
Val Thr Glu Ala Glu Gly Val Pro Leu Gly Phe Thr Asn Asp Leu Asp
20 25 30
Ile Ala Asp Asp Gly Thr Val Tyr Phe Thr Asp Ser Ser Ile Ser Tyr
35 40 45
Gln Arg Arg Asn Phe Leu Gln Leu Val Phe Ser Gly Asp Asn Thr Gly
50 55 60
Arg Val Leu Lys Tyr Asp Pro Val Ala Lys Lys Ala Val Val Leu Val
65 70 75 80
Ser Asn Leu Gln Phe Pro Asn Gly Val Ser Ile Ser Arg Asp Gly Ser
85 90 95
Phe Phe Val Phe Cys Glu Gly Asp Ile Gly Ser Leu Arg Arg Tyr Trp
100 105 110
Leu Lys Gly Glu Lys Ala Gly Thr Thr Asp Val Phe Ala Tyr Leu Pro
115 120 125
Gly His Pro Asp Asn Val Arg Thr Asn Gln Lys Gly Glu Phe Trp Val
130 135 140
Ala Leu His Cys Arg Arg Asn Tyr Tyr Ser Tyr Leu Met Ala Arg Tyr
145 150 155 160
Pro Lys Leu Arg Met Phe Ile Leu Arg Leu Pro Ile Thr Ala Arg Thr
165 170 175
His Tyr Ser Phe Gln Ile Gly Leu Arg Pro His Gly Leu Val Val Lys
180 185 190
Tyr Ser Pro Glu Gly Lys Leu Met His Val Leu Glu Asp Ser Glu Gly
195 200 205
Lys Val Val Arg Ser Val Ser Glu Val Glu Glu Lys Asp Gly Lys Leu

210 215 220
Trp Met Gly Ser Val Leu Met Asn Phe Val Ala Val Tyr Asp Leu
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
atcaccattg ctttgttttg ttcgtcaaat ataatcaatt ttaaatttct tctcttctct      60
tcaaacgaat cgcctttttc gataatctct ttgcatcgat ttcacatggg ctactcaaac      120
ggatctcgct cagcccaagc ttgatatgac caaggaggag aaagagaggt tgaagtattt      180
gcaattcgct caagctgctg ctgtggaagc tctgcttcgc tttgctctta tttacgctaa      240
ggcaaaggac aagtctggct ctttgaaacc tgggtgtgaa tctgttgaag gagctgtcaa      300
gactgtcggt ggtcctgtct acgagaaata ccacgacgtc cctgttgagg tccttaaata      360
catggaccag aagggtacaat ttgactcctt tccctatctt tggatccttg tgaaagtgcc      420
tttgttgatg aacaatgaat gaatctgtgt tgttgattgt atatccactt catcgaacat      480
atgtgattaa aaaagtacag ttaaagttgt gatgatttca tatcatctct ttggtagaag      540
gttcaggtta acgggtcaat gtcattatgt tctgtagagt cctctttttt gaagctgaca      600
agtttgtttt gcgttggttg aggttgatat gtctgtgact gagcttgacc gtcgtgtccc      660
accagtcgtc aagcaagtgt ctgcccaagc catctccgct gctcagatag caccattgt      720
ggcactgctg ttggcctctg aggttcgacg tgctggtgtt gttgaaaccg cttctggaat      780
ggctaaatcc gtctactcca agtacgagcc tgctgctaag gagttgtatg caaactatga      840
gccaaaagca aagcagtgtg ccgtttcagc ttggaagaag cttaccagc ttcctctatt      900
cccaaggctg gctcaagtgt ctgtaccaac agctgctttc tgctctgaga agtacaatga      960
tactgtgggt aaggctgcag agaaagggtg cagagtcaca tcgtacatgc cattggttcc      1020
aacagagagg atctcaaaaa tcttcgctga ggagaaagct gagaccgagc ctttgagatt      1080
ccatccactt gattgatatg ggtgttttgt tagtgtgatt ttttgttttg ttgggattaa      1140
ggtgaaccgg atcttggtta gcgattgatc tctggttctc gttctttttt ttctttgtca      1200
tgaacttttg ttgtttcggt taataatcaa aagttgtata atctaagttt gggattacca      1260
ccctattgag tattgagt
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Ser Val Thr Glu Leu Asp Arg Arg Pro Pro Val Val Lys Gln
1          5          10          15
Val Ser Ala Gln Ala Ile Ser Ala Ala Gln Ile Ala Pro Ile Val Ala
20          25          30
Arg Ala Leu Ala Ser Glu Val Arg Arg Ala Gly Val Val Glu Thr Ala
35          40          45
Ser Gly Met Ala Lys Ser Val Tyr Ser Lys Tyr Glu Pro Ala Ala Lys
50          55          60
Glu Leu Tyr Ala Asn Tyr Glu Pro Lys Ala Lys Gln Cys Ala Val Ser
65          70          75          80
```

Ala Trp Lys Lys Leu Asn Gln Leu Pro Leu Phe Pro Arg Leu Ala Gln
85 90 95
Val Ala Val Pro Thr Ala Ala Phe Cys Ser Glu Lys Tyr Asn Asp Thr
100 105 110
Val Val Lys Ala Ala Glu Lys Gly Tyr Arg Val Thr Ser Tyr Met Pro
115 120 125
Leu Val Pro Thr Glu Arg Ile Ser Lys Ile Phe Ala Glu Glu Lys Ala
130 135 140
Glu Thr Glu Pro Leu Glu Phe His Pro Leu Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Lys Ser Val Tyr Ser Lys Tyr Glu Pro Ala Ala Lys Glu Leu
1 5 10 15
Tyr Ala Asn Tyr Glu Pro Lys Ala Lys Gln Cys Ala Val Ser Ala Trp
20 25 30
Lys Lys Leu Asn Gln Leu Pro Leu Phe Pro Arg Leu Ala Gln Val Ala
35 40 45
Val Pro Thr Ala Ala Phe Cys Ser Glu Lys Tyr Asn Asp Thr Val Val
50 55 60
Lys Ala Ala Glu Lys Gly Tyr Arg Val Thr Ser Tyr Met Pro Leu Val
65 70 75 80
Pro Thr Glu Arg Ile Ser Lys Ile Phe Ala Glu Glu Lys Ala Glu Thr
85 90 95
Glu Pro Leu Glu Phe His Pro Leu Asp
100 105

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gln Thr Met Ser Gln Lys Gln Ser Ser Val Pro Phe Gln Leu Gly
1 5 10 15
Arg Ser Leu Thr Ser Phe Leu Tyr Ser Gln Gly Trp Leu Lys Leu Leu
20 25 30
Tyr Gln Gln Leu Leu Ser Ala Leu Arg Ser Thr Met Ile Leu Trp Leu
35 40 45
Arg Leu Gln Arg Lys Gly Thr Glu Ser His Arg Thr Cys His Trp Phe
50 55 60
Gln Gln Arg Gly Ser Gln Lys Ser Ser Leu Arg Arg Lys Leu Arg Pro
65 70 75 80
Ser Leu Trp Ser Ser Ile His Leu Ile Asp Met Gly Val Leu Leu Val

85

90

95

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

aacatcctaa	tcgaaaaaaaa	aaaacataaa	acacataggg	gtgggtctct	ctcctccgga	60
attcgatcac	gacggcaagg	acgacgcac	tccttctccc	acagggctgg	agatggatct	120
ggtccggtga	tttctgagat	ttaagtcgat	cgagtttcca	gatatatctc	tcaagtagag	180
atggcctggg	tcagtggcaa	agtttctctg	ggaggattcc	cagatctcac	tggcgctgtc	240
aataaattcc	agagagcggt	aaaaacattg	aaaagaattt	cgacaacgcc	cttggcttcg	300
acgacaagtc	cgattctgcc	gctgaagatg	cagcttcaag	tatgtggcca	cctgcagttg	360
ataccaaaag	cctctttgat	cccgttatgt	ccttcatggg	taacacctct	gatgagaaac	420
ctgatacatt	ggaagactct	gtgcgtacag	aaaatccgtc	tcaaattgaa	caaaaagaag	480
aagaagctgg	atcggttaag	ctagctactg	aacaagcagt	atctggtgaa	gcaaataaag	540
aaacaaacat	gagaagagaa	gctgatcaag	cagataatcc	tgaggtaaca	gaaactgttg	600
ttttggatcc	caacgatgat	gaaccgcaat	cgcagatact	tctcgaagag	tcctctgaat	660
attctcttca	gactcctgaa	tcctcagggt	acaagactag	tcttcaacct	aatgaaaagc	720
tggaaatgac	agcttctcaa	gattcacagc	ccgagcaacc	caagtcagag	gctgaggaat	780
cacagcctga	ggattctgaa	gcaaaagagg	ttactgtaga	aaacaaagac	actgttcact	840
cccctgtgtt	agatggacag	cataagatta	cttatatgga	tgagacaaca	aatgaacaag	900
aaattctggg	tgaaaatctg	gaagggagaa	cctcgtctaa	aatttttgaa	gtttcaccag	960
atatcaatca	tgtaaataag	atagagtcce	ttgttgctca	tccgtcttta	atttttgagt	1020
ctgatgggtc	tccttacgag	tcttctatac	caaagagatc	gtcgtcagat	gaaatttcgg	1080
agagaattgt	ggattttgtt	tctcgtgaaa	tagattcaag	actggatact	agtgaagtta	1140
atgaaagcca	gcgttcaagc	tctgcgacaa	atgtttccga	ctctgctgat	gttattctgg	1200
aattagagaa	g					

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Trp	Pro	Pro	Ala	Val	Asp	Thr	Lys	Ser	Leu	Phe	Asp	Pro	Val	Met
1			5					10						15	
Ser	Phe	Met	Gly	Asn	Thr	Ser	Asp	Glu	Lys	Pro	Asp	Thr	Leu	Glu	Asp
			20					25					30		
Ser	Val	Arg	Thr	Glu	Asn	Pro	Ser	Gln	Ile	Glu	Gln	Lys	Glu	Glu	Glu
			35				40					45			
Ala	Gly	Ser	Val	Lys	Leu	Ala	Thr	Glu	Gln	Ala	Val	Ser	Val	Glu	Ala
			50				55				60				
Asn	Lys	Glu	Thr	Asn	Met	Arg	Arg	Glu	Ala	Asp	Gln	Ala	Asp	Asn	Pro
65					70				75					80	
Glu	Val	Thr	Glu	Thr	Val	Val	Leu	Asp	Pro	Asn	Asp	Asp	Glu	Pro	Gln

	85		90		95										
Ser	Gln	Ile	Leu	Leu	Glu	Glu	Ser	Ser	Glu	Tyr	Ser	Leu	Gln	Thr	Pro
	100							105					110		
Glu	Ser	Ser	Gly	Tyr	Lys	Thr	Ser	Leu	Gln	Pro	Asn	Glu	Lys	Leu	Glu
	115							120					125		
Met	Thr	Ala	Ser	Gln	Asp	Ser	Gln	Pro	Glu	Gln	Pro	Lys	Ser	Glu	Ala
	130						135					140			
Glu	Glu	Ser	Gln	Pro	Glu	Asp	Ser	Glu	Ala	Lys	Glu	Val	Thr	Val	Glu
145					150					155					160
Asn	Lys	Asp	Thr	Val	His	Ser	Pro	Val	Leu	Asp	Gly	Gln	His	Lys	Ile
			165						170					175	
Thr	Tyr	Met	Asp	Glu	Thr	Thr	Asn	Glu	Gln	Glu	Ile	Leu	Gly	Glu	Asn
			180					185					190		
Leu	Glu	Gly	Arg	Thr	Ser	Ser	Lys	Ile	Phe	Glu	Val	Ser	Pro	Asp	Ile
			195				200						205		
Asn	His	Val	Asn	Arg	Ile	Glu	Ser	Leu	Val	Ala	His	Pro	Ser	Leu	Ile
	210					215						220			
Phe	Glu	Ser	Asp	Gly	Ser	Pro	Tyr	Glu	Ser	Ser	Ile	Pro	Lys	Arg	Ser
225					230					235					240
Ser	Ser	Asp	Glu	Ile	Ser	Glu	Arg	Ile	Val	Asp	Phe	Val	Ser	Arg	Glu
			245						250					255	
Ile	Asp	Ser	Arg	Leu	Asp	Thr	Ser	Glu	Leu	Asn	Glu	Ser	Gln	Arg	Ser
			260					265					270		
Ser	Ser	Ala	Thr	Asn	Val	Ser	Asp	Ser	Ala	Asp	Val	Ile	Leu	Glu	Leu
		275					280					285			
Glu	Lys														
290															

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ser	Phe	Met	Gly	Asn	Thr	Ser	Asp	Glu	Lys	Pro	Asp	Thr	Leu	Glu
1				5					10					15	
Asp	Ser	Val	Arg	Thr	Glu	Asn	Pro	Ser	Gln	Ile	Glu	Gln	Lys	Glu	Glu
		20						25					30		
Glu	Ala	Gly	Ser	Val	Lys	Leu	Ala	Thr	Glu	Gln	Ala	Val	Ser	Val	Glu
		35					40					45			
Ala	Asn	Lys	Glu	Thr	Asn	Met	Arg	Arg	Glu	Ala	Asp	Gln	Ala	Asp	Asn
	50					55				60					
Pro	Glu	Val	Thr	Glu	Thr	Val	Val	Leu	Asp	Pro	Asn	Asp	Asp	Glu	Pro
65					70					75				80	
Gln	Ser	Gln	Ile	Leu	Leu	Glu	Glu	Ser	Ser	Glu	Tyr	Ser	Leu	Gln	Thr
			85					90					95		
Pro	Glu	Ser	Ser	Gly	Tyr	Lys	Thr	Ser	Leu	Gln	Pro	Asn	Glu	Lys	Leu
		100						105					110		
Glu	Met	Thr	Ala	Ser	Gln	Asp	Ser	Gln	Pro	Glu	Gln	Pro	Lys	Ser	Glu
	115					120						125			
Ala	Glu	Glu	Ser	Gln	Pro	Glu	Asp	Ser	Glu	Ala	Lys	Glu	Val	Thr	Val
	130					135					140				
Glu	Asn	Lys	Asp	Thr	Val	His	Ser	Pro	Val	Leu	Asp	Gly	Gln	His	Lys
145					150					155					160

Ile	Thr	Tyr	Met	Asp	Glu	Thr	Thr	Asn	Glu	Gln	Glu	Ile	Leu	Gly	Glu	
				165					170					175		
Asn	Leu	Glu	Gly	Arg	Thr	Ser	Ser	Lys	Ile	Phe	Glu	Val	Ser	Pro	Asp	
			180					185					190			
Ile	Asn	His	Val	Asn	Arg	Ile	Glu	Ser	Leu	Val	Ala	His	Pro	Ser	Leu	
		195					200					205				
Ile	Phe	Glu	Ser	Asp	Gly	Ser	Pro	Tyr	Glu	Ser	Ser	Ile	Pro	Lys	Arg	
	210					215					220					
Ser	Ser	Ser	Asp	Glu	Ile	Ser	Glu	Arg	Ile	Val	Asp	Phe	Val	Ser	Arg	
225					230					235					240	
Glu	Ile	Asp	Ser	Arg	Leu	Asp	Thr	Ser	Glu	Leu	Asn	Glu	Ser	Gln	Arg	
				245					250					255		
Ser	Ser	Ser	Ala	Thr	Asn	Val	Ser	Asp	Ser	Ala	Asp	Val	Ile	Leu	Glu	
			260					265					270			
Leu	Glu	Lys														
		275														

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Asn	Thr	Ser	Asp	Glu	Lys	Pro	Asp	Thr	Leu	Glu	Asp	Ser	Val	
1				5					10					15		
Arg	Thr	Glu	Asn	Pro	Ser	Gln	Ile	Glu	Gln	Lys	Glu	Glu	Glu	Ala	Gly	
			20					25					30			
Ser	Val	Lys	Leu	Ala	Thr	Glu	Gln	Ala	Val	Ser	Val	Glu	Ala	Asn	Lys	
		35					40					45				
Glu	Thr	Asn	Met	Arg	Arg	Glu	Ala	Asp	Gln	Ala	Asp	Asn	Pro	Glu	Val	
	50					55					60					
Thr	Glu	Thr	Val	Val	Leu	Asp	Pro	Asn	Asp	Asp	Glu	Pro	Gln	Ser	Gln	
65					70					75					80	
Ile	Leu	Leu	Glu	Glu	Ser	Ser	Glu	Tyr	Ser	Leu	Gln	Thr	Pro	Glu	Ser	
			85					90						95		
Ser	Gly	Tyr	Lys	Thr	Ser	Leu	Gln	Pro	Asn	Glu	Lys	Leu	Glu	Met	Thr	
			100					105					110			
Ala	Ser	Gln	Asp	Ser	Gln	Pro	Glu	Gln	Pro	Lys	Ser	Glu	Ala	Glu	Glu	
		115					120					125				
Ser	Gln	Pro	Glu	Asp	Ser	Glu	Ala	Lys	Glu	Val	Thr	Val	Glu	Asn	Lys	
		130				135					140					
Asp	Thr	Val	His	Ser	Pro	Val	Leu	Asp	Gly	Gln	His	Lys	Ile	Thr	Tyr	
145					150					155					160	
Met	Asp	Glu	Thr	Thr	Asn	Glu	Gln	Glu	Ile	Leu	Gly	Glu	Asn	Leu	Glu	
				165				170						175		
Gly	Arg	Thr	Ser	Ser	Lys	Ile	Phe	Glu	Val	Ser	Pro	Asp	Ile	Asn	His	
			180					185					190			
Val	Asn	Arg	Ile	Glu	Ser	Leu	Val	Ala	His	Pro	Ser	Leu	Ile	Phe	Glu	
		195					200					205				
Ser	Asp	Gly	Ser	Pro	Tyr	Glu	Ser	Ser	Ile	Pro	Lys	Arg	Ser	Ser	Ser	
	210					215					220					
Asp	Glu	Ile	Ser	Glu	Arg	Ile	Val	Asp	Phe	Val	Ser	Arg	Glu	Ile	Asp	
225					230					235					240	
Ser	Arg	Leu	Asp	Thr	Ser	Glu	Leu	Asn	Glu	Ser	Gln	Arg	Ser	Ser	Ser	

	245		250		255										
Ala	Thr	Asn	Val	Ser	Asp	Ser	Ala	Asp	Val	Ile	Leu	Glu	Leu	Glu	Lys
	260						265						270		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

cta	atc	gaaa	aaaa	agcgag	aaaga	aagac	gaact	gatca	gcaat	gggaa	gctta	agggt	60
gag	cac	agtt	gttat	tcag	tagtg	gcttg	tctct	ccatc	ctcct	catat	ctcct	acaga	120
agta	gat	ggg	cgttt	agtgt	gtgac	actcc	agcgg	gtaca	tgtac	ctcga	gctct	acttg	180
caat	gac	caa	tgca	atacat	ggggc	ggcaa	ttat	agtga	ggcga	aatgtg	cagatt	caag	240
cttt	cct	ggt	taa	agtatat	gttat	tgctg	ccatt	atgta	gggag	cagtg	ctgaa	atgga	300
aag	cat	gtga	ttgc	agatga	tagaa	aacga	cgtc	gccttg	tgtgc	gtatg	tgtgt	gtttt	360
ttg	cta	atcg	catg	tttatg	ctttc	atttc	acat	cctatg	ttttg	agtgt	ttgc	ctttgt	420
act	ttg	ttgt	tgtg	cttctg	tttgt	ttttgc	gttgt	caagt	atcaa	ataaaa	gttgg	agtg	480
gttt	taaca	aatga	ttttt	ttatt	tctt	tggtg	tattt	agcta	atttta	ttttat	tttaa	540	
gagt	gtttta	ttttat	caaa	taata	ataat	cata	attgcg	gtttg	ttgtg	cg			

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu	Ile	Glu	Lys	Lys	Ala	Arg	Lys	Lys	Asp	Glu	Leu	Ile	Ser	Asn	Gly
1				5				10						15	
Lys	Leu	Lys	Gly	Glu	His	Ser	Cys	Tyr	Cys	Ser	Ser	Gly	Leu	Ser	Leu
		20					25					30			
His	Pro	Pro	His	Ile	Ser	Tyr	Arg	Ser	Arg	Trp	Ala	Phe	Ser	Val	
	35					40					45				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Ser	Leu	Arg	Val	Ser	Thr	Val	Val	Ile	Ala	Val	Val	Ala	Cys
1			5					10					15		

(2) INFORMATION FOR SEO ID NO:18:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1481375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Cys	Val	Phe	Phe	Ala	Asn	Arg	Met	Phe	Met	Leu	Ser	Phe	His	Ile
1				5					10					15	
Leu	Cys	Phe	Glu	Cys	Leu	Pro	Leu	Tyr	Phe	Val	Val	Val	Leu	Leu	Phe
			20					25					30		
Val	Leu	Arg	Cys	Gln	Val	Ser	Asn	Lys	Val	Gly	Val	Cys	Phe		
		35					40					45			

(2) INFORMATION FOR SEO ID NO:19:

(A) LENGTH: 1135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1135

(D) OTHER INFORMATION: / Ceres Seq. ID 1481388

(xi) SEQUENCE DESCRIPTION: SEO ID NO:19:

taaatgagat	gaatagaggt	ccacgagcta	agggtttcaa	cagccaagat	ggttccaag	60
tgatggctgt	gtctttgaag	gagcagagag	tgactgagac	tgagaaactc	agtgaagatg	120
tgtctctttt	agatcccaag	gactacaata	agatagattt	ccctgagacc	tacacagaag	180
caaagtttta	tgtaatcaaa	tcgtacagtg	aagatgatat	tcataaaagt	atcaaataca	240
gtgtttggtc	cagcactcct	aatggttaaca	agaagctgga	tgccatcatat	aacgaggcaa	300
aacagaagtc	agatggctgt	cccggtgtttc	tactttttctc	tgtaaacact	agtggacaat	360
ttgttggttt	agccgagatg	gtaggccctg	ttgatttcaa	taagactggt	gaatactggc	420
aacaggacaa	atgggatgtg	tgcttccctg	ttagtggga	tttcgttaaa	gataacccta	480
atagctcctt	ggagcatata	actctggaga	acaatgagaa	caagccggtt	actaatagca	540
gagacacaca	ggaagtaaag	ctcgagcaag	gcattaaagt	catcaagatt	ttcaaggacc	600
acgcaagcaa	gacatgcata	ctcgatgatt	ttgagttcta	tgagaatcgt	caaaagatta	660
tccaagaaag	gaaaagcaaa	cacctgcaga	tcaaaaaaca	gacattggtg	gccaatgcag	720
acaaaggtgt	aatgtcaaaa	attaatcttg	tgaaacctca	agagtctact	acagcctcag	780
aagatgcagc	agcactagga	gttgcggtctg	aagtgactaa	agaatcgaaa	gtggtgaaag	840
agaccgagtt	acctgtggag	aaaaatgctg	ttgctactgc	ctgctgaacc	aacctttggt	900
tttaagtggg	aactgagtg	gctgttttag	gctattttaga	gcgtttctct	agttttgttt	960
ccattcctga	atttgcagac	tttttttttt	tttttttttg	aaccgagttg	agagggtagt	1020
ggcttagtag	atgaagtttt	ggcatgagca	ttcatcatct	tcgagttatt	ctctatccct	1080
ttagtaatgg	tccaacatat	gaggatatgg	gtaaaaqatt	qgtattqaat	caqct	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asn Glu Met Asn Arg Gly Pro Arg Ala Lys Gly Phe Asn Ser Gln Asp
1 5 10 15
Gly Ser Lys Val Met Ala Val Ser Leu Lys Glu Gln Arg Val Thr Glu
20 25 30
Thr Glu Lys Leu Ser Glu Asp Val Ser Leu Leu Asp Pro Lys Asp Tyr
35 40 45
Asn Lys Ile Asp Phe Pro Glu Thr Tyr Thr Glu Ala Lys Phe Tyr Val
50 55 60
Ile Lys Ser Tyr Ser Glu Asp Asp Ile His Lys Ser Ile Lys Tyr Ser
65 70 75 80
Val Trp Ser Ser Thr Pro Asn Gly Asn Lys Lys Leu Asp Ala Ser Tyr
85 90 95
Asn Glu Ala Lys Gln Lys Ser Asp Gly Cys Pro Val Phe Leu Leu Phe
100 105 110
Ser Val Asn Thr Ser Gly Gln Phe Val Gly Leu Ala Glu Met Val Gly
115 120 125
Pro Val Asp Phe Asn Lys Thr Val Glu Tyr Trp Gln Gln Asp Lys Trp
130 135 140
Ile Gly Cys Phe Pro Val Lys Trp His Phe Val Lys Asp Ile Pro Asn
145 150 155 160
Ser Ser Leu Arg His Ile Thr Leu Glu Asn Asn Glu Asn Lys Pro Val
165 170 175
Thr Asn Ser Arg Asp Thr Gln Glu Val Lys Leu Glu Gln Gly Ile Lys
180 185 190
Val Ile Lys Ile Phe Lys Asp His Ala Ser Lys Thr Cys Ile Leu Asp
195 200 205
Asp Phe Glu Phe Tyr Glu Asn Arg Gln Lys Ile Ile Gln Glu Arg Lys
210 215 220
Ser Lys His Leu Gln Ile Lys Lys Gln Thr Leu Val Ala Asn Ala Asp
225 230 235 240
Lys Gly Val Met Ser Lys Ile Asn Leu Val Lys Pro Gln Glu Ser Thr
245 250 255
Thr Ala Ser Glu Asp Ala Ala Ala Leu Gly Val Ala Ala Glu Val Thr
260 265 270
Lys Glu Ser Lys Val Val Lys Glu Thr Glu Leu Pro Val Glu Lys Asn
275 280 285
Ala Val Ala Thr Ala Cys
290

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1481390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Asn	Arg	Gly	Pro	Arg	Ala	Lys	Gly	Phe	Asn	Ser	Gln	Asp	Gly	Ser
1				5					10					15	
Lys	Val	Met	Ala	Val	Ser	Leu	Lys	Glu	Gln	Arg	Val	Thr	Glu	Thr	Glu
			20					25					30		
Lys	Leu	Ser	Glu	Asp	Val	Ser	Leu	Asp	Pro	Lys	Asp	Tyr	Asn	Lys	
			35				40				45				
Ile	Asp	Phe	Pro	Glu	Thr	Tyr	Thr	Glu	Ala	Lys	Phe	Tyr	Val	Ile	Lys
	50					55					60				
Ser	Tyr	Ser	Glu	Asp	Asp	Ile	His	Lys	Ser	Ile	Lys	Tyr	Ser	Val	Trp
65					70					75				80	
Ser	Ser	Thr	Pro	Asn	Gly	Asn	Lys	Lys	Leu	Asp	Ala	Ser	Tyr	Asn	Glu
				85					90					95	
Ala	Lys	Gln	Lys	Ser	Asp	Gly	Cys	Pro	Val	Phe	Leu	Leu	Phe	Ser	Val
			100					105					110		
Asn	Thr	Ser	Gly	Gln	Phe	Val	Gly	Leu	Ala	Glu	Met	Val	Gly	Pro	Val
			115				120					125			
Asp	Phe	Asn	Lys	Thr	Val	Glu	Tyr	Trp	Gln	Gln	Asp	Lys	Trp	Ile	Gly
	130					135					140				
Cys	Phe	Pro	Val	Lys	Trp	His	Phe	Val	Lys	Asp	Ile	Pro	Asn	Ser	Ser
145					150					155				160	
Leu	Arg	His	Ile	Thr	Leu	Glu	Asn	Asn	Glu	Asn	Lys	Pro	Val	Thr	Asn
				165					170					175	
Ser	Arg	Asp	Thr	Gln	Glu	Val	Lys	Leu	Glu	Gln	Gly	Ile	Lys	Val	Ile
			180					185					190		
Lys	Ile	Phe	Lys	Asp	His	Ala	Ser	Lys	Thr	Cys	Ile	Leu	Asp	Asp	Phe
			195				200					205			
Glu	Phe	Tyr	Glu	Asn	Arg	Gln	Lys	Ile	Ile	Gln	Glu	Arg	Lys	Ser	Lys
	210					215					220				
His	Leu	Gln	Ile	Lys	Lys	Gln	Thr	Leu	Val	Ala	Asn	Ala	Asp	Lys	Gly
225					230					235				240	
Val	Met	Ser	Lys	Ile	Asn	Leu	Val	Lys	Pro	Gln	Glu	Ser	Thr	Thr	Ala
				245					250					255	
Ser	Glu	Asp	Ala	Ala	Ala	Leu	Gly	Val	Ala	Ala	Glu	Val	Thr	Lys	Glu
			260				265						270		
Ser	Lys	Val	Val	Lys	Glu	Thr	Glu	Leu	Pro	Val	Glu	Lys	Asn	Ala	Val
			275				280						285		
Ala	Thr	Ala	Cys												
			290												

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1481391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Ala	Val	Ser	Leu	Lys	Glu	Gln	Arg	Val	Thr	Glu	Thr	Glu	Lys	Leu
1				5						10				15	
Ser	Glu	Asp	Val	Ser	Leu	Leu	Asp	Pro	Lys	Asp	Tyr	Asn	Lys	Ile	Asp
			20					25					30		
Phe	Pro	Glu	Thr	Tyr	Thr	Glu	Ala	Lys	Phe	Tyr	Val	Ile	Lys	Ser	Tyr
			35				40						45		

Ser Glu Asp Asp Ile His Lys Ser Ile Lys Tyr Ser Val Trp Ser Ser
50 55 60
Thr Pro Asn Gly Asn Lys Lys Leu Asp Ala Ser Tyr Asn Glu Ala Lys
65 70 75 80
Gln Lys Ser Asp Gly Cys Pro Val Phe Leu Leu Phe Ser Val Asn Thr
85 90 95
Ser Gly Gln Phe Val Gly Leu Ala Glu Met Val Gly Pro Val Asp Phe
100 105 110
Asn Lys Thr Val Glu Tyr Trp Gln Gln Asp Lys Trp Ile Gly Cys Phe
115 120 125
Pro Val Lys Trp His Phe Val Lys Asp Ile Pro Asn Ser Ser Leu Arg
130 135 140
His Ile Thr Leu Glu Asn Asn Glu Asn Lys Pro Val Thr Asn Ser Arg
145 150 155 160
Asp Thr Gln Glu Val Lys Leu Glu Gln Gly Ile Lys Val Ile Lys Ile
165 170 175
Phe Lys Asp His Ala Ser Lys Thr Cys Ile Leu Asp Asp Phe Glu Phe
180 185 190
Tyr Glu Asn Arg Gln Lys Ile Ile Gln Glu Arg Lys Ser Lys His Leu
195 200 205
Gln Ile Lys Lys Gln Thr Leu Val Ala Asn Ala Asp Lys Gly Val Met
210 215 220
Ser Lys Ile Asn Leu Val Lys Pro Gln Glu Ser Thr Thr Ala Ser Glu
225 230 235 240
Asp Ala Ala Ala Leu Gly Val Ala Ala Glu Val Thr Lys Glu Ser Lys
245 250 255
Val Val Lys Glu Thr Glu Leu Pro Val Glu Lys Asn Ala Val Ala Thr
260 265 270
Ala Cys

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..796
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

catcctaatac gaaaaaaagc aaccaaacac ataaaagaga gatttaatac aaaagaaaga	60
gaaaaaagaa agatatggca ggactcatca acaagatcgg agacgcactc cacaggtcga	120
aggcgaatat ctcaaagata tcagaaacgc caaggatttt acaatacaca gcgttgcgaa	180
gtggctcgat gcacagcttc cattgcatcc gcggttgaaa gctttcttta ggacaatttc	240
tccgaggcat tttaaaaacg gagattggaa tacagggtgga aactgtaaca acacggttcc	300
tttgtctaga ggcagcgaaa tcacagggga tgatggatcg atcgatgcaa cagttgagag	360
tgctgtgaac gggacaagga tcaagattct tgacataact gcactttctg agctaagaga	420
cgaagctcat atctcagggt ctaaactcaa accccgaaaa ccgaagaagg caagtaacgt	480
gacctcaact ccaacgatca acgattgctt gcattgggtgc ttaccaggga tcccagatac	540
ttggaatgaa cttttcattg ctcagatttg aagtattcaa catcatcaca cacacaaagc	600
tagctcaatg gattggctct gttgattctt tgttatagaa aggttttttt ttcagattct	660
ttcttgggag aataacaaag tttcagttct taaaaatagg ttttagatgg tttgtcagta	720
aatgattcat ctgtaacaat cacaatctgg tttttaatta tacacgagaa cattgaaatt	780
gaaacaatct ttttcc	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..76
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481424
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
His Pro Asn Arg Lys Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn
1           5           10           15
Thr Lys Glu Arg Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg
          20          25          30
Ser Glu Thr His Ser Thr Gly Arg Arg Arg Ile Ser Gln Arg Tyr Gln
          35          40          45
Lys Arg Gln Gly Phe Tyr Asn Thr Gln Arg Cys Glu Val Ala Arg Cys
          50          55          60
Thr Ala Ser Ile Ala Ser Ala Val Glu Ser Phe Leu
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..47
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Arg Ser Lys
1           5           10           15
Ala Asn Ile Ser Lys Ile Ser Glu Thr Pro Arg Ile Leu Gln Tyr Thr
          20          25          30
Ala Leu Arg Ser Gly Ser Met His Ser Phe His Cys Ile Arg Gly
          35          40          45
```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..492
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
acttcgcctt gaatcgagtc ttcgacgagt ctccggctgc gagtttctct tgctccggca      60
aacagacctg tcattgcttc tctctccggc taactacaca gaagcatggt gtttgacaaa      120
gtagtaatag gtcctccagg atcgggaaag accacttatt gcaatggaat gtctcagttc      180
ctctctctaa tgggcaggaa gggtgctatt gttaatctgg atcctgcaaa tgatgcatta      240
ccttatgagt gtgctgtgaa tatagaagaa ttgatcaagt tagaagatgt tatgtcggaa      300
cactcgcttg gtcctaattg aggtcttgta tattgtatgg agtacttgga gaaaaacatt      360
gactggctgg aatctaaact aaagcctctt ctgaaggatc attacattct ctttgatttt      420
cctggccaag tggaattggt cttcattcat gacagtacca agaattgtct sncgaagctg      480
attaaatcat tg
```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481472
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr
1          5          10          15
Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys
          20          25          30
Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu
          35          40          45
Cys Ala Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser
          50          55          60
Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr
65          70          75          80
Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu
          85          90          95
Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe
          100          105          110
Phe Ile His Asp Ser Thr Lys Asn Val Xaa Xaa Lys Leu Ile Lys Ser
          115          120          125
Leu
```

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481473
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys Val Ala Ile Val Asn
1          5          10          15
Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu Cys Ala Val Asn Ile
          20          25          30
Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser Glu His Ser Leu Gly
          35          40          45
Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr Leu Glu Lys Asn Ile
          50          55          60
Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu Lys Asp His Tyr Ile
65          70          75          80
Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe Phe Ile His Asp Ser
          85          90          95
Thr Lys Asn Val Xaa Xaa Lys Leu Ile Lys Ser Leu
          100          105
```

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1481474
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gly Arg Lys Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala
1 5 10 15
Leu Pro Tyr Glu Cys Ala Val Asn Ile Glu Glu Leu Ile Lys Leu Glu
20 25 30
Asp Val Met Ser Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr
35 40 45
Cys Met Glu Tyr Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu
50 55 60
Lys Pro Leu Leu Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln
65 70 75 80
Val Glu Leu Phe Phe Ile His Asp Ser Thr Lys Asn Val Xaa Xaa Lys
85 90 95
Leu Ile Lys Ser Leu
100

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1189
(D) OTHER INFORMATION: / Ceres Seq. ID 1481479
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

cagctcacgg aggaaccagt gttgctcctc aaactccaaa cagaaaaggg agtgtacaca 60
tagctcgctc tcgctctgtg ccccttaacg acaaggaatt aagcctgaag ggaatggatt 120
catttttccag agtaattcct tcgactcctc gtgttaagga aggagacgtt ttctcaaagt 180
catcagagggc tggtaatact gaaacagggtg atgctgatgg agaagacata cctgaggatg 240
aagcagtttg taggatttgt ttggtagagc tctgtgaagg aggagaaacc ttaaaaaatgg 300
agtgtagttg caaaggcgaa cttgctcttg cccacaaaga ttgtgctctt aaatggttca 360
ccataaaggg taacaagact tgtgaggtgt gtaaacaaga agttaagaac ttacctgtaa 420
cactcttacg catccaaagc cttcgaaatt ctgggtgtcc tcagctagat gtctctggct 480
atagggtgtg gcaggaggta ccggttctag taatcatcag catgctcgct tacttctgct 540
tcctcgagca gctcctggtt gagaatatgg gtacagggtg catcgctata tcaactgccg 600
tttcttgat tcttggtctt cttgcatcca tgaccgcac aaccatggta atgagaagat 660
ttgtctggat ttacgcactt gtccagtttg cgttggtcgt tctcttcgcc catatatttt 720
actctgtggt gaagttgcaa ccagttctgt cagttcttct gtcaacattt gctggatttg 780
gtgtatgcat atgcggaagt tcagtgatgg ttgagtttgt gagatggaga cgaagatggc 840
gagccagaag gctagagcaa cagctgaacc atgctttgac tctgtcacia ccgccgcaac 900
cactggatcc aacaacctct ctgcatcatt caaatacctc atagagagcc aagaagtgga 960
cagatgattt tacatttata cagtgtagtt tggtaaatg ttatgtaatg atttgtataa 1020
aagaaaaaga gaaagtgatc caaggaatgc ttaaagatyg ytccttttgt ttgttttaca 1080
tacacatttg tattgttgta agtttgtaac tttggtttgc tcaatctctg caaatgaaat 1140
gtttgtagca gtattggtt ctctgtataa taaaagatt taaaattgt

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..313
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala	His	Gly	Gly	Thr	Ser	Val	Ala	Pro	Gln	Thr	Pro	Asn	Arg	Lys	Gly	
1				5					10					15		
Ser	Val	His	Ile	Ala	Arg	Ser	Arg	Ser	Val	Pro	Leu	Asn	Asp	Lys	Glu	
			20					25					30			
Leu	Ser	Leu	Lys	Gly	Met	Asp	Ser	Phe	Phe	Arg	Val	Ile	Pro	Ser	Thr	
		35				40						45				
Pro	Arg	Val	Lys	Glu	Gly	Asp	Val	Phe	Ser	Asn	Ala	Ser	Glu	Ala	Gly	
		50				55					60					
Asn	Thr	Glu	Thr	Gly	Asp	Ala	Asp	Gly	Glu	Asp	Ile	Pro	Glu	Asp	Glu	
65					70					75					80	
Ala	Val	Cys	Arg	Ile	Cys	Leu	Val	Glu	Leu	Cys	Glu	Gly	Gly	Glu	Thr	
			85					90						95		
Leu	Lys	Met	Glu	Cys	Ser	Cys	Lys	Gly	Glu	Leu	Ala	Leu	Ala	His	Lys	
			100					105						110		
Asp	Cys	Ala	Leu	Lys	Trp	Phe	Thr	Ile	Lys	Gly	Asn	Lys	Thr	Cys	Glu	
		115					120						125			
Val	Cys	Lys	Gln	Glu	Val	Lys	Asn	Leu	Pro	Val	Thr	Leu	Leu	Arg	Ile	
		130				135					140					
Gln	Ser	Leu	Arg	Asn	Ser	Gly	Val	Pro	Gln	Leu	Asp	Val	Ser	Gly	Tyr	
145				150						155					160	
Arg	Val	Trp	Gln	Glu	Val	Pro	Val	Leu	Val	Ile	Ile	Ser	Met	Leu	Ala	
			165					170						175		
Tyr	Phe	Cys	Phe	Leu	Glu	Gln	Leu	Leu	Val	Glu	Asn	Met	Gly	Thr	Gly	
			180					185					190			
Ala	Ile	Ala	Ile	Ser	Leu	Pro	Phe	Ser	Cys	Ile	Leu	Gly	Leu	Leu	Ala	
		195					200					205				
Ser	Met	Thr	Ala	Ser	Thr	Met	Val	Met	Arg	Arg	Phe	Val	Trp	Ile	Tyr	
	210					215					220					
Ala	Ser	Val	Gln	Phe	Ala	Leu	Val	Val	Leu	Phe	Ala	His	Ile	Phe	Tyr	
225				230						235					240	
Ser	Val	Val	Lys	Leu	Gln	Pro	Val	Leu	Ser	Val	Leu	Leu	Ser	Thr	Phe	
			245					250						255		
Ala	Gly	Phe	Gly	Val	Cys	Ile	Cys	Gly	Ser	Ser	Val	Met	Val	Glu	Phe	
		260						265					270			
Val	Arg	Trp	Arg	Arg	Arg	Trp	Arg	Ala	Arg	Arg	Leu	Glu	Gln	Gln	Leu	
		275				280							285			
Asn	His	Ala	Leu	Thr	Leu	Ser	Gln	Pro	Pro	Gln	Pro	Leu	Asp	Pro	Thr	
	290					295						300				
Thr	Ser	Leu	His	His	Ser	Asn	Thr	Ser								
305					310											

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..276
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asp Ser Phe Phe Arg Val Ile Pro Ser Thr Pro Arg Val Lys Glu
1 5 10 15
Gly Asp Val Phe Ser Asn Ala Ser Glu Ala Gly Asn Thr Glu Thr Gly
20 25 30
Asp Ala Asp Gly Glu Asp Ile Pro Glu Asp Glu Ala Val Cys Arg Ile
35 40 45
Cys Leu Val Glu Leu Cys Glu Gly Gly Glu Thr Leu Lys Met Glu Cys
50 55 60
Ser Cys Lys Gly Glu Leu Ala Leu Ala His Lys Asp Cys Ala Leu Lys
65 70 75 80
Trp Phe Thr Ile Lys Gly Asn Lys Thr Cys Glu Val Cys Lys Gln Glu
85 90 95
Val Lys Asn Leu Pro Val Thr Leu Leu Arg Ile Gln Ser Leu Arg Asn
100 105 110
Ser Gly Val Pro Gln Leu Asp Val Ser Gly Tyr Arg Val Trp Gln Glu
115 120 125
Val Pro Val Leu Val Ile Ile Ser Met Leu Ala Tyr Phe Cys Phe Leu
130 135 140
Glu Gln Leu Leu Val Glu Asn Met Gly Thr Gly Ala Ile Ala Ile Ser
145 150 155 160
Leu Pro Phe Ser Cys Ile Leu Gly Leu Leu Ala Ser Met Thr Ala Ser
165 170 175
Thr Met Val Met Arg Arg Phe Val Trp Ile Tyr Ala Ser Val Gln Phe
180 185 190
Ala Leu Val Val Leu Phe Ala His Ile Phe Tyr Ser Val Val Lys Leu
195 200 205
Gln Pro Val Leu Ser Val Leu Leu Ser Thr Phe Ala Gly Phe Gly Val
210 215 220
Cys Ile Cys Gly Ser Ser Val Met Val Glu Phe Val Arg Trp Arg Arg
225 230 235 240
Arg Trp Arg Ala Arg Arg Leu Glu Gln Gln Leu Asn His Ala Leu Thr
245 250 255
Leu Ser Gln Pro Pro Gln Pro Leu Asp Pro Thr Thr Ser Leu His His
260 265 270
Ser Asn Thr Ser
275

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1481482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Glu Cys Ser Cys Lys Gly Glu Leu Ala Leu Ala His Lys Asp Cys
1 5 10 15
Ala Leu Lys Trp Phe Thr Ile Lys Gly Asn Lys Thr Cys Glu Val Cys
20 25 30
Lys Gln Glu Val Lys Asn Leu Pro Val Thr Leu Leu Arg Ile Gln Ser
35 40 45
Leu Arg Asn Ser Gly Val Pro Gln Leu Asp Val Ser Gly Tyr Arg Val
50 55 60
Trp Gln Glu Val Pro Val Leu Val Ile Ile Ser Met Leu Ala Tyr Phe
65 70 75 80
Cys Phe Leu Glu Gln Leu Leu Val Glu Asn Met Gly Thr Gly Ala Ile

(2) INFORMATION FOR SEO ID NO:34:

(A) LENGTH: 643 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (q

FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..643

(D) OTHER INFORMATION: / Ceres Seq. ID 1481483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ataatttcgag	ctgttttttt	gctgtaataa	tttcacaatt	ctcttttttt	ttcgctttta	60
aataattttg	tctotccatc	ttcttctctt	ttgctagtct	ctcatatcag	ctaagaaaag	120
aaatttcagaa	caaaaaaata	acacaaagct	ctgtgtttct	gtctatctgt	tgaatcaa	180
catatggaag	acgatcgaaa	agagaagaac	actccgtggc	tatcagtgcc	acagtttggt	240
gattgggacc	aaaaaggagg	aggaacaatg	cctgattact	ctatggattt	cactaagatt	300
agagagatga	ggaaacaaaa	caagagagac	ccttctcgag	ccagtttagg	caatgaggaa	360
gagctcatta	agccacccga	gtcagcaaca	tcaactgctg	agcttaccac	ggtccaaagt	420
gaaaaccgac	gagagttctc	tcccagccac	catcatcaac	cacattctcc	ttctacgagg	480
agaagtatgt	tcagctgctt	caactgctgc	gttaaagctt	gaagatttct	tcttgagcaa	540
agtagcagtt	tattatttga	cttctgattt	gaatgtggaa	atgtgttaat	gtcatgacac	600
tttaatatat	gttccaatcc	atttttcttt	tcttttggga	acc		

(2) INFORMATION FOR SEQ ID NO:35:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME

(B) LOCATION: 1..112

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Asp Asp Arg Lys Glu Lys Asn Thr Pro

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Gln	Phe	Gly	Asp	Trp	Asp	Gln	Lys	Gly	Gly	Gly	Thr	Met	Pro	Asp	Tyr
			20					25					30		
Ser	Met	Asp	Phe	Thr	Lys	Ile	Arg	Glu	Met	Arg	Lys	Gln	Asn	Lys	Arg
			35				40					45			
Asp	Pro	Ser	Arg	Ala	Ser	Leu	Gly	Asn	Glu	Glu	Glu	Leu	Ile	Lys	Pro

50					55					60							
Pro	Glu	Ser	Ala	Thr	Ser	Thr	Ala	Glu	Leu	Thr	Thr	Val	Gln	Ser	Glu		
65					70					75					80		
Asn	Arg	Arg	Glu	Phe	Ser	Pro	Ser	His	His	His	Gln	Pro	His	Ser	Pro		
				85					90						95		
Ser	Thr	Arg	Arg	Ser	Met	Phe	Ser	Cys	Phe	Asn	Cys	Cys	Val	Lys	Ala		
				100					105						110		

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1481485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Pro	Asp	Tyr	Ser	Met	Asp	Phe	Thr	Lys	Ile	Arg	Glu	Met	Arg	Lys		
1				5				10						15			
Gln	Asn	Lys	Arg	Asp	Pro	Ser	Arg	Ala	Ser	Leu	Gly	Asn	Glu	Glu	Glu		
			20					25						30			
Leu	Ile	Lys	Pro	Pro	Glu	Ser	Ala	Thr	Ser	Thr	Ala	Glu	Leu	Thr	Thr		
		35					40					45					
Val	Gln	Ser	Glu	Asn	Arg	Arg	Glu	Phe	Ser	Pro	Ser	His	His	His	Gln		
	50					55				60							
Pro	His	Ser	Pro	Ser	Thr	Arg	Arg	Ser	Met	Phe	Ser	Cys	Phe	Asn	Cys		
65					70					75					80		
Cys	Val	Lys	Ala														

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1481486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Asp	Phe	Thr	Lys	Ile	Arg	Glu	Met	Arg	Lys	Gln	Asn	Lys	Arg	Asp		
1				5				10						15			
Pro	Ser	Arg	Ala	Ser	Leu	Gly	Asn	Glu	Glu	Glu	Leu	Ile	Lys	Pro	Pro		
			20					25						30			
Glu	Ser	Ala	Thr	Ser	Thr	Ala	Glu	Leu	Thr	Thr	Val	Gln	Ser	Glu	Asn		
		35					40					45					
Arg	Arg	Glu	Phe	Ser	Pro	Ser	His	His	His	Gln	Pro	His	Ser	Pro	Ser		
	50					55				60							
Thr	Arg	Arg	Ser	Met	Phe	Ser	Cys	Phe	Asn	Cys	Cys	Val	Lys	Ala			
65					70					75							

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 760 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..760
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481487
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
gcmccmbtyy cattayytag aacatcctaw hraaaaaaca aaagtgatca gttttgtttt      60
ctcggggaaa ttttctgaaa gtgaagaaaag ggaaagcaag ttttttttga agtggggaga      120
gagatgggag aaatggggaa ggcgatggga ttgctgatta gcgggacgct tgtgtattac      180
cattgtgcat atcgtaacgc gactcttctc tctctcttct ccgatgtttt cattgttctc      240
ttatgtcttc tcgccattct cgggtctcctt tttcgccaac tcaatgtctc ggtaccagtg      300
gatccactag agtggcaaat atcacaggac acagcaagta acatcgttgc acgcttagct      360
aataccgttg gagcagcaga ggggtgttctg aggggttgacg caactggaca tgacaagaga      420
ctttttgtca aggtcgtaat ttgccttttac ttcttatcag cgcttgggag actcatatca      480
ggygtaaccg ttgcttatgc aggactatgc ttgttctgtc tctccatgct ctgtcagact      540
tctcaatctc ttggaaactg tgtactaaag cgaggaaatg gccagatttt agaacaagaa      600
gcacattctg atacataata tgtctagctt ttgtttatac ttttcgtctt ttctcatgct      660
tacatgctca tagcttcagt cttcagagta gtttcccttt atgtacattg gatttgttgc      720
atactacctt gtgaaaaatg taatgatatt gtttaacctc
```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481488
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
Met Gly Glu Met Gly Lys Ala Met Gly Leu Leu Ile Ser Gly Thr Leu
1      5      10      15
Val Tyr Tyr His Cys Ala Tyr Arg Asn Ala Thr Leu Leu Ser Leu Phe
20     25     30
Ser Asp Val Phe Ile Val Leu Leu Cys Ser Leu Ala Ile Leu Gly Leu
35     40     45
Leu Phe Arg Gln Leu Asn Val Ser Val Pro Val Asp Pro Leu Glu Trp
50     55     60
Gln Ile Ser Gln Asp Thr Ala Ser Asn Ile Val Ala Arg Leu Ala Asn
65     70     75     80
Thr Val Gly Ala Ala Glu Gly Val Leu Arg Val Ala Ala Thr Gly His
85     90     95
Asp Lys Arg Leu Phe Val Lys Val Val Ile Cys Leu Tyr Phe Leu Ser
100    105    110
Ala Leu Gly Arg Leu Ile Ser Xaa Val Thr Val Ala Tyr Ala Gly Leu
115    120    125
Cys Leu Phe Cys Leu Ser Met Leu Cys Gln Thr Ser Gln Ser Leu Gly
130    135    140
Asn Cys Val Leu Lys Arg Gly Asn Gly Gln Ile Leu Glu Gln Glu Ala
145    150    155    160
His Ser Asp Thr
```

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1481489
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Gly Lys Ala Met Gly Leu Leu Ile Ser Gly Thr Leu Val Tyr Tyr
1 5 10 15
His Cys Ala Tyr Arg Asn Ala Thr Leu Leu Ser Leu Phe Ser Asp Val
20 25 30
Phe Ile Val Leu Leu Cys Ser Leu Ala Ile Leu Gly Leu Leu Phe Arg
35 40 45
Gln Leu Asn Val Ser Val Pro Val Asp Pro Leu Glu Trp Gln Ile Ser
50 55 60
Gln Asp Thr Ala Ser Asn Ile Val Ala Arg Leu Ala Asn Thr Val Gly
65 70 75 80
Ala Ala Glu Gly Val Leu Arg Val Ala Ala Thr Gly His Asp Lys Arg
85 90 95
Leu Phe Val Lys Val Val Ile Cys Leu Tyr Phe Leu Ser Ala Leu Gly
100 105 110
Arg Leu Ile Ser Xaa Val Thr Val Ala Tyr Ala Gly Leu Cys Leu Phe
115 120 125
Cys Leu Ser Met Leu Cys Gln Thr Ser Gln Ser Leu Gly Asn Cys Val
130 135 140
Leu Lys Arg Gly Asn Gly Gln Ile Leu Glu Gln Glu Ala His Ser Asp
145 150 155 160
Thr

- (2) INFORMATION FOR SEQ ID NO:41:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1481490
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Gly Leu Leu Ile Ser Gly Thr Leu Val Tyr Tyr His Cys Ala Tyr
1 5 10 15
Arg Asn Ala Thr Leu Leu Ser Leu Phe Ser Asp Val Phe Ile Val Leu
20 25 30
Leu Cys Ser Leu Ala Ile Leu Gly Leu Leu Phe Arg Gln Leu Asn Val
35 40 45
Ser Val Pro Val Asp Pro Leu Glu Trp Gln Ile Ser Gln Asp Thr Ala
50 55 60
Ser Asn Ile Val Ala Arg Leu Ala Asn Thr Val Gly Ala Ala Glu Gly
65 70 75 80
Val Leu Arg Val Ala Ala Thr Gly His Asp Lys Arg Leu Phe Val Lys
85 90 95
Val Val Ile Cys Leu Tyr Phe Leu Ser Ala Leu Gly Arg Leu Ile Ser
100 105 110
Xaa Val Thr Val Ala Tyr Ala Gly Leu Cys Leu Phe Cys Leu Ser Met
115 120 125
Leu Cys Gln Thr Ser Gln Ser Leu Gly Asn Cys Val Leu Lys Arg Gly

130 135 140
Asn Gly Gln Ile Leu Glu Gln Glu Ala His Ser Asp Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..661
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

mcacaaaaya	actaaaaaac	aatcagatct	gagatcgaac	aaaacaacat	gaacacgtta	60
atcccatcgg	agaaaagatg	gatcatcacc	ggcgttttac	tagccgggtt	agttggcggg	120
gctttgcttt	tcacaagctt	catcacgagc	gctgacgaaa	cgctcttcct	ctgttccaca	180
gcaagcgcca	aaagcagagc	ggtggctgcg	gcagctgatt	acgaagcgac	tccgattcag	240
cttcaagcga	tcgtccacta	cgcgacatct	aacgttgttc	cacaacagaa	tcttgctgag	300
atctcgatct	ctttcaacat	cttgaaaaag	ctagctccgg	ctaactttct	cgtgttcggg	360
ctcggctcgtg	actcgctcat	gtgggcttct	ttaaattccac	gtggcaaaac	cttgttcttg	420
gaagaagatc	ttgaatggtt	tcagaaagtg	accaaagact	ctcctttctt	acgtgcgcac	480
cacgtgcgtt	acaggacgca	gcttcaacaa	gccgattcgc	ttctacgttc	gtacaaaacg	540
gagcctaact	gttttccggc	gaaatcttat	ctccggggaa	acgagaagtg	taagctagct	600
ctcacgggac	tgcccgatga	gttctacgat	acagagtggg	atctgctgat	ggtcgatgct	660

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Asn	Thr	Leu	Ile	Pro	Ser	Glu	Lys	Arg	Trp	Ile	Ile	Thr	Gly	Val
1				5					10					15	
Leu	Leu	Ala	Gly	Leu	Val	Gly	Gly	Ala	Leu	Leu	Phe	Thr	Ser	Phe	Ile
		20				25					30				
Arg	Ala	Ala	Asp	Glu	Thr	Leu	Phe	Leu	Cys	Ser	Thr	Ala	Ser	Ala	Lys
		35				40					45				
Ser	Arg	Ala	Val	Ala	Ala	Ala	Ala	Asp	Tyr	Glu	Ala	Thr	Pro	Ile	Gln
		50				55				60					
Leu	Gln	Ala	Ile	Val	His	Tyr	Ala	Thr	Ser	Asn	Val	Val	Pro	Gln	Gln
65				70					75					80	
Asn	Leu	Ala	Glu	Ile	Ser	Ile	Ser	Phe	Asn	Ile	Leu	Lys	Lys	Leu	Ala
			85						90					95	
Pro	Ala	Asn	Phe	Leu	Val	Phe	Gly	Leu	Gly	Arg	Asp	Ser	Leu	Met	Trp
		100						105					110		
Ala	Ser	Leu	Asn	Pro	Arg	Gly	Lys	Thr	Leu	Phe	Leu	Glu	Glu	Asp	Leu
		115					120					125			
Glu	Trp	Phe	Gln	Lys	Val	Thr	Lys	Asp	Ser	Pro	Phe	Leu	Arg	Ala	His
		130					135				140				
His	Val	Arg	Tyr	Arg	Thr	Gln	Leu	Gln	Gln	Ala	Asp	Ser	Leu	Leu	Arg
145					150					155					160

Ser Tyr Lys Thr Glu Pro Asn Cys Phe Pro Ala Lys Ser Tyr Leu Arg
165 170 175
Gly Asn Glu Lys Cys Lys Leu Ala Leu Thr Gly Leu Pro Asp Glu Phe
180 185 190
Tyr Asp Thr Glu Trp Asp Leu Leu Met Val Asp Ala
195 200

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

aatgctcgt	agttcaagca	aaatcacaag	agcgagagag	atggtgacga	aaacagagga	60
gaagcaattg	aaccagctag	agattcaagt	cgataatggc	ggaggtggaa	catgggagta	120
tctttgtctc	gttcgtaatc	tcaaaacttcg	tcggtcggag	aaagtattaa	aacacggttc	180
ctcgattttg	aatgatccga	ggaaacgatac	tgctctcggg	ccatatgaat	ggacactaaa	240
tgagcaggtg	gcaattgcag	ctatggactg	tcaatgtctc	ggtgtcgcac	agagttgcat	300
taaggctttg	cagaagaaat	ttcctgggag	caaaagggtt	gggaggcttg	aggcattgct	360
tcttgaagca	aagggattat	ggggagaggg	tgaggaagca	tatgcgagtc	ttttggaaga	420
taatccactc	gaccaagcga	tacacaaacg	aagagtgggt	atatccaagg	cactaggaaa	480
accttcata	gccattgagc	ttcttaacaa	atatcttgaa	ctattcatgg	ctgatcatga	540
tgcatggaga	gaacttgacg	agctttatct	ttccttgcaa	atgtataagc	aagcagcttt	600
ctgctatgaa	gagctcatac	tatctcagcc	tactgttcca	ttgtaccacc	tcgcatatgc	660
tgaggttctc	tatacaatcg	gtggagtaga	aaacattatc	tcagcaagaa	aatactatgc	720
agcgaccgta	gatttaacag	gcggcaaaaa	cactagagct	cttctcggaa	tctgcttggtg	780
tgcatcgccc	attgcacagc	tctcaaaaagg	caggaacaaa	gaggacaaa	acgctacggc	840
agccccagag	cttcattccc	tggtctgcagc	tgcaagtagag	aaagaatata	agcaaaaagc	900
cccggacaaa	cttcagctca	tctcttccgc	gttaagaatc	ttgaagactt	gacgcgaagt	960
aaacgatggt	ctggcccaca	agacgcaaac	gacttagcag	tagtagatag	tcggaaaata	1020
tcgaactcta	aattcaaata	actttcttta	aagtttaaac	caaagagaat	tttgattact	1080
gttagatacc	aaaaccaa	aactgtatca	ctccttagcc	tttacgggtt	ccatgcttgc	1140
gacgtgcagc	ttcttttgta	tcg				

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Leu	Val	Ser	Ser	Lys	Ile	Thr	Arg	Ala	Arg	Glu	Met	Val	Thr
1			5				10						15	
Lys	Thr	Glu	Glu	Lys	Gln	Leu	Asn	Gln	Leu	Glu	Ile	Gln	Val	Asp
			20				25						30	
Gly	Gly	Gly	Gly	Thr	Trp	Glu	Tyr	Leu	Cys	Leu	Val	Arg	Asn	Leu
			35				40					45		
Leu	Arg	Arg	Ser	Glu	Lys	Val	Leu	Lys	His	Gly	Ser	Ser	Ile	Leu
			50			55					60			
Asp	Pro	Arg	Lys	Arg	Ser	Ala	Leu	Gly	Pro	Tyr	Glu	Trp	Thr	Leu

65					70					75					80
Glu	Gln	Val	Ala	Ile	Ala	Ala	Met	Asp	Cys	Gln	Cys	Leu	Gly	Val	Ala
				85					90					95	
Gln	Ser	Cys	Ile	Lys	Ala	Leu	Gln	Lys	Lys	Phe	Pro	Gly	Ser	Lys	Arg
			100					105					110		
Val	Gly	Arg	Leu	Glu	Ala	Leu	Leu	Leu	Glu	Ala	Lys	Gly	Leu	Trp	Gly
		115					120					125			
Glu	Ala	Glu	Glu	Ala	Tyr	Ala	Ser	Leu	Leu	Glu	Asp	Asn	Pro	Leu	Asp
	130						135				140				
Gln	Ala	Ile	His	Lys	Arg	Arg	Val	Ala	Ile	Ser	Lys	Ala	Leu	Gly	Lys
145					150					155					160
Pro	Ser	Ile	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Tyr	Leu	Glu	Leu	Phe	Met
				165					170					175	
Ala	Asp	His	Asp	Ala	Trp	Arg	Glu	Leu	Ala	Glu	Leu	Tyr	Leu	Ser	Leu
			180					185					190		
Gln	Met	Tyr	Lys	Gln	Ala	Ala	Phe	Cys	Tyr	Glu	Glu	Leu	Ile	Leu	Ser
		195					200					205			
Gln	Pro	Thr	Val	Pro	Leu	Tyr	His	Leu	Ala	Tyr	Ala	Glu	Val	Leu	Tyr
	210						215				220				
Thr	Ile	Gly	Gly	Val	Glu	Asn	Ile	Ile	Ser	Ala	Arg	Lys	Tyr	Tyr	Ala
225					230					235					240
Ala	Thr	Val	Asp	Leu	Thr	Gly	Gly	Lys	Asn	Thr	Arg	Ala	Leu	Leu	Gly
				245					250					255	
Ile	Cys	Leu	Cys	Ala	Ser	Ala	Ile	Ala	Gln	Leu	Ser	Lys	Gly	Arg	Asn
			260					265					270		
Lys	Glu	Asp	Lys	Asp	Ala	Thr	Ala	Ala	Pro	Glu	Leu	His	Ser	Leu	Ala
		275					280					285			
Ala	Ala	Ala	Val	Glu	Lys	Glu	Tyr	Lys	Gln	Lys	Ala	Pro	Asp	Lys	Leu
	290						295				300				
Gln	Leu	Ile	Ser	Ser	Ala	Leu	Arg	Ile	Leu	Lys	Thr				
305					310					315					

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Leu	Val	Ser	Ser	Lys	Ile	Thr	Arg	Ala	Arg	Glu	Met	Val	Thr	
1				5				10					15		
Lys	Thr	Glu	Glu	Lys	Gln	Leu	Asn	Gln	Leu	Glu	Ile	Gln	Val	Asp	Asn
			20					25					30		
Gly	Gly	Gly	Gly	Thr	Trp	Glu	Tyr	Leu	Cys	Leu	Val	Arg	Asn	Leu	Lys
			35				40					45			
Leu	Arg	Arg	Ser	Glu	Lys	Val	Leu	Lys	His	Gly	Ser	Ser	Ile	Leu	Asn
	50					55					60				
Asp	Pro	Arg	Lys	Arg	Ser	Ala	Leu	Gly	Pro	Tyr	Glu	Trp	Thr	Leu	Asn
65					70					75					80
Glu	Gln	Val	Ala	Ile	Ala	Ala	Met	Asp	Cys	Gln	Cys	Leu	Gly	Val	Ala
			85						90					95	
Gln	Ser	Cys	Ile	Lys	Ala	Leu	Gln	Lys	Lys	Phe	Pro	Gly	Ser	Lys	Arg
			100					105					110		
Val	Gly	Arg	Leu	Glu	Ala	Leu	Leu	Glu	Ala	Lys	Gly	Leu	Trp	Gly	
		115					120					125			

Glu Ala Glu Glu Ala Tyr Ala Ser Leu Leu Glu Asp Asn Pro Leu Asp
130 135 140
Gln Ala Ile His Lys Arg Arg Val Ala Ile Ser Lys Ala Leu Gly Lys
145 150 155 160
Pro Ser Ile Ala Ile Glu Leu Leu Asn Lys Tyr Leu Glu Leu Phe Met
165 170 175
Ala Asp His Asp Ala Trp Arg Glu Leu Ala Glu Leu Tyr Leu Ser Leu
180 185 190
Gln Met Tyr Lys Gln Ala Ala Phe Cys Tyr Glu Glu Leu Ile Leu Ser
195 200 205
Gln Pro Thr Val Pro Leu Tyr His Leu Ala Tyr Ala Glu Val Leu Tyr
210 215 220
Thr Ile Gly Gly Val Glu Asn Ile Ile Ser Ala Arg Lys Tyr Tyr Ala
225 230 235 240
Ala Thr Val Asp Leu Thr Gly Gly Lys Asn Thr Arg Ala Leu Leu Gly
245 250 255
Ile Cys Leu Cys Ala Ser Ala Ile Ala Gln Leu Ser Lys Gly Arg Asn
260 265 270
Lys Glu Asp Lys Asp Ala Thr Ala Ala Pro Glu Leu His Ser Leu Ala
275 280 285
Ala Ala Ala Val Glu Lys Glu Tyr Lys Gln Lys Ala Pro Asp Lys Leu
290 295 300
Gln Leu Ile Ser Ser Ala Leu Arg Ile Leu Lys Thr
305 310 315

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1481507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Val Thr Lys Thr Glu Glu Lys Gln Leu Asn Gln Leu Glu Ile Gln
1 5 10 15
Val Asp Asn Gly Gly Gly Gly Thr Trp Glu Tyr Leu Cys Leu Val Arg
20 25 30
Asn Leu Lys Leu Arg Arg Ser Glu Lys Val Leu Lys His Gly Ser Ser
35 40 45
Ile Leu Asn Asp Pro Arg Lys Arg Ser Ala Leu Gly Pro Tyr Glu Trp
50 55 60
Thr Leu Asn Glu Gln Val Ala Ile Ala Ala Met Asp Cys Gln Cys Leu
65 70 75 80
Gly Val Ala Gln Ser Cys Ile Lys Ala Leu Gln Lys Lys Phe Pro Gly
85 90 95
Ser Lys Arg Val Gly Arg Leu Glu Ala Leu Leu Leu Glu Ala Lys Gly
100 105 110
Leu Trp Gly Glu Ala Glu Glu Ala Tyr Ala Ser Leu Leu Glu Asp Asn
115 120 125
Pro Leu Asp Gln Ala Ile His Lys Arg Arg Val Ala Ile Ser Lys Ala
130 135 140
Leu Gly Lys Pro Ser Ile Ala Ile Glu Leu Leu Asn Lys Tyr Leu Glu
145 150 155 160
Leu Phe Met Ala Asp His Asp Ala Trp Arg Glu Leu Ala Glu Leu Tyr
165 170 175
Leu Ser Leu Gln Met Tyr Lys Gln Ala Ala Phe Cys Tyr Glu Glu Leu

	180		185		190										
Ile	Leu	Ser	Gln	Pro	Thr	Val	Pro	Leu	Tyr	His	Leu	Ala	Tyr	Ala	Glu
	195		200		205										
Val	Leu	Tyr	Thr	Ile	Gly	Gly	Val	Glu	Asn	Ile	Ile	Ser	Ala	Arg	Lys
	210		215		220										
Tyr	Tyr	Ala	Ala	Thr	Val	Asp	Leu	Thr	Gly	Gly	Lys	Asn	Thr	Arg	Ala
225				230		235									240
Leu	Leu	Gly	Ile	Cys	Leu	Cys	Ala	Ser	Ala	Ile	Ala	Gln	Leu	Ser	Lys
			245			250								255	
Gly	Arg	Asn	Lys	Glu	Asp	Lys	Asp	Ala	Thr	Ala	Ala	Pro	Glu	Leu	His
		260				265							270		
Ser	Leu	Ala	Ala	Ala	Ala	Val	Glu	Lys	Glu	Tyr	Lys	Gln	Lys	Ala	Pro
	275					280						285			
Asp	Lys	Leu	Gln	Leu	Ile	Ser	Ser	Ala	Leu	Arg	Ile	Leu	Lys	Thr	
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1259
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

atttcacttt	ccgattttat	aaaattgatt	cttctcttct	tcttaaacc	atgaagagtt	60
catgatttct	taagctcgca	gcataatcga	tggcgaattt	gagtttgagc	ttgtatctaa	120
tcctccggat	ttacgctctt	ttgttgctgt	tcaatgtctc	cttcgctaaa	acacttaaac	180
gagacatgaa	agctttgaat	gagataaaga	aattgggtggg	atggagattg	gtataactctt	240
gggttgagga	tgatccttgt	ggcgtaggag	ttttgcctcc	gtggctctgga	gttaacttgct	300
ctaaagttgg	cgattatcgt	gtcgtcgtca	agctagaagt	gtattcaatg	tcgatagttg	360
ggaatttccc	aaaggctata	acgaagctct	tagatctcac	tgttttggat	atgcataata	420
acaaattaac	aggctctatt	cctccagaaa	ttgggcggct	taagcggctt	atcacactga	480
atttgagggtg	gaacaaactt	caacaggcac	tgcctcctga	aattgggtgga	ttgaagagtc	540
taacttatct	gtacctgagt	tttaacaatt	tcaaaggaga	aatccccaaa	gaacttgcaa	600
atctccatga	gctccagtac	ttacatattc	aggagaatca	ttttactggg	cgaattccag	660
cagagctggg	aacattacaa	aaacttcgcc	acttggtatg	tggcaacaat	aacttagtgg	720
ggagtataag	cgatcttttt	cgcattgaag	gatgctttcc	agctcttaga	aacctgtttt	780
taaacaataa	ttacttgact	ggaggactcc	caaacaagct	tgcaaatacta	acaaacctgg	840
agatcttgta	cttatctttc	aacaaaatga	ctggagcaat	acccgctgca	cttgccagta	900
taccaagact	aactaacttg	cacttggacc	acaatctatt	caatggaagt	atacctgaag	960
ccttctacaa	gcataccaaac	ctaaaagata	tgtacataga	agggaaatgct	ttcaaatcag	1020
acgtgaaggc	gattgggtgca	cataaggctc	tcgaactttc	tgacacagac	ttccttggtt	1080
agttatgtat	agcacaaactt	tgtttcatct	acagatagga	atttggcagt	gttatctggt	1140
tatttaagat	tcattttctc	tgttaaagcg	agattgtagt	tgatgtgttt	tctgaatgta	1200
aaagattcct	tatccatgta	tgaaaattga	atataaaggg	aatctggttt	gttctttcc	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Ala	Asn	Leu	Ser	Leu	Ser	Leu	Tyr	Leu	Ile	Leu	Arg	Ile	Tyr	Ala
1				5					10					15	
Leu	Leu	Leu	Leu	Phe	Asn	Val	Ser	Phe	Ala	Lys	Thr	Leu	Lys	Arg	Asp
			20					25					30		
Met	Lys	Ala	Leu	Asn	Glu	Ile	Lys	Lys	Leu	Val	Gly	Trp	Arg	Leu	Val
		35					40					45			
Tyr	Ser	Trp	Val	Gly	Asp	Asp	Pro	Cys	Gly	Asp	Gly	Val	Leu	Pro	Pro
	50					55					60				
Trp	Ser	Gly	Val	Thr	Cys	Ser	Lys	Val	Gly	Asp	Tyr	Arg	Val	Val	Val
65					70					75				80	
Lys	Leu	Glu	Val	Tyr	Ser	Met	Ser	Ile	Val	Gly	Asn	Phe	Pro	Lys	Ala
				85					90					95	
Ile	Thr	Lys	Leu	Leu	Asp	Leu	Thr	Val	Leu	Asp	Met	His	Asn	Asn	Lys
			100					105					110		
Leu	Thr	Gly	Pro	Ile	Pro	Pro	Glu	Ile	Gly	Arg	Leu	Lys	Arg	Leu	Ile
		115					120						125		
Thr	Leu	Asn	Leu	Arg	Trp	Asn	Lys	Leu	Gln	Gln	Ala	Leu	Pro	Pro	Glu
	130					135					140				
Ile	Gly	Gly	Leu	Lys	Ser	Leu	Thr	Tyr	Leu	Tyr	Leu	Ser	Phe	Asn	Asn
145					150					155				160	
Phe	Lys	Gly	Glu	Ile	Pro	Lys	Glu	Leu	Ala	Asn	Leu	His	Glu	Leu	Gln
				165					170					175	
Tyr	Leu	His	Ile	Gln	Glu	Asn	His	Phe	Thr	Gly	Arg	Ile	Pro	Ala	Glu
		180						185					190		
Leu	Gly	Thr	Leu	Gln	Lys	Leu	Arg	His	Leu	Asp	Ala	Gly	Asn	Asn	Asn
		195					200					205			
Leu	Val	Gly	Ser	Ile	Ser	Asp	Leu	Phe	Arg	Ile	Glu	Gly	Cys	Phe	Pro
	210					215					220				
Ala	Leu	Arg	Asn	Leu	Phe	Leu	Asn	Asn	Asn	Tyr	Leu	Thr	Gly	Gly	Leu
225					230					235				240	
Pro	Asn	Lys	Leu	Ala	Asn	Leu	Thr	Asn	Leu	Glu	Ile	Leu	Tyr	Leu	Ser
				245					250					255	
Phe	Asn	Lys	Met	Thr	Gly	Ala	Ile	Pro	Ala	Ala	Leu	Ala	Ser	Ile	Pro
		260						265					270		
Arg	Leu	Thr	Asn	Leu	His	Leu	Asp	His	Asn	Leu	Phe	Asn	Gly	Ser	Ile
		275					280					285			
Pro	Glu	Ala	Phe	Tyr	Lys	His	Pro	Asn	Leu	Lys	Asp	Met	Tyr	Ile	Glu
	290					295					300				
Gly	Asn	Ala	Phe	Lys	Ser	Asp	Val	Lys	Ala	Ile	Gly	Ala	His	Lys	Val
305					310					315				320	
Leu	Glu	Leu	Ser	Asp	Thr	Asp	Phe	Leu	Val						
				325					330						

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Lys	Ala	Leu	Asn	Glu	Ile	Lys	Lys	Leu	Val	Gly	Trp	Arg	Leu	Val
1				5					10					15	
Tyr	Ser	Trp	Val	Gly	Asp	Asp	Pro	Cys	Gly	Asp	Gly	Val	Leu	Pro	Pro
		20						25					30		

Trp	Ser	Gly	Val	Thr	Cys	Ser	Lys	Val	Gly	Asp	Tyr	Arg	Val	Val	Val
		35					40					45			
Lys	Leu	Glu	Val	Tyr	Ser	Met	Ser	Ile	Val	Gly	Asn	Phe	Pro	Lys	Ala
	50					55					60				
Ile	Thr	Lys	Leu	Leu	Asp	Leu	Thr	Val	Leu	Asp	Met	His	Asn	Asn	Lys
65					70					75				80	
Leu	Thr	Gly	Pro	Ile	Pro	Pro	Glu	Ile	Gly	Arg	Leu	Lys	Arg	Leu	Ile
				85					90					95	
Thr	Leu	Asn	Leu	Arg	Trp	Asn	Lys	Leu	Gln	Gln	Ala	Leu	Pro	Pro	Glu
			100					105					110		
Ile	Gly	Gly	Leu	Lys	Ser	Leu	Thr	Tyr	Leu	Tyr	Leu	Ser	Phe	Asn	Asn
		115					120					125			
Phe	Lys	Gly	Glu	Ile	Pro	Lys	Glu	Leu	Ala	Asn	Leu	His	Glu	Leu	Gln
	130					135				140					
Tyr	Leu	His	Ile	Gln	Glu	Asn	His	Phe	Thr	Gly	Arg	Ile	Pro	Ala	Glu
145					150					155					160
Leu	Gly	Thr	Leu	Gln	Lys	Leu	Arg	His	Leu	Asp	Ala	Gly	Asn	Asn	Asn
				165					170					175	
Leu	Val	Gly	Ser	Ile	Ser	Asp	Leu	Phe	Arg	Ile	Glu	Gly	Cys	Phe	Pro
			180					185					190		
Ala	Leu	Arg	Asn	Leu	Phe	Leu	Asn	Asn	Asn	Tyr	Leu	Thr	Gly	Gly	Leu
		195					200					205			
Pro	Asn	Lys	Leu	Ala	Asn	Leu	Thr	Asn	Leu	Glu	Ile	Leu	Tyr	Leu	Ser
	210					215					220				
Phe	Asn	Lys	Met	Thr	Gly	Ala	Ile	Pro	Ala	Ala	Leu	Ala	Ser	Ile	Pro
225					230					235					240
Arg	Leu	Thr	Asn	Leu	His	Leu	Asp	His	Asn	Leu	Phe	Asn	Gly	Ser	Ile
			245					250						255	
Pro	Glu	Ala	Phe	Tyr	Lys	His	Pro	Asn	Leu	Lys	Asp	Met	Tyr	Ile	Glu
			260					265					270		
Gly	Asn	Ala	Phe	Lys	Ser	Asp	Val	Lys	Ala	Ile	Gly	Ala	His	Lys	Val
	275					280						285			
Leu	Glu	Leu	Ser	Asp	Thr	Asp	Phe	Leu	Val						
	290					295									

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..244
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Ser	Ile	Val	Gly	Asn	Phe	Pro	Lys	Ala	Ile	Thr	Lys	Leu	Leu	Asp
1				5					10					15	
Leu	Thr	Val	Leu	Asp	Met	His	Asn	Asn	Lys	Leu	Thr	Gly	Pro	Ile	Pro
		20						25					30		
Pro	Glu	Ile	Gly	Arg	Leu	Lys	Arg	Leu	Ile	Thr	Leu	Asn	Leu	Arg	Trp
		35					40					45			
Asn	Lys	Leu	Gln	Gln	Ala	Leu	Pro	Pro	Glu	Ile	Gly	Gly	Leu	Lys	Ser
	50					55					60				
Leu	Thr	Tyr	Leu	Tyr	Leu	Ser	Phe	Asn	Asn	Phe	Lys	Gly	Glu	Ile	Pro
65					70					75				80	
Lys	Glu	Leu	Ala	Asn	Leu	His	Glu	Leu	Gln	Tyr	Leu	His	Ile	Gln	Glu
			85						90				95		
Asn	His	Phe	Thr	Gly	Arg	Ile	Pro	Ala	Glu	Leu	Gly	Thr	Leu	Gln	Lys

	100		105		110
Leu Arg His	Leu Asp Ala Gly Asn Asn Asn Leu Val Gly Ser Ile Ser				
	115		120		125
Asp Leu Phe Arg Ile Glu Gly Cys Phe Pro Ala Leu Arg Asn Leu Phe					
	130		135		140
Leu Asn Asn Asn Tyr Leu Thr Gly Gly Leu Pro Asn Lys Leu Ala Asn					
	145		150		155
Leu Thr Asn Leu Glu Ile Leu Tyr Leu Ser Phe Asn Lys Met Thr Gly					
	165		170		175
Ala Ile Pro Ala Ala Leu Ala Ser Ile Pro Arg Leu Thr Asn Leu His					
	180		185		190
Leu Asp His Asn Leu Phe Asn Gly Ser Ile Pro Glu Ala Phe Tyr Lys					
	195		200		205
His Pro Asn Leu Lys Asp Met Tyr Ile Glu Gly Asn Ala Phe Lys Ser					
	210		215		220
Asp Val Lys Ala Ile Gly Ala His Lys Val Leu Glu Leu Ser Asp Thr					
	225		230		235
Asp Phe Leu Val					240

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..860
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

cattaagctg	actaagttcg	agaacgagga	agctgtctgc	aacccccaaa	gaactcgtgc	60
taatgatatg	aagaatttag	ccactgctgc	tgtaaaagca	agcagatttt	atagggagtt	120
gaattcccaa	actgtcaaac	acttgacac	actccatgag	taccttgga	tgatgatggc	180
tgtccaaggc	gcatttgcag	atagatctag	tgctttactg	acagttcaga	cgcttctatc	240
agagcttctt	tctctgcaaa	ctagagttga	gaagctagag	gctgcatcat	cgaagggtatt	300
tggtggtgac	aaatcaagga	tccgaaaaat	agaagagtta	aaagaaacaa	tcaagggtcac	360
tgaggatgca	aaaaatggtg	ccatcaaagg	gtatgagcga	atcaaggaaa	acaaccgatc	420
tgaggttgag	aggttggaca	gagaaaggcg	tgcagacttc	atgaacatga	tgaagggttt	480
tgttgttaac	caggttggat	acgcagagaa	aatgggaaac	gtctgggcaa	aggttgcaga	540
agagaccagc	caatacgata	gagagaagca	gagcagctaa	caaacacaga	aaaaaagaga	600
gtgaacgatg	ttcatttttg	cataaccata	ccaaatccat	gtatggcaca	gaatcacatt	660
gcgtaataat	ggtttgtcaa	aaagtgtagt	ttcctttttc	atatgttgta	tctatcttga	720
tagagattgg	taaacgttct	tgtttgtttt	ctttagttgc	tgtaaattag	ttttctagaa	780
gcattctctg	ctacagctgc	attgactcat	acccattgtt	ttctggtata	tgccgcaaaa	840
gatatatctg	atagtttggc					

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ile Lys Leu Thr Lys Phe Glu Asn Glu Glu Ala Val Cys Asn Pro Gln

1		5		10		15									
Arg	Thr	Arg	Ala	Asn	Asp	Met	Lys	Asn	Leu	Ala	Thr	Ala	Ala	Val	Lys
		20		25		30									
Ala	Ser	Arg	Phe	Tyr	Arg	Glu	Leu	Asn	Ser	Gln	Thr	Val	Lys	His	Leu
		35		40		45									
Asp	Thr	Leu	His	Glu	Tyr	Leu	Gly	Met	Met	Met	Ala	Val	Gln	Gly	Ala
		50		55		60									
Phe	Ala	Asp	Arg	Ser	Ser	Ala	Leu	Leu	Thr	Val	Gln	Thr	Leu	Leu	Ser
		65		70		75									80
Glu	Leu	Pro	Ser	Leu	Gln	Thr	Arg	Val	Glu	Lys	Leu	Glu	Ala	Ala	Ser
			85			90									95
Ser	Lys	Val	Phe	Gly	Gly	Asp	Lys	Ser	Arg	Ile	Arg	Lys	Ile	Glu	Glu
		100		105		110									
Leu	Lys	Glu	Thr	Ile	Lys	Val	Thr	Glu	Asp	Ala	Lys	Asn	Val	Ala	Ile
		115		120		125									
Lys	Gly	Tyr	Glu	Arg	Ile	Lys	Glu	Asn	Asn	Arg	Ser	Glu	Val	Glu	Arg
		130		135		140									
Leu	Asp	Arg	Glu	Arg	Arg	Ala	Asp	Phe	Met	Asn	Met	Met	Lys	Gly	Phe
		145		150		155									160
Val	Val	Asn	Gln	Val	Gly	Tyr	Ala	Glu	Lys	Met	Gly	Asn	Val	Trp	Ala
			165			170									175
Lys	Val	Ala	Glu	Thr	Ser	Gln	Tyr	Asp	Arg	Glu	Lys	Gln	Ser	Ser	
		180				185									190

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1481522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Lys	Asn	Leu	Ala	Thr	Ala	Ala	Val	Lys	Ala	Ser	Arg	Phe	Tyr	Arg
1			5					10						15	
Glu	Leu	Asn	Ser	Gln	Thr	Val	Lys	His	Leu	Asp	Thr	Leu	His	Glu	Tyr
			20				25						30		
Leu	Gly	Met	Met	Met	Ala	Val	Gln	Gly	Ala	Phe	Ala	Asp	Arg	Ser	Ser
		35					40					45			
Ala	Leu	Leu	Thr	Val	Gln	Thr	Leu	Leu	Ser	Glu	Leu	Pro	Ser	Leu	Gln
		50				55					60				
Thr	Arg	Val	Glu	Lys	Leu	Glu	Ala	Ala	Ser	Ser	Lys	Val	Phe	Gly	Gly
		65			70					75					80
Asp	Lys	Ser	Arg	Ile	Arg	Lys	Ile	Glu	Glu	Leu	Lys	Glu	Thr	Ile	Lys
			85				90							95	
Val	Thr	Glu	Asp	Ala	Lys	Asn	Val	Ala	Ile	Lys	Gly	Tyr	Glu	Arg	Ile
			100				105							110	
Lys	Glu	Asn	Asn	Arg	Ser	Glu	Val	Glu	Arg	Leu	Asp	Arg	Glu	Arg	Arg
		115					120						125		
Ala	Asp	Phe	Met	Asn	Met	Met	Lys	Gly	Phe	Val	Val	Asn	Gln	Val	Gly
		130				135					140				
Tyr	Ala	Glu	Lys	Met	Gly	Asn	Val	Trp	Ala	Lys	Val	Ala	Glu	Glu	Thr
		145			150					155					160
Ser	Gln	Tyr	Asp	Arg	Glu	Lys	Gln	Ser	Ser						
			165					170							

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Met Met Ala Val Gln Gly Ala Phe Ala Asp Arg Ser Ser Ala Leu
1 5 10 15
Leu Thr Val Gln Thr Leu Leu Ser Glu Leu Pro Ser Leu Gln Thr Arg
20 25 30
Val Glu Lys Leu Glu Ala Ala Ser Lys Val Phe Gly Gly Asp Lys
35 40 45
Ser Arg Ile Arg Lys Ile Glu Glu Leu Lys Glu Thr Ile Lys Val Thr
50 55 60
Glu Asp Ala Lys Asn Val Ala Ile Lys Gly Tyr Glu Arg Ile Lys Glu
65 70 75 80
Asn Asn Arg Ser Glu Val Glu Arg Leu Asp Arg Glu Arg Arg Ala Asp
85 90 95
Phe Met Asn Met Met Lys Gly Phe Val Val Asn Gln Val Gly Tyr Ala
100 105 110
Glu Lys Met Gly Asn Val Trp Ala Lys Val Ala Glu Glu Thr Ser Gln
115 120 125
Tyr Asp Arg Glu Lys Gln Ser Ser
130 135

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

attactcaat tagtacaagt tggtatacaa ctaaattcttc atttggtaaa tcactctttac 60
tcaaattgaa tagtagtggt cgtgtgaaaa caagaaaagt ggaaaaggac aaaagagaga 120
gtaaaggacg cctcctaata aagcactctt cttccttttc actttcctca ttgaagagag 180
agccaaattc agcttaaagc cccataagcg taagcgtaag cgtaagcgta agcgtaagcg 240
taagcgtaag cgtaagcgta agcgtaagcg taagcgtaag cgcggggata aatctctctc 300
ttcctcacct gcgttttcgt ggagcatctt cttcaacaat ggctgcttct ccgatctgat 360
catatcctga tttgaatttt gctatctctc atgcctcgaa ctgcgtttgt cgacgtagca 420
tcctagtgcg tgaggaagaa gaagaagatg agcttcttta tcctctccgt cgctgctttc 480
gtttctctcg ctttcttctc tcttcgcgat tccgttgatt catctgtttc cgcttcacag 540
gacctctca gactcatatt aggttcacgg aattttggaa catggaaagg tggaatctca 600
ttagcaccag gacctgaatc tgatgatgtt gtctctgatt acctcctctt agcagctcat 660
agaaccaaga gacctgacat tcttagagct ttttaagcctt accatggtgg ctggaacatc 720
accaataatc actattgggc ttctgttgga tttacaggtg ctcttggttt catactagct 780
gttatctggc tcttgtcttt tggtctctct cttgttggtt atcattgctt caaatggaga 840
atatgtgata aagctaaagg atcatcattc gatacacgaa gaatctgttt cattttgttg 900
attgtgttta catgtgttgc agcgggtgga tgcattcttt tatctgttgg acaagataag 960
tttcataccg aagctatgca tactcttaag tatgttgtaa accagtcaga ctacactgtg 1020

(2) INFORMATION FOR SEQ ID NO:57:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1481525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Ser	Phe	Phe	Ile	Leu	Ser	Val	Val	Val	Phe	Val	Ser	Leu	Ala	Phe
1				5						10				15	
Phe	Ser	Leu	Pro	His	Ser	Val	Asp	Ser	Ser	Val	Ser	Ala	Ser	Gln	Asp
			20					25					30		
Pro	Leu	Arg	Leu	Ile	Leu	Gly	Ser	Pro	Asn	Phe	Gly	Thr	Trp	Lys	Gly
			35				40					45			
Gly	Ile	Ser	Leu	Ala	Pro	Gly	Pro	Glu	Ser	Asp	Asp	Val	Val	Ser	Asp
			50			55					60				
Tyr	Leu	Leu	Leu	Ala	Ala	His	Arg	Thr	Lys	Arg	Pro	Asp	Ile	Leu	Arg
65					70					75					80
Ala	Phe	Lys	Pro	Tyr	His	Gly	Gly	Trp	Asn	Ile	Thr	Asn	Asn	His	Tyr
				85					90					95	
Trp	Ala	Ser	Val	Gly	Phe	Thr	Gly	Ala	Pro	Gly	Phe	Ile	Leu	Ala	Val
			100					105					110		
Ile	Trp	Leu	Leu	Ser	Phe	Gly	Ser	Leu	Leu	Val	Val	Tyr	His	Cys	Phe
			115				120					125			
Lys	Trp	Arg	Ile	Cys	Asp	Lys	Ala	Lys	Gly	Ser	Ser	Phe	Asp	Thr	Arg
			130			135					140				
Arg	Ile	Cys	Phe	Ile	Leu	Leu	Ile	Val	Phe	Thr	Cys	Val	Ala	Ala	Val
145					150					155					160
Gly	Cys	Ile	Leu	Leu	Ser	Val	Gly	Gln	Asp	Lys	Phe	His	Thr	Glu	Ala
				165					170					175	
Met	His	Thr	Leu	Lys	Tyr	Val	Val	Asn	Gln	Ser	Asp	Tyr	Thr	Val	Glu
			180					185					190		
Ile	Leu	Gln	Asn	Val	Thr	Gln	Tyr	Leu	Ser	Leu	Ala	Lys	Thr	Ile	Asn
			195				200					205			
Val	Thr	Gln	Ile	Val	Ile	Pro	Ser	Asp	Val	Met	Gly	Glu	Ile	Asp	Lys

210	215	220
Leu Asn Val Asn Leu Asn Thr Ala Ala Val Thr Leu Gly Glu Thr Thr		
225	230	235
Thr Asp Lys Arg Cys		240
	245	

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1481526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Leu	Ile	Leu	Ser	Phe	Val	Gly	Leu	Leu	Ser	Val	Leu	Arg	His
1				5				10					15	
Gln	His	Val	Val	His	Ile	Phe	Val	Val	Ser	Gly	Trp	Ile	Leu	Val
		20						25					30	
Val	Thr	Phe	Val	Leu	Cys	Gly	Val	Phe	Leu	Ile	Leu	Asn	Asn	Ala
		35					40					45		
Ser	Asp	Thr	Cys	Val	Ala	Met	Lys	Glu	Trp	Val	Asp	Asn	Pro	His
	50					55					60			
Glu	Thr	Ala	Leu	Ser	Ser	Ile	Leu	Pro	Cys	Val	Asp	Gln	Gln	Thr
	65				70					75				80
Asn	Gln	Thr	Leu	Ser	Gln	Ser	Lys	Val	Val	Ile	Asn	Ser	Ile	Val
			85						90					95
Val	Val	Asn	Thr	Phe	Val	Tyr	Ala	Val	Ala	Asn	Thr	Asn	Pro	Ala
		100						105					110	
Gly	Gln	Asp	Arg	Tyr	Tyr	Asn	Gln	Ser	Gly	Pro	Pro	Met	Pro	Pro
	115						120					125		
Cys	Ile	Pro	Phe	Asp	Ala	Asn	Met	Glu	Asp	Arg	Gln	Cys	Ser	Pro
	130					135					140			
Glu	Leu	Ser	Ile	Glu	Asn	Ala	Ser	Ser	Val	Trp	Glu	Asn	Tyr	Lys
	145				150					155				160
Glu	Val	Thr	Pro	Ser	Gly	Ile	Cys	Thr	Thr	Val	Gly	Arg	Val	Thr
			165						170					175
Asp	Thr	Phe	Gly	Gln	Leu	Val	Ala	Ala	Val	Asn	Glu	Ser	Tyr	Ala
		180						185					190	
Glu	His	Tyr	Thr	Pro	Pro	Leu	Leu	Ser	Phe	Arg	Asp	Cys	Asn	Phe
	195						200					205		
Arg	Glu	Thr	Phe	Met	Ser	Ile	Thr	Ser	Asp	Tyr	Cys	Pro	Pro	Leu
	210					215					220			
Arg	Asn	Leu	Arg	Ile	Val	Asn	Ala	Gly	Leu	Gly	Leu	Ile	Ser	Val
	225				230					235				240
Val	Leu	Leu	Cys	Leu	Val	Leu	Trp	Ile	Phe	Tyr	Ala	Asn	Pro	Pro
			245						250					255
Gly	Arg	Lys	Cys	Leu	Arg	Ile	His	Thr	Leu	Lys	Glu	Lys	Met	Ile
		260					265						270	
Leu	Val	Thr	Ala	Trp	Ile	Leu	Ile	Thr	Gln	Met	Thr	Asn	Leu	Ser
		275					280						285	

Leu

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..235
(D) OTHER INFORMATION: / Ceres Seq. ID 1481527
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
Met Lys Glu Trp Val Asp Asn Pro His Ala Glu Thr Ala Leu Ser Ser
1 5 10 15
Ile Leu Pro Cys Val Asp Gln Gln Thr Thr Asn Gln Thr Leu Ser Gln
20 25 30
Ser Lys Val Val Ile Asn Ser Ile Val Thr Val Val Asn Thr Phe Val
35 40 45
Tyr Ala Val Ala Asn Thr Asn Pro Ala Pro Gly Gln Asp Arg Tyr Tyr
50 55 60
Asn Gln Ser Gly Pro Pro Met Pro Pro Leu Cys Ile Pro Phe Asp Ala
65 70 75 80
Asn Met Glu Asp Arg Gln Cys Ser Pro Trp Glu Leu Ser Ile Glu Asn
85 90 95
Ala Ser Ser Val Trp Glu Asn Tyr Lys Cys Glu Val Thr Pro Ser Gly
100 105 110
Ile Cys Thr Thr Val Gly Arg Val Thr Pro Asp Thr Phe Gly Gln Leu
115 120 125
Val Ala Ala Val Asn Glu Ser Tyr Ala Leu Glu His Tyr Thr Pro Pro
130 135 140
Leu Leu Ser Phe Arg Asp Cys Asn Phe Val Arg Glu Thr Phe Met Ser
145 150 155 160
Ile Thr Ser Asp Tyr Cys Pro Pro Leu Val Arg Asn Leu Arg Ile Val
165 170 175
Asn Ala Gly Leu Gly Leu Ile Ser Val Gly Val Leu Leu Cys Leu Val
180 185 190
Leu Trp Ile Phe Tyr Ala Asn Pro Lys Gly Arg Lys Cys Leu Arg
195 200 205
Ile His Thr Leu Lys Glu Lys Met Ile Ala Leu Val Thr Ala Trp Ile
210 215 220
Leu Ile Thr Gln Met Thr Asn Leu Ser Phe Leu
225 230 235

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..634
(D) OTHER INFORMATION: / Ceres Seq. ID 1481532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

aaaacatctc	tcgccgtcag	gttacatcta	tcgccaccgc	aaagagacca	ccgtctcctc	60
cgcaatcttc	ataacctaaa	caaccctcat	cccctggtac	ttaaacaatg	ggaaagagga	120
aatcaagagc	aaagcctgct	cctacgaagc	gaatggataa	gcttgacaca	atctttagtt	180
gtcctttctg	caatcacggg	tctagtgtcg	aatgcatcat	tgatatgaag	catctgattg	240
gtaaagcagc	ttgtagaatc	tgtgaagaaa	gctttaggta	ctactatcac	agctttgact	300
gaagctatag	acatttatag	cgaatggatc	gatgagtgcg	agagggttaa	taccgcggaa	360
gatgatgttg	tgcaagaaga	ggaggatgat	gaagatgacc	atgtctctgt	caaaaggaag	420
tataacttct	gagacgagtg	ttttatcgaa	aatcatgtaa	gtcgtcgtct	tagagttatc	480
tgctttatgt	tgtaatatct	atctgatgaa	atcacaagaa	caatctttag	tgttttctca	540

gtgtctgata gagaaacata catttaagt aacaatcttt aatcacaata acagtgtatg 600
attatgattt gtaagtggat ttaaggcttt gctt

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys	Thr	Ser	Leu	Ala	Val	Arg	Leu	His	Leu	Ser	Pro	Pro	Gln	Arg	Asp
1				5					10					15	
His	Arg	Leu	Leu	Arg	Asn	Leu	His	Asn	Leu	Asn	Asn	Pro	His	Pro	Leu
		20						25					30		
Val	Leu	Lys	Gln	Trp	Glu	Arg	Gly	Asn	Gln	Glu	Gln	Ser	Leu	Leu	Leu
		35					40					45			
Arg	Ser	Glu	Trp	Ile	Ser	Leu	Thr	Gln	Ser	Leu	Val	Val	Leu	Ser	Ala
		50				55					60				
Ile	Thr	Gly	Leu	Val	Ser	Asn	Ala	Ser	Leu	Ile					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Gly	Lys	Arg	Lys	Ser	Arg	Ala	Lys	Pro	Ala	Pro	Thr	Lys	Arg	Met
1				5					10					15	
Asp	Lys	Leu	Asp	Thr	Ile	Phe	Ser	Cys	Pro	Phe	Cys	Asn	His	Gly	Ser
		20						25					30		
Ser	Val	Glu	Cys	Ile	Ile	Asp	Met	Lys	His	Leu	Ile	Gly	Lys	Ala	Ala
		35					40					45			
Cys	Arg	Ile	Cys	Glu	Glu	Ser	Phe	Arg	Tyr	Tyr	Tyr	His	Ser	Phe	Asp
		50				55						60			

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Asp Lys Leu Asp Thr Ile Phe Ser Cys Pro Phe Cys Asn His Gly

1	5	10	15
Ser Ser Val Glu Cys Ile Ile Asp Met Lys His Leu Ile Gly Lys Ala			
	20	25	30
Ala Cys Arg Ile Cys Glu Glu Ser Phe Arg Tyr Tyr Tyr His Ser Phe			
	35	40	45

Asp

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

atctgcattg ttctccgcct ctctctctca aactcttcag tttgcaaaac ccttaagaag	60
gtgtgaatta gtaagtaatg gggaagaaga agttttattga taagaaaaag gcggcgactt	120
tcgagttgtg tcctcgtgat acgtcagacc caagatacag tgatgcacca ggtggtgata	180
agatcttctt acgagttgat caaaaccctg ttaacatcaa tggtttcatt gaagaagatg	240
aagaagattt tagagttagg gtatcctgat gatggttata attacttga gcatthtga	300
gagattaaga atactggttg tggttctaatt ttctatgtga atcctaagta tgaggttgct	360
cagttacctc gtgatgttaa ggcttatgat gcgtctcgtg ttaagatctc tggtatggtg	420
aatgaagaag gtaatgataa taagttgatg tatagtgttg cgtccaagac tgtaaacgtc	480
aaggtgcaga aagctattga tcctgaagtt gctgcgttgc ttgaaaacag tgatgggtct	540
gagtttggtt ctgatgttga ggatttgga gaagattttg ttgttcaagc taatcttact	600
caaaaggggtg aatcttcttg tgtgagcaat ggagagctcg agttttctgt aagacgtgag	660
gtagagagaaa gagaaagtga tgaacctgtg gctgaaaacc cgagagttcc tcgtcaaatt	720
gatgagctat ttgatcagct cgaactcaat gaatatggaa gtgatagtga cggtgatggt	780
tacatagctg aagatggaga agaagaagaa gaagaagact tcatggctca agaagttcag	840
aatcttattc atgggaaggc aaaagattat gagcttgaag aaaaatatat gaaccctgcg	900
gatatactga agaacagtga ctctgtcaga gataaagagg aagtggacac tgctgctcat	960
gttatccgcc gaactgtaga atatggtgaa aattttgata acgggaatga agatgaattt	1020
gtagagctga ctgaagaaag cagcgatgaa agcgagaagc atgattgtga aaccatagtc	1080
tcaacatact cgaatctcga taacctccct ggtaaaatcc ttgctgcaga gtcagctagg	1140
cagaagaagc tgagtgaaac attagctaac gcattgagtt caaatggaag aatcattaat	1200
ctccaaggga gagagaggat tcctgtcagag tttttacctg gtaggagagc tgaacaaacc	1260
gatgtcaaag cggaaatccc aaaagctgaa ccgatcaaga ggaagactca tggtaagag	1320
tcgaaagaag agaagaaga gcggaaaaat gctgtaaaag ccgaaaagcg agaagcaagg	1380
ataattaaga aacagacaaa gatgctgtat tgcggtgaaa cgcagcgtgc tcaaagagct	1440
gttgctacct ctggtccatc gtcgagacct ctaaaataat atgttactaa ggtaaaaacaa	1500
aacaattctc agactgttta aaaccagttt ttccagccat ttcgtgtaat atttgctgtt	1560
tgtttttttc tttttcatca agatttgaaa atcttgaatc ttgttttgga tgtggacgtt	1620
ttgaatatta tttattactt ttactagtct aatttcgaga aagtgatg	

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..438
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met His Gln Val Val Ile Arg Ser Ser Tyr Glu Leu Ile Lys Thr Leu
1 5 10 15
Leu Thr Ser Met Val Ser Leu Lys Lys Met Lys Lys Ile Leu Glu Leu
20 25 30
Gly Tyr Pro Asp Asp Gly Tyr Asn Tyr Leu Glu His Leu Arg Glu Ile
35 40 45
Lys Asn Thr Gly Gly Gly Ser Asn Phe Tyr Val Asn Pro Lys Tyr Glu
50 55 60
Val Ala Gln Leu Pro Arg Asp Val Lys Ala Tyr Asp Ala Ser Arg Val
65 70 75 80
Lys Ile Ser Gly Met Val Asn Glu Glu Gly Asn Asp Asn Lys Leu Met
85 90 95
Tyr Ser Val Ala Ser Lys Thr Val Asn Val Lys Val Gln Lys Ala Ile
100 105 110
Asp Pro Glu Val Ala Ala Leu Leu Glu Asn Ser Asp Gly Ser Glu Phe
115 120 125
Gly Ser Asp Val Glu Asp Leu Glu Glu Asp Phe Val Val Gln Ala Asn
130 135 140
Leu Thr Gln Lys Gly Glu Ser Ser Gly Val Ser Asn Gly Glu Leu Glu
145 150 155 160
Phe Ser Val Arg Arg Glu Val Arg Glu Arg Glu Ser Asp Glu Pro Val
165 170 175
Ala Glu Asn Pro Arg Val Pro Arg Gln Ile Asp Glu Leu Phe Asp Gln
180 185 190
Leu Glu Leu Asn Glu Tyr Gly Ser Asp Ser Asp Gly Asp Gly Tyr Ile
195 200 205
Ala Glu Asp Gly Glu Glu Glu Glu Glu Asp Phe Met Ala Gln Glu
210 215 220
Val Gln Asn Leu Ile His Gly Lys Ala Lys Asp Tyr Glu Leu Glu Glu
225 230 235 240
Lys Tyr Met Asn Pro Ala Asp Ile Leu Lys Asn Ser Asp Ser Val Arg
245 250 255
Asp Lys Glu Glu Val Asp Thr Ala Ala His Val Ile Arg Arg Thr Val
260 265 270
Glu Tyr Gly Glu Asn Phe Asp Asn Gly Asn Glu Asp Glu Phe Val Glu
275 280 285
Leu Thr Glu Glu Ser Ser Asp Glu Ser Glu Lys His Asp Cys Glu Thr
290 295 300
Ile Val Ser Thr Tyr Ser Asn Leu Asp Asn Leu Pro Gly Lys Ile Leu
305 310 315 320
Ala Ala Glu Ser Ala Arg Gln Lys Lys Leu Ser Glu Thr Leu Ala Asn
325 330 335
Ala Leu Ser Ser Asn Gly Arg Ile Ile Asn Leu Gln Gly Arg Glu Arg
340 345 350
Ile Pro Val Glu Phe Leu Pro Gly Arg Arg Ala Glu Gln Thr Asp Val
355 360 365
Lys Ala Glu Ile Pro Lys Ala Glu Pro Ile Lys Arg Lys Thr His Gly
370 375 380
Gln Glu Ser Lys Glu Glu Lys Lys Glu Arg Lys Asn Ala Val Lys Ala
385 390 395 400
Glu Lys Arg Glu Ala Arg Ile Ile Lys Lys Gln Thr Lys Met Leu Tyr
405 410 415
Cys Gly Glu Thr Gln Arg Ala Gln Arg Ala Val Ala Thr Ser Gly Pro
420 425 430
Ser Ser Arg Pro Leu Lys
435

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..419
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Val	Ser	Leu	Lys	Lys	Met	Lys	Lys	Ile	Leu	Glu	Leu	Gly	Tyr	Pro
1			5						10					15	
Asp	Asp	Gly	Tyr	Asn	Tyr	Leu	Glu	His	Leu	Arg	Glu	Ile	Lys	Asn	Thr
		20						25					30		
Gly	Gly	Gly	Ser	Asn	Phe	Tyr	Val	Asn	Pro	Lys	Tyr	Glu	Val	Ala	Gln
		35					40					45			
Leu	Pro	Arg	Asp	Val	Lys	Ala	Tyr	Asp	Ala	Ser	Arg	Val	Lys	Ile	Ser
	50					55					60				
Gly	Met	Val	Asn	Glu	Glu	Gly	Asn	Asp	Asn	Lys	Leu	Met	Tyr	Ser	Val
65				70						75				80	
Ala	Ser	Lys	Thr	Val	Asn	Val	Lys	Val	Gln	Lys	Ala	Ile	Asp	Pro	Glu
			85						90					95	
Val	Ala	Ala	Leu	Leu	Glu	Asn	Ser	Asp	Gly	Ser	Glu	Phe	Gly	Ser	Asp
		100						105					110		
Val	Glu	Asp	Leu	Glu	Glu	Asp	Phe	Val	Val	Gln	Ala	Asn	Leu	Thr	Gln
		115					120						125		
Lys	Gly	Glu	Ser	Ser	Gly	Val	Ser	Asn	Gly	Glu	Leu	Glu	Phe	Ser	Val
	130					135					140				
Arg	Arg	Glu	Val	Arg	Glu	Arg	Glu	Ser	Asp	Glu	Pro	Val	Ala	Glu	Asn
145				150						155				160	
Pro	Arg	Val	Pro	Arg	Gln	Ile	Asp	Glu	Leu	Phe	Asp	Gln	Leu	Glu	Leu
			165						170					175	
Asn	Glu	Tyr	Gly	Ser	Asp	Ser	Asp	Gly	Asp	Gly	Tyr	Ile	Ala	Glu	Asp
		180						185					190		
Gly	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Phe	Met	Ala	Gln	Glu	Val	Gln	Asn
		195					200					205			
Leu	Ile	His	Gly	Lys	Ala	Lys	Asp	Tyr	Glu	Leu	Glu	Glu	Lys	Tyr	Met
	210					215					220				
Asn	Pro	Ala	Asp	Ile	Leu	Lys	Asn	Ser	Asp	Ser	Val	Arg	Asp	Lys	Glu
225				230						235				240	
Glu	Val	Asp	Thr	Ala	Ala	His	Val	Ile	Arg	Arg	Thr	Val	Glu	Tyr	Gly
			245						250					255	
Glu	Asn	Phe	Asp	Asn	Gly	Asn	Glu	Asp	Glu	Phe	Val	Glu	Leu	Thr	Glu
		260						265					270		
Glu	Ser	Ser	Asp	Glu	Ser	Glu	Lys	His	Asp	Cys	Glu	Thr	Ile	Val	Ser
		275					280					285			
Thr	Tyr	Ser	Asn	Leu	Asp	Asn	Leu	Pro	Gly	Lys	Ile	Leu	Ala	Ala	Glu
	290					295					300				
Ser	Ala	Arg	Gln	Lys	Lys	Leu	Ser	Glu	Thr	Leu	Ala	Asn	Ala	Leu	Ser
305				310						315				320	
Ser	Asn	Gly	Arg	Ile	Asn	Leu	Gln	Gly	Arg	Glu	Arg	Ile	Pro	Val	
			325					330					335		
Glu	Phe	Leu	Pro	Gly	Arg	Arg	Ala	Glu	Gln	Thr	Asp	Val	Lys	Ala	Glu
		340						345					350		
Ile	Pro	Lys	Ala	Glu	Pro	Ile	Lys	Arg	Lys	Thr	His	Gly	Gln	Glu	Ser
		355					360					365			
Lys	Glu	Glu	Lys	Lys	Glu	Arg	Lys	Asn	Ala	Val	Lys	Ala	Glu	Lys	Arg
	370					375					380				
Glu	Ala	Arg	Ile	Ile	Lys	Lys	Gln	Thr	Lys	Met	Leu	Tyr	Cys	Gly	Glu
385				390						395				400	

Thr Gln Arg Ala Gln Arg Ala Val Ala Thr Ser Gly Pro Ser Ser Arg
405 410 415
Pro Leu Lys

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1481543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Lys	Lys	Ile	Leu	Glu	Leu	Gly	Tyr	Pro	Asp	Asp	Gly	Tyr	Asn	Tyr
1			5					10						15	
Leu	Glu	His	Leu	Arg	Glu	Ile	Lys	Asn	Thr	Gly	Gly	Gly	Ser	Asn	Phe
			20				25						30		
Tyr	Val	Asn	Pro	Lys	Tyr	Glu	Val	Ala	Gln	Leu	Pro	Arg	Asp	Val	Lys
		35				40						45			
Ala	Tyr	Asp	Ala	Ser	Arg	Val	Lys	Ile	Ser	Gly	Met	Val	Asn	Glu	Glu
	50				55						60				
Gly	Asn	Asp	Asn	Lys	Leu	Met	Tyr	Ser	Val	Ala	Ser	Lys	Thr	Val	Asn
65				70					75						80
Val	Lys	Val	Gln	Lys	Ala	Ile	Asp	Pro	Glu	Val	Ala	Ala	Leu	Leu	Glu
			85						90					95	
Asn	Ser	Asp	Gly	Ser	Glu	Phe	Gly	Ser	Asp	Val	Glu	Asp	Leu	Glu	Glu
			100					105					110		
Asp	Phe	Val	Val	Gln	Ala	Asn	Leu	Thr	Gln	Lys	Gly	Glu	Ser	Ser	Gly
	115						120					125			
Val	Ser	Asn	Gly	Glu	Leu	Glu	Phe	Ser	Val	Arg	Arg	Glu	Val	Arg	Glu
	130					135						140			
Arg	Glu	Ser	Asp	Glu	Pro	Val	Ala	Glu	Asn	Pro	Arg	Val	Pro	Arg	Gln
145				150						155					160
Ile	Asp	Glu	Leu	Phe	Asp	Gln	Leu	Glu	Leu	Asn	Glu	Tyr	Gly	Ser	Asp
			165						170					175	
Ser	Asp	Gly	Asp	Gly	Tyr	Ile	Ala	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Glu
		180						185					190		
Glu	Asp	Phe	Met	Ala	Gln	Glu	Val	Gln	Asn	Leu	Ile	His	Gly	Lys	Ala
	195					200						205			
Lys	Asp	Tyr	Glu	Leu	Glu	Glu	Lys	Tyr	Met	Asn	Pro	Ala	Asp	Ile	Leu
	210					215					220				
Lys	Asn	Ser	Asp	Ser	Val	Arg	Asp	Lys	Glu	Glu	Val	Asp	Thr	Ala	Ala
225				230						235					240
His	Val	Ile	Arg	Arg	Thr	Val	Glu	Tyr	Gly	Glu	Asn	Phe	Asp	Asn	Gly
			245						250					255	
Asn	Glu	Asp	Glu	Phe	Val	Glu	Leu	Thr	Glu	Glu	Ser	Ser	Asp	Glu	Ser
		260						265					270		
Glu	Lys	His	Asp	Cys	Glu	Thr	Ile	Val	Ser	Thr	Tyr	Ser	Asn	Leu	Asp
		275					280					285			
Asn	Leu	Pro	Gly	Lys	Ile	Leu	Ala	Ala	Glu	Ser	Ala	Arg	Gln	Lys	Lys
	290					295					300				
Leu	Ser	Glu	Thr	Leu	Ala	Asn	Ala	Leu	Ser	Ser	Asn	Gly	Arg	Ile	Ile
305				310						315					320
Asn	Leu	Gln	Gly	Arg	Glu	Arg	Ile	Pro	Val	Glu	Phe	Leu	Pro	Gly	Arg
			325						330					335	
Arg	Ala	Glu	Gln	Thr	Asp	Val	Lys	Ala	Glu	Ile	Pro	Lys	Ala	Glu	Pro

```

          340          345          350
Ile Lys Arg Lys Thr His Gly Gln Glu Ser Lys Glu Glu Lys Lys Glu
          355          360          365
Arg Lys Asn Ala Val Lys Ala Glu Lys Arg Glu Ala Arg Ile Ile Lys
          370          375          380
Lys Gln Thr Lys Met Leu Tyr Cys Gly Glu Thr Gln Arg Ala Gln Arg
          385          390          395          400
Ala Val Ala Thr Ser Gly Pro Ser Ser Arg Pro Leu Lys
          405          410
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1601
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

aatcttcctc attcgaaggt tactcgcaact tcctctgcac acttcttcct ctccatctaa      60
cctcagttact cctacaatcc tctaagaatc catagatcta ctgctgggaa aagcttcgcg      120
acaatgtctt ggcctacgga ttctgagtta aattccataa aggaggcagt ggctcagatg      180
agtggaagag ataaaggaga agttcgagtg gtggtcgctc cttatcgtat atgtccttta      240
ggagctcaca ttgatcacca ggggtgaact gtatcagta tgacgattaa agggatcctt      300
cttggttttg ttccatcggg tgatactcag gtccagttgc gctctgcaca atttgaagga      360
gaagtatgtt tcagagtaga tgaaatccag cacccaatag gcctagcaaa caagaatggt      420
gcaagcacgc catctccatc gaaggaaaaa agtatctggg gtacttatgc cagaggagca      480
gtttatgcgt tacagagcag caaaaagaat ctcaaacagg gcattattgg ttacctcagt      540
ggctcaaagt gactagatag ctccgggctt agctcatcag ctgctgttgg tgtggcatag      600
ctgctagctc tagagaatgc aaacgaattg actgtatccc caacagaaaa tatcgaatat      660
gacaggctta ttgagaatgt gtatctgggt ctgcggaatg gaattttgga tcaatcagct      720
atthttgctt cgaattatgg gtgtctaaca tacatggact gcaagacttt ggaccacgag      780
cttgtacagg ctctgaact ggagaaaccg ttcaggatat tgtagcatt ctcaggcttg      840
aggcaggcgt tgaccaccaa cccaggatat aatctgcgag tttctgagtg tcaagaggca      900
gcaaaagtgc ttttgactgc atctgggaac agtgagctgg aacctacgtt gtgcaatgtt      960
gagcatgcgg tctatgaagc tcacaagcat gagctgaaac cggtttttagc taaaagagca     1020
gagcattatt tctcggagaa catgcgagtt atcaaaggac gggaagcctg ggcttcaggg     1080
aatcttgaag aatttggaag gctaatttca gcatccggct tgagttccat tgagaattac     1140
gaatgcggtg cggagccact gatccagcta tacaagattc ttctgaaggc tcctggtgta     1200
tatggagcta gattcagcgg tgcaggtttc aggggatgtt gtctagcctt tgtagatgca     1260
gtaaaagctg aggcagctgc ttcatatgtg aaggatgaat atgaaaaggc ccaaccgag      1320
tttgctaaca atctaaatgg aggaaaacct gttctcatct gtgaagcagg tgacgctgct      1380
cgtgttcttc tctgatcaat cctggagttt ttggtttctt cccacttaa actcgatttt      1440
tttgtccctt atatctctca cgcttattga ttctttgctt gtttatctct ttttgatcct      1500
gtctgagaaa ttctctggtc tctttggtcg gagtttcatc attgcttgat acattttttt      1560
tgctacaaat acataatgta aatcattctc taccgttttc c
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..423
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ser	Trp	Pro	Thr	Asp	Ser	Glu	Leu	Asn	Ser	Ile	Lys	Glu	Ala	Val
1				5					10					15	
Ala	Gln	Met	Ser	Gly	Arg	Asp	Lys	Gly	Glu	Val	Arg	Val	Val	Val	Ala
		20					25					30			
Pro	Tyr	Arg	Ile	Cys	Pro	Leu	Gly	Ala	His	Ile	Asp	His	Gln	Gly	Gly
	35					40					45				
Thr	Val	Ser	Ala	Met	Thr	Ile	Lys	Gly	Ile	Leu	Leu	Gly	Phe	Val	Pro
	50				55					60					
Ser	Gly	Asp	Thr	Gln	Val	Gln	Leu	Arg	Ser	Ala	Gln	Phe	Glu	Gly	Glu
65				70					75					80	
Val	Cys	Phe	Arg	Val	Asp	Glu	Ile	Gln	His	Pro	Ile	Gly	Leu	Ala	Asn
			85					90						95	
Lys	Asn	Gly	Ala	Ser	Thr	Pro	Ser	Pro	Ser	Lys	Glu	Lys	Ser	Ile	Trp
	100						105						110		
Gly	Thr	Tyr	Ala	Arg	Gly	Ala	Val	Tyr	Ala	Leu	Gln	Ser	Ser	Lys	Lys
	115						120					125			
Asn	Leu	Lys	Gln	Gly	Ile	Ile	Gly	Tyr	Leu	Ser	Gly	Ser	Asn	Gly	Leu
	130				135					140					
Asp	Ser	Ser	Gly	Leu	Ser	Ser	Ser	Ala	Ala	Val	Gly	Val	Ala	Tyr	Leu
145				150						155				160	
Leu	Ala	Leu	Glu	Asn	Ala	Asn	Glu	Leu	Thr	Val	Ser	Pro	Thr	Glu	Asn
			165					170						175	
Ile	Glu	Tyr	Asp	Arg	Leu	Ile	Glu	Asn	Val	Tyr	Leu	Gly	Leu	Arg	Asn
	180						185						190		
Gly	Ile	Leu	Asp	Gln	Ser	Ala	Ile	Leu	Leu	Ser	Asn	Tyr	Gly	Cys	Leu
	195						200					205			
Thr	Tyr	Met	Asp	Cys	Lys	Thr	Leu	Asp	His	Glu	Leu	Val	Gln	Ala	Pro
	210					215					220				
Glu	Leu	Glu	Lys	Pro	Phe	Arg	Ile	Leu	Leu	Ala	Phe	Ser	Gly	Leu	Arg
225				230						235				240	
Gln	Ala	Leu	Thr	Thr	Asn	Pro	Gly	Tyr	Asn	Leu	Arg	Val	Ser	Glu	Cys
			245						250					255	
Gln	Glu	Ala	Ala	Lys	Val	Leu	Leu	Thr	Ala	Ser	Gly	Asn	Ser	Glu	Leu
	260						265						270		
Glu	Pro	Thr	Leu	Cys	Asn	Val	Glu	His	Ala	Val	Tyr	Glu	Ala	His	Lys
	275						280					285			
His	Glu	Leu	Lys	Pro	Val	Leu	Ala	Lys	Arg	Ala	Glu	His	Tyr	Phe	Ser
	290					295					300				
Glu	Asn	Met	Arg	Val	Ile	Lys	Gly	Arg	Glu	Ala	Trp	Ala	Ser	Gly	Asn
305				310						315				320	
Leu	Glu	Glu	Phe	Gly	Lys	Leu	Ile	Ser	Ala	Ser	Gly	Leu	Ser	Ser	Ile
			325						330					335	
Glu	Asn	Tyr	Glu	Cys	Gly	Ala	Glu	Pro	Leu	Ile	Gln	Leu	Tyr	Lys	Ile
	340						345					350			
Leu	Leu	Lys	Ala	Pro	Gly	Val	Tyr	Gly	Ala	Arg	Phe	Ser	Gly	Ala	Gly
	355						360					365			
Phe	Arg	Gly	Cys	Cys	Leu	Ala	Phe	Val	Asp	Ala	Val	Lys	Ala	Glu	Ala
	370					375					380				
Ala	Ala	Ser	Tyr	Val	Lys	Asp	Glu	Tyr	Glu	Lys	Ala	Gln	Pro	Glu	Phe
385				390						395				400	
Ala	Asn	Asn	Leu	Asn	Gly	Gly	Lys	Pro	Val	Leu	Ile	Cys	Glu	Ala	Gly
			405						410					415	
Asp	Ala	Ala	Arg	Val	Leu	Leu									
			420												

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid


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      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..405
      (D) OTHER INFORMATION: / Ceres Seq. ID 1481546
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

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[illegible]

405

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1481547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met	Thr	Ile	Lys	Gly	Ile	Leu	Leu	Gly	Phe	Val	Pro	Ser	Gly	Asp	Thr
1				5					10					15	
Gln	Val	Gln	Leu	Arg	Ser	Ala	Gln	Phe	Glu	Gly	Glu	Val	Cys	Phe	Arg
			20					25					30		
Val	Asp	Glu	Ile	Gln	His	Pro	Ile	Gly	Leu	Ala	Asn	Lys	Asn	Gly	Ala
			35				40					45			
Ser	Thr	Pro	Ser	Pro	Ser	Lys	Glu	Lys	Ser	Ile	Trp	Gly	Thr	Tyr	Ala
			50			55					60				
Arg	Gly	Ala	Val	Tyr	Ala	Leu	Gln	Ser	Ser	Lys	Lys	Asn	Leu	Lys	Gln
65					70					75				80	
Gly	Ile	Ile	Gly	Tyr	Leu	Ser	Gly	Ser	Asn	Gly	Leu	Asp	Ser	Ser	Gly
				85					90					95	
Leu	Ser	Ser	Ser	Ala	Ala	Val	Gly	Val	Ala	Tyr	Leu	Leu	Ala	Leu	Glu
			100					105					110		
Asn	Ala	Asn	Glu	Leu	Thr	Val	Ser	Pro	Thr	Glu	Asn	Ile	Glu	Tyr	Asp
			115				120						125		
Arg	Leu	Ile	Glu	Asn	Val	Tyr	Leu	Gly	Leu	Arg	Asn	Gly	Ile	Leu	Asp
			130				135					140			
Gln	Ser	Ala	Ile	Leu	Leu	Ser	Asn	Tyr	Gly	Cys	Leu	Thr	Tyr	Met	Asp
145					150					155				160	
Cys	Lys	Thr	Leu	Asp	His	Glu	Leu	Val	Gln	Ala	Pro	Glu	Leu	Glu	Lys
				165					170					175	
Pro	Phe	Arg	Ile	Leu	Leu	Ala	Phe	Ser	Gly	Leu	Arg	Gln	Ala	Leu	Thr
			180					185					190		
Thr	Asn	Pro	Gly	Tyr	Asn	Leu	Arg	Val	Ser	Glu	Cys	Gln	Glu	Ala	Ala
			195				200					205			
Lys	Val	Leu	Leu	Thr	Ala	Ser	Gly	Asn	Ser	Glu	Leu	Glu	Pro	Thr	Leu
			210			215					220				
Cys	Asn	Val	Glu	His	Ala	Val	Tyr	Glu	Ala	His	Lys	His	Glu	Leu	Lys
225					230					235				240	
Pro	Val	Leu	Ala	Lys	Arg	Ala	Glu	His	Tyr	Phe	Ser	Glu	Asn	Met	Arg
				245					250					255	
Val	Ile	Lys	Gly	Arg	Glu	Ala	Trp	Ala	Ser	Gly	Asn	Leu	Glu	Glu	Phe
			260					265					270		
Gly	Lys	Leu	Ile	Ser	Ala	Ser	Gly	Leu	Ser	Ser	Ile	Glu	Asn	Tyr	Glu
			275				280						285		
Cys	Gly	Ala	Glu	Pro	Leu	Ile	Gln	Leu	Tyr	Lys	Ile	Leu	Leu	Lys	Ala
			290			295					300				
Pro	Gly	Val	Tyr	Gly	Ala	Arg	Phe	Ser	Gly	Ala	Gly	Phe	Arg	Gly	Cys
305					310					315				320	
Cys	Leu	Ala	Phe	Val	Asp	Ala	Val	Lys	Ala	Glu	Ala	Ala	Ala	Ser	Tyr
				325					330					335	
Val	Lys	Asp	Glu	Tyr	Glu	Lys	Ala	Gln	Pro	Glu	Phe	Ala	Asn	Asn	Leu
			340					345					350		
Asn	Gly	Gly	Lys	Pro	Val	Leu	Ile	Cys	Glu	Ala	Gly	Asp	Ala	Ala	Arg
			355				360						365		

Val Leu Leu
370

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..915
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

caaaagagag	aaaaggatgg	tcaataacgg	tccatgatct	ctccggttca	cccgtggcta	60
tggcctctat	ggtaacacct	ttcgtacct	ctcctggttc	gaaccgggtg	actcgggtcaa	120
gtcccggagc	gtggcttatt	cttcgacctg	acggttgac	atggaagcca	tggggaagac	180
tagaagcatg	gcgtgaggct	ggttactctg	acactctagg	ttatcgtttc	gagcttttcc	240
aagacggtat	agccaccgca	gtttctgcat	cgctcgat	cagtttgaaa	aatggcggga	300
gttttggtat	tgatgttacc	ggcgggtaca	gcacaacggc	gtctacgccg	acaacgagtc	360
ctcaaggaag	ctgggatctc	ggatccgggt	caagcgccgg	ttcaagaccc	gcgtcgagac	420
caggatcagg	atccgggtcg	gatttcggat	atctactacc	gcaacatccg	tctgcggccg	480
cgcaaaacag	agggttcggt	atgtcggcta	cggttgaaag	agttgggaaa	cgaagcaaac	540
cagaagtaga	agtcgggtgtg	acgcacgtga	catgtacgga	ggatgcagca	gcgcacgtgg	600
cattagctgc	ggcgggtgat	ctgagtttgg	atgcttgacg	gcttttctca	cacaagctaa	660
ggaaagagct	gagacagcaa	agccagcttg	gtgtcggttg	acttggttcg	ctttgtcggt	720
ttaccaattc	atgagttgtc	ttccactcac	atttttttgg	tttgaatttt	ctattttttt	780
ctttttaaga	tagcgtagg	aattagccag	ccattttttt	gagaggtgga	tgtcatcatt	840
attaaaaatt	gttaatatct	ttctcagtac	agctaagaaa	tgacagtaac	aactaacaaa	900
caactcatta	tctcc					

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Lys	Glu	Arg	Lys	Gly	Trp	Ser	Ile	Thr	Val	His	Asp	Leu	Ser	Gly	Ser
1			5					10					15		
Pro	Val	Ala	Met	Ala	Ser	Met	Val	Thr	Pro	Phe	Val	Pro	Ser	Pro	Gly
			20					25				30			
Ser	Asn	Arg	Val	Thr	Arg	Ser	Ser	Pro	Gly	Ala	Trp	Leu	Ile	Leu	Arg
			35				40				45				
Pro	Asp	Gly	Cys	Thr	Trp	Lys	Pro	Trp	Gly	Arg	Leu	Glu	Ala	Trp	Arg
			50			55				60					
Glu	Ala	Gly	Tyr	Ser	Asp	Thr	Leu	Gly	Tyr	Arg	Phe	Glu	Leu	Phe	Gln
					70				75					80	
Asp	Gly	Ile	Ala	Thr	Ala	Val	Ser	Ala	Ser	Ser	Ser	Ile	Ser	Leu	Lys
				85				90					95		
Asn	Gly	Gly	Ser	Phe	Val	Ile	Asp	Val	Thr	Gly	Gly	Thr	Ser	Thr	Thr
				100				105				110			
Ala	Ser	Thr	Pro	Thr	Thr	Ser	Pro	Gln	Gly	Ser	Trp	Asp	Leu	Gly	Ser
				115			120					125			
Gly	Ser	Ser	Ala	Gly	Ser	Arg	Pro	Ala	Ser	Arg	Pro	Gly	Ser	Gly	Ser

130	135	140
Gly Ser Asp Phe Gly Tyr Leu Leu Pro Gln His Pro Ser Ala Ala Ala		
145	150	155
Gln Asn Arg Gly Phe Val Met Ser Ala Thr Val Glu Gly Val Gly Lys		160
	165	170
Arg Ser Lys Pro Glu Val Glu Val Gly Val Thr His Val Thr Cys Thr		175
	180	185
Glu Asp Ala Ala His Val Ala Leu Ala Ala Ala Val Asp Leu Ser		190
	195	200
Leu Asp Ala Cys Arg Leu Phe Ser His Lys Leu Arg Lys Glu Leu Arg		205
	210	215
Gln Gln Ser Gln Leu Gly Val Val		220
225	230	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1481566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Ala Ser Met Val Thr Pro Phe Val Pro Ser Pro Gly Ser Asn Arg		
1	5	10
Val Thr Arg Ser Ser Pro Gly Ala Trp Leu Ile Leu Arg Pro Asp Gly		15
	20	25
Cys Thr Trp Lys Pro Trp Gly Arg Leu Glu Ala Trp Arg Glu Ala Gly		30
	35	40
Tyr Ser Asp Thr Leu Gly Tyr Arg Phe Glu Leu Phe Gln Asp Gly Ile		45
	50	55
Ala Thr Ala Val Ser Ala Ser Ser Ser Ile Ser Leu Lys Asn Gly Gly		60
65	70	75
Ser Phe Val Ile Asp Val Thr Gly Gly Thr Ser Thr Thr Ala Ser Thr		80
	85	90
Pro Thr Thr Ser Pro Gln Gly Ser Trp Asp Leu Gly Ser Gly Ser Ser		95
	100	105
Ala Gly Ser Arg Pro Ala Ser Arg Pro Gly Ser Gly Ser Gly Ser Asp		110
	115	120
Phe Gly Tyr Leu Leu Pro Gln His Pro Ser Ala Ala Ala Gln Asn Arg		125
	130	135
Gly Phe Val Met Ser Ala Thr Val Glu Gly Val Gly Lys Arg Ser Lys		140
145	150	155
Pro Glu Val Glu Val Gly Val Thr His Val Thr Cys Thr Glu Asp Ala		160
	165	170
Ala Ala His Val Ala Leu Ala Ala Ala Val Asp Leu Ser Leu Asp Ala		175
	180	185
Cys Arg Leu Phe Ser His Lys Leu Arg Lys Glu Leu Arg Gln Gln Ser		190
	195	200
Gln Leu Gly Val Val		205
210		

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..210
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
Met Val Thr Pro Phe Val Pro Ser Pro Gly Ser Asn Arg Val Thr Arg
1          5          10          15
Ser Ser Pro Gly Ala Trp Leu Ile Leu Arg Pro Asp Gly Cys Thr Trp
20          25          30
Lys Pro Trp Gly Arg Leu Glu Ala Trp Arg Glu Ala Gly Tyr Ser Asp
35          40          45
Thr Leu Gly Tyr Arg Phe Glu Leu Phe Gln Asp Gly Ile Ala Thr Ala
50          55          60
Val Ser Ala Ser Ser Ser Ile Ser Leu Lys Asn Gly Gly Ser Phe Val
65          70          75          80
Ile Asp Val Thr Gly Thr Ser Thr Thr Ala Ser Thr Pro Thr Thr
85          90          95
Ser Pro Gln Gly Ser Trp Asp Leu Gly Ser Gly Ser Ser Ala Gly Ser
100         105         110
Arg Pro Ala Ser Arg Pro Gly Ser Gly Ser Gly Ser Asp Phe Gly Tyr
115         120         125
Leu Leu Pro Gln His Pro Ser Ala Ala Ala Gln Asn Arg Gly Phe Val
130         135         140
Met Ser Ala Thr Val Glu Gly Val Gly Lys Arg Ser Lys Pro Glu Val
145         150         155         160
Glu Val Gly Val Thr His Val Thr Cys Thr Glu Asp Ala Ala Ala His
165         170         175
Val Ala Leu Ala Ala Ala Val Asp Leu Ser Leu Asp Ala Cys Arg Leu
180         185         190
Phe Ser His Lys Leu Arg Lys Glu Leu Arg Gln Gln Ser Gln Leu Gly
195         200         205
Val Val
210
```

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1330
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
atcccaaagt ctcctaaggc gagaagggat cgggtcgctg cactagggttt ccttttcttt      60
tttttttttg gtttcaaatt ttttcatcat atctcctgaa aatcttcttc attcgctcc      120
aattttgctc atgttcgtcc gatccaacat tcttcgtgct ctgattttta ctgtgctgga      180
aacagttacc tcctcttgat tcagttttga ttcttcaaag cctcagagat aatttggttt      240
tctctaattc cttgtaagga gaaaacttgc ttggagatca aaatgatgca ttcaagctgc      300
aaaggacttg tgctgcttct attcttattt gtcgttgat tcattggaaa caccgatgcg      360
aatgctcagt gggagggttt acataaagta agagcttctc cccatgaaaa catgggacgt      420
aatgttattg acggaagtgg tgtagagaaa acgttacatg acattggaat gggtgaaaag      480
agaggcactc acaacaaagt ttcagtctca acagttgcgt tgttcacctt ggctatggct      540
gctgccactg ggtaggtgct tgtgcccttc ttctttggtg agcttgatcc tcaatgggct      600
ggaatttgca atggcatggc tgctggttga tgttggccgc tagctttgat cttgttaagg      660
aagggcagga acatggctct ggaaactggg ttgttactgg gatcctagcc ggtgctttgt      720
tcatttggct ctgtaagcag attcttgaac aatatggtga agttagtatg ctggatatta      780
```

aaggcgcaga	tgcaactaaa	gttggttctcg	tcataggaat	tatgacactt	cattcttttcg	840
gggaaggatc	aggggttggt	gtatcattcg	ctggctcaaa	agggttttagc	caagggcttc	900
tggtcacttt	ggccatagct	gttcataaca	ttccagaagg	gttggtctgtt	agcatgggtg	960
tggtcatcaag	gggtgtctct	ccacaaaatg	ccatgctctg	gagtataata	acatccttac	1020
ctcagcctct	cgtcgccgtg	ccagcttttt	tatgcgctga	tgcgttcagc	aagtttttgc	1080
ctttttgcac	tggatttgct	gccggatgca	tgatttggat	ggttattgct	gaagtgtctc	1140
ctgatgcttt	taaggaagcg	tctccttcgc	aagtggcatc	tgcagccacc	atatcagtag	1200
catccatgga	agctcttagc	actcttttgc	agagtttcac	acatgattac	aactcagagg	1260
atgcttctgg	cttcttcgtt	tcactcctct	ttggtctggg	tccattgctt	gggggagtat	1320
ttctggttgc						

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met	Gly	Trp	Asn	Leu	Gln	Trp	His	Gly	Cys	Trp	Leu	Met	Leu	Ala	Ala	
1				5					10					15		
Ser	Phe	Asp	Leu	Val	Lys	Glu	Gly	Gln	Glu	His	Gly	Ser	Gly	Asn	Trp	
			20					25					30			
Val	Val	Thr	Gly	Ile	Leu	Ala	Gly	Ala	Leu	Phe	Ile	Trp	Leu	Cys	Lys	
			35					40				45				
Gln	Ile	Leu	Glu	Gln	Tyr	Gly	Glu	Val	Ser	Met	Leu	Asp	Ile	Lys	Gly	
			50				55				60					
Ala	Asp	Ala	Thr	Lys	Val	Val	Leu	Val	Ile	Gly	Ile	Met	Thr	Leu	His	
65					70					75				80		
Ser	Phe	Gly	Glu	Gly	Ser	Gly	Val	Gly	Val	Ser	Phe	Ala	Gly	Ser	Lys	
				85					90					95		
Gly	Phe	Ser	Gln	Gly	Leu	Leu	Val	Thr	Leu	Ala	Ile	Ala	Val	His	Asn	
			100					105					110			
Ile	Pro	Glu	Gly	Leu	Ala	Val	Ser	Met	Val	Leu	Ala	Ser	Arg	Gly	Val	
			115					120					125			
Ser	Pro	Gln	Asn	Ala	Met	Leu	Trp	Ser	Ile	Ile	Thr	Ser	Leu	Pro	Gln	
			130			135					140					
Pro	Leu	Val	Ala	Val	Pro	Ala	Phe	Leu	Cys	Ala	Asp	Ala	Phe	Ser	Lys	
145					150					155				160		
Phe	Leu	Pro	Phe	Cys	Thr	Gly	Phe	Ala	Ala	Gly	Cys	Met	Ile	Trp	Met	
				165					170					175		
Val	Ile	Ala	Glu	Val	Leu	Pro	Asp	Ala	Phe	Lys	Glu	Ala	Ser	Pro	Ser	
			180					185					190			
Gln	Val	Ala	Ser	Ala	Ala	Thr	Ile	Ser	Val	Ala	Ser	Met	Glu	Ala	Leu	
			195				200					205				
Ser	Thr	Leu	Phe	Glu	Ser	Phe	Thr	His	Asp	Tyr	Asn	Ser	Glu	Asp	Ala	
			210				215				220					
Ser	Gly	Phe	Phe	Val	Ser	Leu	Leu	Phe	Gly	Leu	Gly	Pro	Leu	Leu	Gly	
225					230					235					240	
Gly	Val	Phe	Leu	Val												
				245												

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..233
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481582
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Leu Ala Ala Ser Phe Asp Leu Val Lys Glu Gly Gln Glu His Gly
1 5 10 15
Ser Gly Asn Trp Val Val Thr Gly Ile Leu Ala Gly Ala Leu Phe Ile
 20 25 30
Trp Leu Cys Lys Gln Ile Leu Glu Gln Tyr Gly Glu Val Ser Met Leu
 35 40 45
Asp Ile Lys Gly Ala Asp Ala Thr Lys Val Val Leu Val Ile Gly Ile
50 55 60
Met Thr Leu His Ser Phe Gly Glu Gly Ser Gly Val Gly Val Ser Phe
65 70 75 80
Ala Gly Ser Lys Gly Phe Ser Gln Gly Leu Leu Val Thr Leu Ala Ile
 85 90 95
Ala Val His Asn Ile Pro Glu Gly Leu Ala Val Ser Met Val Leu Ala
 100 105 110
Ser Arg Gly Val Ser Pro Gln Asn Ala Met Leu Trp Ser Ile Ile Thr
115 120 125
Ser Leu Pro Gln Pro Leu Val Ala Val Pro Ala Phe Leu Cys Ala Asp
130 135 140
Ala Phe Ser Lys Phe Leu Pro Phe Cys Thr Gly Phe Ala Ala Gly Cys
145 150 155 160
Met Ile Trp Met Val Ile Ala Glu Val Leu Pro Asp Ala Phe Lys Glu
 165 170 175
Ala Ser Pro Ser Gln Val Ala Ser Ala Ala Thr Ile Ser Val Ala Ser
180 185 190
Met Glu Ala Leu Ser Thr Leu Phe Glu Ser Phe Thr His Asp Tyr Asn
195 200 205
Ser Glu Asp Ala Ser Gly Phe Phe Val Ser Leu Leu Phe Gly Leu Gly
210 215 220
Pro Leu Leu Gly Gly Val Phe Leu Val
225 230

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..187
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481583
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Leu Asp Ile Lys Gly Ala Asp Ala Thr Lys Val Val Leu Val Ile
1 5 10 15
Gly Ile Met Thr Leu His Ser Phe Gly Glu Gly Ser Gly Val Gly Val
 20 25 30
Ser Phe Ala Gly Ser Lys Gly Phe Ser Gln Gly Leu Leu Val Thr Leu
35 40 45
Ala Ile Ala Val His Asn Ile Pro Glu Gly Leu Ala Val Ser Met Val
50 55 60
Leu Ala Ser Arg Gly Val Ser Pro Gln Asn Ala Met Leu Trp Ser Ile
65 70 75 80

Ile Thr Ser Leu Pro Gln Pro Leu Val Ala Val Pro Ala Phe Leu Cys
85 90 95
Ala Asp Ala Phe Ser Lys Phe Leu Pro Phe Cys Thr Gly Phe Ala Ala
100 105 110
Gly Cys Met Ile Trp Met Val Ile Ala Glu Val Leu Pro Asp Ala Phe
115 120 125
Lys Glu Ala Ser Pro Ser Gln Val Ala Ser Ala Ala Thr Ile Ser Val
130 135 140
Ala Ser Met Glu Ala Leu Ser Thr Leu Phe Glu Ser Phe Thr His Asp
145 150 155 160
Tyr Asn Ser Glu Asp Ala Ser Gly Phe Phe Val Ser Leu Leu Phe Gly
165 170 175
Leu Gly Pro Leu Leu Gly Gly Val Phe Leu Val
180 185

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

acaatttctaa aaccctaatac tcacaaaaaa ccctaattctc acaaaaaccc tcctctcttc	60
atcgacatct ctcttttcaact gcttcaatgg cgtcttttga gcgttttgac gacatgtgtg	120
acctgagatt gaaacctaac attctccgaa accttctctc cgaatatgtt cccaacgaga	180
agcagcctct caccaacttt ctatcactct ccaaggttgt atcaaccatc tccacacaca	240
agctcttatac tgagtctcct ccagcttcaa ttgaccagaa gcttcatgct aaatcgaaat	300
cagccgttga tgattgggtt gctagattat cagctttgat ttcttctgat atgccggata	360
aaagctgggt gggtatttgt ttgattggag taacatgtca agaatgtagc tcagatcggt	420
tctttaagtc atactctgtt tggtttaaca gtttattatc acatcttaag aatccagcaa	480
gttctagaat tgtccgagtg gcttcatgta cctcaatctc tgatctactt acaaggctgt	540
ctagattttc gaatacgaag aaagatgcag ttccacacgc ttcgaaacta atcctgccta	600
tcattaaatt attggatgaa gattcttcag aagcactatt ggaaggcatt gtccatctgc	660
taagtacaat tgtactcttg tttcctgctg ccttccacag taattatgac aagattgaag	720
ccgctattgc ctccaaaata ttttcggcga aaaccagttc taatatgtta aagaaatttg	780
cccactttct agcattgctc cccaaagcta aagggtgacga gggcacctgg tccttgatga	840
tgcaaaagct gctgatatac ataaacgtac atttaaataa ttttttccaa ggtctagaag	900
aagaaacaaa aggaacaaaa gcaatccaac gattgactcc tcctggaaaa gactctcctt	960
tgccccctcg aggtcaaaaat gggggattgg atgatgcata atggaactct gaacaattga	1020
ttgtatccag agtttctgca cttatgttct gcacctcaac gatgttaact acctcgata	1080
aatccaagat taatattcca gttggctcat tgttatccct tgttgagcga gtgctgttgg	1140
tgaacggctc tctacctga gccatgtcac ccttcatgac	

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..392
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Asn Ser Lys Thr Leu Ile Ser Gln Lys Thr Leu Ile Ser Gln Lys Pro

1		5		10		15
Ser	Ser	Leu	His	Arg	His	Leu
		20				25
Glu	Arg	Phe	Asp	Asp	Met	Cys
		35				40
Arg	Asn	Leu	Leu	Ser	Glu	Tyr
		50				55
Asn	Phe	Leu	Ser	Leu	Ser	Lys
		65				70
Leu	Leu	Ser	Glu	Ser	Pro	Pro
						85
Lys	Ser	Lys	Ser	Ala	Val	Asp
						100
Ile	Ser	Ser	Asp	Met	Pro	Asp
						115
Gly	Val	Thr	Cys	Gln	Glu	Cys
						130
Ser	Val	Trp	Phe	Asn	Ser	Leu
						145
Ser	Arg	Ile	Val	Arg	Val	Ala
						160
Thr	Arg	Leu	Ser	Arg	Phe	Ser
						180
Ala	Ser	Lys	Leu	Ile	Leu	Pro
						195
Ser	Glu	Ala	Leu	Leu	Glu	Gly
						210
Leu	Leu	Phe	Pro	Ala	Ala	Phe
						225
Ala	Ile	Ala	Ser	Lys	Ile	Phe
						240
Lys	Lys	Phe	Ala	His	Phe	Leu
						260
Glu	Gly	Thr	Trp	Ser	Leu	Met
						275
Val	His	Leu	Asn	Asn	Phe	Phe
						290
Thr	Lys	Ala	Ile	Gln	Arg	Leu
						305
Pro	Leu	Gly	Gly	Gln	Asn	Gly
						320
Glu	Gln	Leu	Ile	Val	Ser	Arg
						340
Thr	Met	Leu	Thr	Thr	Ser	Tyr
						355
Ser	Leu	Leu	Ser	Leu	Val	Glu
						370
Pro	Arg	Ala	Met	Ser	Pro	Phe
						385

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1481598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Ala	Ser	Phe	Glu	Arg	Phe	Asp	Asp	Met	Cys	Asp	Leu	Arg	Leu	Lys
1				5					10					15	
Pro	Asn	Ile	Leu	Arg	Asn	Leu	Leu	Ser	Glu	Tyr	Val	Pro	Asn	Glu	Lys
		20						25					30		
Gln	Pro	Leu	Thr	Asn	Phe	Leu	Ser	Leu	Ser	Lys	Val	Val	Ser	Thr	Ile
		35						40				45			
Ser	Thr	His	Lys	Leu	Leu	Ser	Glu	Ser	Pro	Pro	Ala	Ser	Ile	Asp	Gln
	50						55				60				
Lys	Leu	His	Ala	Lys	Ser	Lys	Ser	Ala	Val	Asp	Asp	Trp	Val	Ala	Arg
65					70					75					80
Leu	Ser	Ala	Leu	Ile	Ser	Ser	Asp	Met	Pro	Asp	Lys	Ser	Trp	Val	Gly
				85					90					95	
Ile	Cys	Leu	Ile	Gly	Val	Thr	Cys	Gln	Glu	Cys	Ser	Ser	Asp	Arg	Phe
		100						105					110		
Phe	Lys	Ser	Tyr	Ser	Val	Trp	Phe	Asn	Ser	Leu	Leu	Ser	His	Leu	Lys
		115						120					125		
Asn	Pro	Ala	Ser	Ser	Arg	Ile	Val	Arg	Val	Ala	Ser	Cys	Thr	Ser	Ile
	130					135						140			
Ser	Asp	Leu	Leu	Thr	Arg	Leu	Ser	Arg	Phe	Ser	Asn	Thr	Lys	Lys	Asp
145					150					155					160
Ala	Val	Ser	His	Ala	Ser	Lys	Leu	Ile	Leu	Pro	Ile	Ile	Lys	Leu	Leu
				165					170					175	
Asp	Glu	Asp	Ser	Ser	Glu	Ala	Leu	Leu	Glu	Gly	Ile	Val	His	Leu	Leu
		180						185					190		
Ser	Thr	Ile	Val	Leu	Leu	Phe	Pro	Ala	Ala	Phe	His	Ser	Asn	Tyr	Asp
		195					200						205		
Lys	Ile	Glu	Ala	Ala	Ile	Ala	Ser	Lys	Ile	Phe	Ser	Ala	Lys	Thr	Ser
	210					215					220				
Ser	Asn	Met	Leu	Lys	Lys	Phe	Ala	His	Phe	Leu	Ala	Leu	Leu	Pro	Lys
225					230					235					240
Ala	Lys	Gly	Asp	Glu	Gly	Thr	Trp	Ser	Leu	Met	Met	Gln	Lys	Leu	Leu
			245						250					255	
Ile	Ser	Ile	Asn	Val	His	Leu	Asn	Asn	Phe	Phe	Gln	Gly	Leu	Glu	Glu
		260					265						270		
Glu	Thr	Lys	Gly	Thr	Lys	Ala	Ile	Gln	Arg	Leu	Thr	Pro	Pro	Gly	Lys
		275					280						285		
Asp	Ser	Pro	Leu	Pro	Leu	Gly	Gly	Gln	Asn	Gly	Gly	Leu	Asp	Asp	Ala
	290					295					300				
Ser	Trp	Asn	Ser	Glu	Gln	Leu	Ile	Val	Ser	Arg	Val	Ser	Ala	Leu	Met
305					310					315					320
Phe	Cys	Thr	Ser	Thr	Met	Leu	Thr	Thr	Ser	Tyr	Lys	Ser	Lys	Ile	Asn
				325					330					335	
Ile	Pro	Val	Gly	Ser	Leu	Leu	Ser	Leu	Val	Glu	Arg	Val	Leu	Leu	Val
		340						345					350		
Asn	Gly	Ser	Leu	Pro	Arg	Ala	Met	Ser	Pro	Phe	Met				
		355					360								

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1481599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met Cys Asp Leu Arg Leu Lys Pro Asn Ile Leu Arg Asn Leu Leu Ser
1 5 10 15
Glu Tyr Val Pro Asn Glu Lys Gln Pro Leu Thr Asn Phe Leu Ser Leu
20 25 30
Ser Lys Val Val Ser Thr Ile Ser Thr His Lys Leu Leu Ser Glu Ser
35 40 45
Pro Pro Ala Ser Ile Asp Gln Lys Leu His Ala Lys Ser Lys Ser Ala
50 55 60
Val Asp Asp Trp Val Ala Arg Leu Ser Ala Leu Ile Ser Ser Asp Met
65 70 75 80
Pro Asp Lys Ser Trp Val Gly Ile Cys Leu Ile Gly Val Thr Cys Gln
85 90 95
Glu Cys Ser Ser Asp Arg Phe Phe Lys Ser Tyr Ser Val Trp Phe Asn
100 105 110
Ser Leu Leu Ser His Leu Lys Asn Pro Ala Ser Ser Arg Ile Val Arg
115 120 125
Val Ala Ser Cys Thr Ser Ile Ser Asp Leu Leu Thr Arg Leu Ser Arg
130 135 140
Phe Ser Asn Thr Lys Lys Asp Ala Val Ser His Ala Ser Lys Leu Ile
145 150 155 160
Leu Pro Ile Ile Lys Leu Leu Asp Glu Asp Ser Ser Glu Ala Leu Leu
165 170 175
Glu Gly Ile Val His Leu Leu Ser Thr Ile Val Leu Leu Phe Pro Ala
180 185 190
Ala Phe His Ser Asn Tyr Asp Lys Ile Glu Ala Ala Ile Ala Ser Lys
195 200 205
Ile Phe Ser Ala Lys Thr Ser Ser Asn Met Leu Lys Lys Phe Ala His
210 215 220
Phe Leu Ala Leu Leu Pro Lys Ala Lys Gly Asp Glu Gly Thr Trp Ser
225 230 235 240
Leu Met Met Gln Lys Leu Leu Ile Ser Ile Asn Val His Leu Asn Asn
245 250 255
Phe Phe Gln Gly Leu Glu Glu Glu Thr Lys Gly Thr Lys Ala Ile Gln
260 265 270
Arg Leu Thr Pro Pro Gly Lys Asp Ser Pro Leu Pro Leu Gly Gly Gln
275 280 285
Asn Gly Gly Leu Asp Asp Ala Ser Trp Asn Ser Glu Gln Leu Ile Val
290 295 300
Ser Arg Val Ser Ala Leu Met Phe Cys Thr Ser Thr Met Leu Thr Thr
305 310 315 320
Ser Tyr Lys Ser Lys Ile Asn Ile Pro Val Gly Ser Leu Leu Ser Leu
325 330 335
Val Glu Arg Val Leu Leu Val Asn Gly Ser Leu Pro Arg Ala Met Ser
340 345 350
Pro Phe Met
355

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1724
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

attcaacctc	tctacttcag	tttctctgtc	cccatTTTTc	atctgagagt	taaaactgta	60
acctcaaaat	ctgagataaa	gtcaaaaaaa	aaacccaggt	ttatgattct	cattttctct	120
ttataatcga	aagcttcgat	ttttaacaaa	accagaatc	tgtgttcttg	tttttttttt	180
tttttggtga	gagttatctt	tttttttttt	ggaatatggg	gtgagaatct	gagtaatggg	240
atttacataa	aatattctat	gtaaabacta	aaataatctg	gaaattatta	aatttccaaa	300
ctttgtgttc	cattttgtgg	actcaaattt	gtttataaag	atctcaaatc	agagagattg	360
agacgaccaa	gaacaagcag	aagaagaaga	agaattgaga	gaatgtgggt	gtgggtcttct	420
tcaactaaa	gtcgttcgaa	tctggagagg	tttcttttag	gaatcactcc	taagcctcct	480
tccttctctc	ttcctcagga	acagggaag	gaggagattg	agtatttcag	gcttgatgat	540
ctctgggatt	gttatgatga	gatgagtgcg	tatggctttg	gcacacaggt	tgatttaaac	600
aatggcgaaa	ccgttatgca	gtactacgtc	ccgtacctat	ccgctatcca	aatccacact	660
aacaaacccg	ccttgctttc	caggaaccag	aatgaggtgg	ctgaatctga	gagtagcgag	720
ggttggagcg	atagtgaag	tgaaaagttg	ttgtcaaggt	caatgagcaa	tgattcaagc	780
aaaacatggg	atgctgtctc	tgaagattcg	gttttcgatc	cggatgggtc	accgttgctg	840
aaagatagac	ttggtaacct	tgactttaag	tacattgaaa	gagatcctcc	gcacaagcgg	900
attcccttaa	ccgacaagat	aaacgtattg	gtggagaaat	atccgggact	catgacctta	960
aggagtgtcg	acatgtctcc	tgcaagttgg	atggctgttg	cgtgggtacc	gatataccac	1020
atcccaacct	gcagggaacg	gaaagatttg	acgacagggt	tcctaactta	tcatactcta	1080
tcttcgtctt	ttcaagataa	tgtgggtgaa	ggagatcaaa	gcaacaacaa	tgaagaaaca	1140
gagttttgtg	aagattccgt	aataaacaag	agaatgccat	tgctccggtt	tggtgtaaca	1200
acttacaaaa	tgcaaggaga	tctttggggg	aagacggggg	ttgaccagga	ccggttgctt	1260
tatcttcaaa	gcgctgcgga	ttcatggctg	aaacagctca	atgttgatca	ccatgactat	1320
aacttcttcc	ttaaactcgag	cttctaaaga	tcaatcgggt	cgttcgtatg	tttatccttc	1380
tccaaacctt	aaacaaaaaa	aaaaagacct	cataaccctt	tttctttggt	gttttcaagc	1440
tccttttggt	tctctgtggt	ttttgttctt	tttggttttg	tctggctcgt	tgtgttggtt	1500
taggtagcaa	ccgccatcgc	ggagtttttt	ctccttttgc	aagccaatca	tggaagtttc	1560
taagaagaaa	acagagcttt	tttttctttt	tttttaacgg	tgttgagaaa	acaagaaagt	1620
tgttttcttt	tcttggtgga	gagatcatgt	aaattgacct	tgaacagagg	actctgtttt	1680
gtacttttct	gtctaaaata	tataaaaaaa	tctgtctttc	ttgt		

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1481614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met	Trp	Trp	Trp	Ser	Ser	Ser	Thr	Lys	Gly	Arg	Ser	Asn	Leu	Glu	Arg
1				5				10					15		
Phe	Leu	Leu	Gly	Ile	Thr	Pro	Lys	Pro	Pro	Ser	Phe	Ser	Leu	Pro	Gln
			20					25					30		
Glu	Gln	Gly	Lys	Glu	Glu	Ile	Glu	Tyr	Phe	Arg	Leu	Asp	Asp	Leu	Trp
			35					40					45		
Asp	Cys	Tyr	Asp	Glu	Met	Ser	Ala	Tyr	Gly	Phe	Gly	Thr	Gln	Val	Asp
	50					55					60				
Leu	Asn	Asn	Gly	Glu	Thr	Val	Met	Gln	Tyr	Tyr	Val	Pro	Tyr	Leu	Ser
65					70					75				80	
Ala	Ile	Gln	Ile	His	Thr	Asn	Lys	Pro	Ala	Leu	Leu	Ser	Arg	Asn	Gln
			85					90						95	
Asn	Glu	Val	Ala	Glu	Ser	Glu	Ser	Ser	Glu	Gly	Trp	Ser	Asp	Ser	Glu
			100					105					110		
Ser	Glu	Lys	Leu	Leu	Ser	Arg	Ser	Met	Ser	Asn	Asp	Ser	Ser	Lys	Thr
		115				120						125			
Trp	Asp	Ala	Val	Ser	Glu	Asp	Ser	Val	Phe	Asp	Pro	Asp	Gly	Ser	Pro
			130			135					140				

Leu Leu Lys Asp Arg Leu Gly Asn Leu Asp Phe Lys Tyr Ile Glu Arg
145 150 155 160
Asp Pro Pro His Lys Arg Ile Pro Leu Thr Asp Lys Ile Asn Val Leu
165 170 175
Val Glu Lys Tyr Pro Gly Leu Met Thr Leu Arg Ser Val Asp Met Ser
180 185 190
Pro Ala Ser Trp Met Ala Val Ala Trp Tyr Pro Ile Tyr His Ile Pro
195 200 205
Thr Cys Arg Asn Glu Lys Asp Leu Thr Thr Gly Phe Leu Thr Tyr His
210 215 220
Thr Leu Ser Ser Ser Phe Gln Asp Asn Val Val Glu Gly Asp Gln Ser
225 230 235 240
Asn Asn Asn Glu Glu Thr Glu Phe Cys Glu Asp Ser Val Ile Asn Lys
245 250 255
Arg Met Pro Leu Pro Pro Phe Gly Val Thr Thr Tyr Lys Met Gln Gly
260 265 270
Asp Leu Trp Gly Lys Thr Gly Phe Asp Gln Asp Arg Leu Leu Tyr Leu
275 280 285
Gln Ser Ala Ala Asp Ser Trp Leu Lys Gln Leu Asn Val Asp His His
290 295 300
Asp Tyr Asn Phe Phe Leu Asn Ser Ser Phe
305 310

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1481615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Ser Ala Tyr Gly Phe Gly Thr Gln Val Asp Leu Asn Asn Gly Glu
1 5 10 15
Thr Val Met Gln Tyr Tyr Val Pro Tyr Leu Ser Ala Ile Gln Ile His
20 25 30
Thr Asn Lys Pro Ala Leu Leu Ser Arg Asn Gln Asn Glu Val Ala Glu
35 40 45
Ser Glu Ser Ser Glu Gly Trp Ser Asp Ser Glu Ser Glu Lys Leu Leu
50 55 60
Ser Arg Ser Met Ser Asn Asp Ser Ser Lys Thr Trp Asp Ala Val Ser
65 70 75 80
Glu Asp Ser Val Phe Asp Pro Asp Gly Ser Pro Leu Leu Lys Asp Arg
85 90 95
Leu Gly Asn Leu Asp Phe Lys Tyr Ile Glu Arg Asp Pro Pro His Lys
100 105 110
Arg Ile Pro Leu Thr Asp Lys Ile Asn Val Leu Val Glu Lys Tyr Pro
115 120 125
Gly Leu Met Thr Leu Arg Ser Val Asp Met Ser Pro Ala Ser Trp Met
130 135 140
Ala Val Ala Trp Tyr Pro Ile Tyr His Ile Pro Thr Cys Arg Asn Glu
145 150 155 160
Lys Asp Leu Thr Thr Gly Phe Leu Thr Tyr His Thr Leu Ser Ser Ser
165 170 175
Phe Gln Asp Asn Val Val Glu Gly Asp Gln Ser Asn Asn Asn Glu Glu
180 185 190
Thr Glu Phe Cys Glu Asp Ser Val Ile Asn Lys Arg Met Pro Leu Pro

195	200	205
Pro Phe Gly Val Thr Thr Tyr Lys Met Gln Gly Asp Leu Trp Gly Lys		
210	215	220
Thr Gly Phe Asp Gln Asp Arg Leu Leu Tyr Leu Gln Ser Ala Ala Asp		
225	230	235
Ser Trp Leu Lys Gln Leu Asn Val Asp His His Asp Tyr Asn Phe Phe		
245	250	255
Leu Asn Ser Ser Phe		
260		

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1481616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Gln	Tyr	Tyr	Val	Pro	Tyr	Leu	Ser	Ala	Ile	Gln	Ile	His	Thr	Asn
1				5					10					15	
Lys	Pro	Ala	Leu	Leu	Ser	Arg	Asn	Gln	Asn	Glu	Val	Ala	Glu	Ser	Glu
			20					25					30		
Ser	Ser	Glu	Gly	Trp	Ser	Asp	Ser	Glu	Ser	Glu	Lys	Leu	Leu	Ser	Arg
		35					40					45			
Ser	Met	Ser	Asn	Asp	Ser	Ser	Lys	Thr	Trp	Asp	Ala	Val	Ser	Glu	Asp
		50				55				60					
Ser	Val	Phe	Asp	Pro	Asp	Gly	Ser	Pro	Leu	Leu	Lys	Asp	Arg	Leu	Gly
65				70					75					80	
Asn	Leu	Asp	Phe	Lys	Tyr	Ile	Glu	Arg	Asp	Pro	Pro	His	Lys	Arg	Ile
			85						90					95	
Pro	Leu	Thr	Asp	Lys	Ile	Asn	Val	Leu	Val	Glu	Lys	Tyr	Pro	Gly	Leu
			100					105					110		
Met	Thr	Leu	Arg	Ser	Val	Asp	Met	Ser	Pro	Ala	Ser	Trp	Met	Ala	Val
		115				120						125			
Ala	Trp	Tyr	Pro	Ile	Tyr	His	Ile	Pro	Thr	Cys	Arg	Asn	Glu	Lys	Asp
		130				135					140				
Leu	Thr	Thr	Gly	Phe	Leu	Thr	Tyr	His	Thr	Leu	Ser	Ser	Ser	Phe	Gln
145				150						155				160	
Asp	Asn	Val	Val	Glu	Gly	Asp	Gln	Ser	Asn	Asn	Asn	Glu	Glu	Thr	Glu
			165						170					175	
Phe	Cys	Glu	Asp	Ser	Val	Ile	Asn	Lys	Arg	Met	Pro	Leu	Pro	Pro	Phe
		180						185				190			
Gly	Val	Thr	Thr	Tyr	Lys	Met	Gln	Gly	Asp	Leu	Trp	Gly	Lys	Thr	Gly
		195				200						205			
Phe	Asp	Gln	Asp	Arg	Leu	Leu	Tyr	Leu	Gln	Ser	Ala	Ala	Asp	Ser	Trp
		210			215						220				
Leu	Lys	Gln	Leu	Asn	Val	Asp	His	His	Asp	Tyr	Asn	Phe	Phe	Leu	Asn
225				230						235				240	
Ser	Ser	Phe													

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1235

(D) OTHER INFORMATION: / Ceres Seq. ID 1481621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

attgacccaa	cgcttcttct	ccggcacgac	tgttcagagt	tcgattttcca	ttttcggggtc	60
gaaaggttga	ttttatttgg	attttggatg	gtagattcag	ttcctaaaca	taggaaactt	120
gaatctcaga	gtttttcgag	ttagggataa	gagaaagaaa	cacagttgga	gttatactga	180
tgaatggagg	aggctcgagt	agtttgcgtt	cagcattgtc	ctattgtgtg	cagcaagtac	240
gaaactatga	ctatcatcac	tacctctgtc	tccttgaact	cccaactgag	atgcgtaaag	300
cagcatttgc	tctccgggct	tttaatgtag	aaaccgcaag	agccatggat	gttgcatctg	360
atcccaaaaat	cggcttgatg	cggttacttt	ggtggcaaga	agcaattgac	aaactctaca	420
ccaaaaagcc	cataaaccat	ccagctgcac	aagctctgtc	ttgggcaata	tcagaacata	480
acatcagtaa	accttggcta	aaacgctcgg	ttgacgctag	aatccgagat	gccccaaagag	540
aagtagacga	tataccagag	agcattgcgg	agctagagaa	atacgcagaa	gacacagttt	600
ccactcttct	gtacaatata	ctccaagcag	gcggaattag	ttcaacaaca	gctgatcatg	660
cagcttcaca	cattggtaaa	gccagtggtc	ttgtcttgct	gcttaaatca	ttaccgtacc	720
actgtaccag	aaaccgtcac	cagagttaca	tccctgcaga	tctcgtctgag	aagcacgggt	780
tgctcgtgaa	acaaggtgga	cgattagaaa	ttcttctgga	taacgattca	agagaaggac	840
taagcaatgt	cgtgtttgag	attgcatctg	ttgccaatgc	acatctcctg	aaagcccgtg	900
aactggcggg	aaaggttcct	gcagaagcta	aaccggctact	gcttcattct	gtgccggtac	960
aagttcttct	ggattcggtt	aataaagtac	aattcgatgt	gtttgatccc	aggattcaaa	1020
gaggagttct	tggtgttcct	ccactcttgt	ttcagtttaa	actcaagtgg	tattcatgga	1080
gagcaatgtt	ttgaaaactt	gtctttatct	cccttttctt	gcctctttta	tttctggttt	1140
caaagacttt	acattaaact	ccagcttact	tgtatttctt	ttgtaataat	acaaaattac	1200
aaatggtgat	gaatacaaaa	taaagaattt	gttttc			

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1481622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met	Asn	Gly	Gly	Gly	Ser	Ser	Ser	Leu	Arg	Ser	Ala	Leu	Ser	Tyr	Cys
1				5					10					15	
Val	Gln	Gln	Val	Arg	Asn	Tyr	Asp	Tyr	His	His	Tyr	Leu	Cys	Leu	Leu
			20					25					30		
Glu	Leu	Pro	Thr	Glu	Met	Arg	Lys	Ala	Ala	Phe	Ala	Leu	Arg	Ala	Phe
			35				40					45			
Asn	Val	Glu	Thr	Ala	Arg	Ala	Met	Asp	Val	Ala	Ser	Asp	Pro	Lys	Ile
			50				55				60				
Gly	Leu	Met	Arg	Leu	Leu	Trp	Trp	Gln	Glu	Ala	Ile	Asp	Lys	Leu	Tyr
65					70				75					80	
Thr	Lys	Lys	Pro	Ile	Asn	His	Pro	Ala	Ala	Gln	Ala	Leu	Ser	Trp	Ala
				85					90					95	
Ile	Ser	Glu	His	Asn	Ile	Ser	Lys	Pro	Trp	Leu	Lys	Arg	Ser	Val	Asp
				100				105					110		
Ala	Arg	Ile	Arg	Asp	Ala	Gln	Arg	Glu	Val	Asp	Asp	Ile	Pro	Glu	Ser
				115			120					125			
Ile	Ala	Glu	Leu	Glu	Lys	Tyr	Ala	Glu	Asp	Thr	Val	Ser	Thr	Leu	Leu
				130			135					140			
Tyr	Asn	Thr	Leu	Gln	Ala	Gly	Gly	Ile	Ser	Ser	Thr	Thr	Ala	Asp	His
145					150					155					160

Ala	Ala	Ser	His	Ile	Gly	Lys	Ala	Ser	Gly	Leu	Val	Leu	Leu	Leu	Lys
				165					170					175	
Ser	Leu	Pro	Tyr	His	Cys	Thr	Arg	Asn	Arg	His	Gln	Ser	Tyr	Ile	Pro
			180					185					190		
Ala	Asp	Leu	Ala	Glu	Lys	His	Gly	Leu	Leu	Val	Lys	Gln	Gly	Gly	Arg
		195					200					205			
Leu	Glu	Ile	Leu	Leu	Asp	Asn	Asp	Ser	Arg	Glu	Gly	Leu	Ser	Asn	Val
	210					215					220				
Val	Phe	Glu	Ile	Ala	Ser	Val	Ala	Asn	Ala	His	Leu	Leu	Lys	Ala	Arg
225					230					235					240
Glu	Leu	Ala	Gly	Lys	Val	Pro	Ala	Glu	Ala	Lys	Pro	Val	Leu	Leu	His
				245					250					255	
Ser	Val	Pro	Val	Gln	Val	Leu	Leu	Asp	Ser	Leu	Asn	Lys	Val	Gln	Phe
			260					265					270		
Asp	Val	Phe	Asp	Pro	Arg	Ile	Gln	Arg	Gly	Val	Leu	Gly	Val	Pro	Pro
		275					280					285			
Leu	Leu	Phe	Gln	Phe	Lys	Leu	Lys	Trp	Tyr	Ser	Trp	Arg	Ala	Met	Phe
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1481623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Arg	Lys	Ala	Ala	Phe	Ala	Leu	Arg	Ala	Phe	Asn	Val	Glu	Thr	Ala
1			5						10					15	
Arg	Ala	Met	Asp	Val	Ala	Ser	Asp	Pro	Lys	Ile	Gly	Leu	Met	Arg	Leu
			20					25					30		
Leu	Trp	Trp	Gln	Glu	Ala	Ile	Asp	Lys	Leu	Tyr	Thr	Lys	Lys	Pro	Ile
		35					40					45			
Asn	His	Pro	Ala	Ala	Gln	Ala	Leu	Ser	Trp	Ala	Ile	Ser	Glu	His	Asn
	50					55					60				
Ile	Ser	Lys	Pro	Trp	Leu	Lys	Arg	Ser	Val	Asp	Ala	Arg	Ile	Arg	Asp
65					70					75				80	
Ala	Gln	Arg	Glu	Val	Asp	Asp	Ile	Pro	Glu	Ser	Ile	Ala	Glu	Leu	Glu
			85						90				95		
Lys	Tyr	Ala	Glu	Asp	Thr	Val	Ser	Thr	Leu	Leu	Tyr	Asn	Thr	Leu	Gln
			100					105					110		
Ala	Gly	Gly	Ile	Ser	Ser	Thr	Thr	Ala	Asp	His	Ala	Ala	Ser	His	Ile
		115					120						125		
Gly	Lys	Ala	Ser	Gly	Leu	Val	Leu	Leu	Leu	Lys	Ser	Leu	Pro	Tyr	His
		130				135					140				
Cys	Thr	Arg	Asn	Arg	His	Gln	Ser	Tyr	Ile	Pro	Ala	Asp	Leu	Ala	Glu
145					150					155				160	
Lys	His	Gly	Leu	Leu	Val	Lys	Gln	Gly	Gly	Arg	Leu	Glu	Ile	Leu	Leu
			165						170				175		
Asp	Asn	Asp	Ser	Arg	Glu	Gly	Leu	Ser	Asn	Val	Val	Phe	Glu	Ile	Ala
			180					185					190		
Ser	Val	Ala	Asn	Ala	His	Leu	Leu	Lys	Ala	Arg	Glu	Leu	Ala	Gly	Lys
		195					200					205			
Val	Pro	Ala	Glu	Ala	Lys	Pro	Val	Leu	Leu	His	Ser	Val	Pro	Val	Gln

210	215	220
Val Leu Leu Asp Ser Leu Asn Lys Val Gln Phe Asp Val Phe Asp Pro		
225	230	235
Arg Ile Gln Arg Gly Val Leu Gly Val Pro Pro Leu Leu Phe Gln Phe		240
	245	250
Lys Leu Lys Trp Tyr Ser Trp Arg Ala Met Phe		255
260	265	

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Asp Val Ala Ser Asp Pro Lys Ile Gly Leu Met Arg Leu Leu Trp
1 5 10 15
Trp Gln Glu Ala Ile Asp Lys Leu Tyr Thr Lys Lys Pro Ile Asn His
20 25 30
Pro Ala Ala Gln Ala Leu Ser Trp Ala Ile Ser Glu His Asn Ile Ser
35 40 45
Lys Pro Trp Leu Lys Arg Ser Val Asp Ala Arg Ile Arg Asp Ala Gln
50 55 60
Arg Glu Val Asp Asp Ile Pro Glu Ser Ile Ala Glu Leu Glu Lys Tyr
65 70 75 80
Ala Glu Asp Thr Val Ser Thr Leu Leu Tyr Asn Thr Leu Gln Ala Gly
85 90 95
Gly Ile Ser Ser Thr Thr Ala Asp His Ala Ala Ser His Ile Gly Lys
100 105 110
Ala Ser Gly Leu Val Leu Leu Leu Lys Ser Leu Pro Tyr His Cys Thr
115 120 125
Arg Asn Arg His Gln Ser Tyr Ile Pro Ala Asp Leu Ala Glu Lys His
130 135 140
Gly Leu Leu Val Lys Gln Gly Gly Arg Leu Glu Ile Leu Leu Asp Asn
145 150 155 160
Asp Ser Arg Glu Gly Leu Ser Asn Val Val Phe Glu Ile Ala Ser Val
165 170 175
Ala Asn Ala His Leu Leu Lys Ala Arg Glu Leu Ala Gly Lys Val Pro
180 185 190
Ala Glu Ala Lys Pro Val Leu Leu His Ser Val Pro Val Gln Val Leu
195 200 205
Leu Asp Ser Leu Asn Lys Val Gln Phe Asp Val Phe Asp Pro Arg Ile
210 215 220
Gln Arg Gly Val Leu Gly Val Pro Pro Leu Leu Phe Gln Phe Lys Leu
225 230 235 240
Lys Trp Tyr Ser Trp Arg Ala Met Phe
245

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1232

(D) OTHER INFORMATION: / Ceres Seq. ID 1481625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ctctctcgcg	ttcggttctta	tccacgagct	ctgcaccgtc	gcaatctccg	tcttctccat	60
ttagatccaa	cacagagcct	tttctacatg	aaattcggca	aagagtttcg	tactcacctc	120
gaagaaactt	taccagagt	gagagacaag	ttcctttgct	ataaaccttt	aaaaaagctt	180
ctcaaatatt	atccttatta	ctccgccgat	tttgaccg	ccaattccga	tcacaacgat	240
tcgcgtccag	tatttgctga	tactactaac	atctcttccg	cgcgcgacga	cggcggtgtg	300
gttcccggcg	tcaggccatc	ggaagatctc	cagggttcgt	ttgtgaggat	acttaacgat	360
gaacttgaga	agttaaacga	tttttacgtt	gataaggaag	aagatttcgt	tatcagatta	420
caggagctca	aggaaagaat	cgagcaagtt	aaagaaaaga	atggggaatt	tgcatacagaa	480
agtgagttca	gcgaagaaat	gatggatatt	cggagagacc	ttgttaccat	tcattggcgag	540
atggtgctcc	tgaaaaacta	cagctcccctt	aattttgcag	gacttgtcaa	gattttgaag	600
aagtacgata	aaagaacagg	tgacttttta	cgtttgccctt	tcacacagct	tgttctccat	660
caacccttct	ttactacaga	gccattact	aggttagtcc	gtgaatgtga	ggccaatctt	720
gagcttcttt	ttccttcaga	agcggaagtt	gtagagtctt	ctagcgcagt	gcaagcacac	780
tcaagctcac	atcagcacaa	ctccccaaga	atctcagctg	agacttcctc	aactctcggc	840
aatgaaaatc	ttgatataata	taagagtaca	ctcgtctgcaa	tgagagctat	aagagggtta	900
caaaaggcta	gctcgacgta	caacccttta	tcattctcat	cgcttcttca	gaacgaggat	960
gatgagacgg	taacagctga	aaactctcca	aactctggga	acaaagatga	ttcagagaag	1020
gaagatactg	gaccttccca	ctgatcagaa	gagaatgatg	ctctttttga	tcaagatttt	1080
gagaatttgc	ttcttgattt	caccctaact	tttcataaaa	ttaacacatt	ttactttact	1140
tcttcacctt	ttgcaggaca	caacttctgt	atgcatttga	attttagtac	agtcgtttat	1200
agattttcaa	tgaaattttc	ctccattgtc	gc			

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1481626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu	Ser	Arg	Val	Arg	Ser	Tyr	Pro	Arg	Ala	Leu	His	Arg	Arg	Asn	Leu	
1			5						10					15		
Arg	Leu	Leu	His	Leu	Asp	Pro	Thr	Gln	Ser	Leu	Phe	Tyr	Met	Lys	Phe	
			20					25					30			
Gly	Lys	Glu	Phe	Arg	Thr	His	Leu	Glu	Glu	Thr	Leu	Pro	Glu	Trp	Arg	
			35				40					45				
Asp	Lys	Phe	Leu	Cys	Tyr	Lys	Pro	Leu	Lys	Lys	Leu	Leu	Lys	Tyr	Tyr	
			50				55				60					
Pro	Tyr	Tyr	Ser	Ala	Asp	Phe	Gly	Pro	Ala	Asn	Ser	Asp	His	Asn	Asp	
65				70						75				80		
Ser	Arg	Pro	Val	Phe	Ala	Asp	Thr	Thr	Asn	Ile	Ser	Ser	Ala	Ala	Asp	
			85						90					95		
Asp	Gly	Gly	Val	Val	Pro	Gly	Val	Arg	Pro	Ser	Glu	Asp	Leu	Gln	Gly	
			100				105						110			
Ser	Phe	Val	Arg	Ile	Leu	Asn	Asp	Glu	Leu	Glu	Lys	Phe	Asn	Asp	Phe	
			115				120					125				
Tyr	Val	Asp	Lys	Glu	Glu	Asp	Phe	Val	Ile	Arg	Leu	Gln	Glu	Leu	Lys	
			130				135				140					
Glu	Arg	Ile	Glu	Gln	Val	Lys	Glu	Lys	Asn	Gly	Glu	Phe	Ala	Ser	Glu	
145				150						155				160		
Ser	Glu	Phe	Ser	Glu	Glu	Met	Met	Asp	Ile	Arg	Arg	Asp	Leu	Val	Thr	
			165						170					175		

Ile His Gly Glu Met Val Leu Leu Lys Asn Tyr Ser Ser Leu Asn Phe
180 185 190
Ala Gly Leu Val Lys Ile Leu Lys Lys Tyr Asp Lys Arg Thr Gly Gly
195 200 205
Leu Leu Arg Leu Pro Phe Thr Gln Leu Val Leu His Gln Pro Phe Phe
210 215 220
Thr Thr Glu Pro Leu Thr Arg Leu Val Arg Glu Cys Glu Ala Asn Leu
225 230 235 240
Glu Leu Leu Phe Pro Ser Glu Ala Glu Val Val Glu Ser Ser Ser Ala
245 250 255
Val Gln Ala His Ser Ser Ser His Gln His Asn Ser Pro Arg Ile Ser
260 265 270
Ala Glu Thr Ser Ser Thr Leu Gly Asn Glu Asn Leu Asp Ile Tyr Lys
275 280 285
Ser Thr Leu Ala Ala Met Arg Ala Ile Arg Gly Leu Gln Lys Ala Ser
290 295 300
Ser Thr Tyr Asn Pro Leu Ser Phe Ser Ser Leu Leu Gln Asn Glu Asp
305 310 315 320
Asp Glu Thr Val Thr Ala Glu Asn Ser Pro Asn Ser Gly Asn Lys Asp
325 330 335
Asp Ser Glu Lys Glu Asp Thr Gly Pro Ser His
340 345

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1481627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met Lys Phe Gly Lys Glu Phe Arg Thr His Leu Glu Glu Thr Leu Pro
1 5 10 15
Glu Trp Arg Asp Lys Phe Leu Cys Tyr Lys Pro Leu Lys Lys Leu Leu
20 25 30
Lys Tyr Tyr Pro Tyr Tyr Ser Ala Asp Phe Gly Pro Ala Asn Ser Asp
35 40 45
His Asn Asp Ser Arg Pro Val Phe Ala Asp Thr Thr Asn Ile Ser Ser
50 55 60
Ala Ala Asp Asp Gly Gly Val Val Pro Gly Val Arg Pro Ser Glu Asp
65 70 75 80
Leu Gln Gly Ser Phe Val Arg Ile Leu Asn Asp Glu Leu Glu Lys Phe
85 90 95
Asn Asp Phe Tyr Val Asp Lys Glu Glu Asp Phe Val Ile Arg Leu Gln
100 105 110
Glu Leu Lys Glu Arg Ile Glu Gln Val Lys Glu Lys Asn Gly Glu Phe
115 120 125
Ala Ser Glu Ser Glu Phe Ser Glu Glu Met Met Asp Ile Arg Arg Asp
130 135 140
Leu Val Thr Ile His Gly Glu Met Val Leu Leu Lys Asn Tyr Ser Ser
145 150 155 160
Leu Asn Phe Ala Gly Leu Val Lys Ile Leu Lys Lys Tyr Asp Lys Arg
165 170 175
Thr Gly Gly Leu Leu Arg Leu Pro Phe Thr Gln Leu Val Leu His Gln
180 185 190
Pro Phe Phe Thr Thr Glu Pro Leu Thr Arg Leu Val Arg Glu Cys Glu

195	200	205
Ala Asn Leu Glu Leu Leu Phe Pro Ser Glu Ala Glu Val Val Glu Ser		
210	215	220
Ser Ser Ala Val Gln Ala His Ser Ser Ser His Gln His Asn Ser Pro		
225	230	235
Arg Ile Ser Ala Glu Thr Ser Ser Thr Leu Gly Asn Glu Asn Leu Asp		240
	245	250
Ile Tyr Lys Ser Thr Leu Ala Ala Met Arg Ala Ile Arg Gly Leu Gln		255
	260	265
Lys Ala Ser Ser Thr Tyr Asn Pro Leu Ser Phe Ser Ser Leu Leu Gln		270
	275	280
Asn Glu Asp Asp Glu Thr Val Thr Ala Glu Asn Ser Pro Asn Ser Gly		285
290	295	300
Asn Lys Asp Asp Ser Glu Lys Glu Asp Thr Gly Pro Ser His		
305	310	315

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1481628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Met Asp Ile Arg Arg Asp Leu Val Thr Ile His Gly Glu Met Val		
1	5	10
Leu Leu Lys Asn Tyr Ser Ser Leu Asn Phe Ala Gly Leu Val Lys Ile		15
	20	25
Leu Lys Lys Tyr Asp Lys Arg Thr Gly Gly Leu Leu Arg Leu Pro Phe		30
	35	40
Thr Gln Leu Val Leu His Gln Pro Phe Phe Thr Thr Glu Pro Leu Thr		45
	50	55
Arg Leu Val Arg Glu Cys Glu Ala Asn Leu Glu Leu Leu Phe Pro Ser		60
65	70	75
Glu Ala Glu Val Val Glu Ser Ser Ser Ala Val Gln Ala His Ser Ser		80
	85	90
Ser His Gln His Asn Ser Pro Arg Ile Ser Ala Glu Thr Ser Ser Thr		95
	100	105
Leu Gly Asn Glu Asn Leu Asp Ile Tyr Lys Ser Thr Leu Ala Ala Met		110
	115	120
Arg Ala Ile Arg Gly Leu Gln Lys Ala Ser Ser Thr Tyr Asn Pro Leu		125
	130	135
Ser Phe Ser Ser Leu Leu Gln Asn Glu Asp Asp Glu Thr Val Thr Ala		140
145	150	155
Glu Asn Ser Pro Asn Ser Gly Asn Lys Asp Asp Ser Glu Lys Glu Asp		160
	165	170
Thr Gly Pro Ser His		175
	180	

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1217

(D) OTHER INFORMATION: / Ceres Seq. ID 1481632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

actccaaaat	gaggacgcgc	cggcaaacat	atccgccgat	cgctgaatcc	ctcacggcga	60
ggtccattgt	tcaggcgctt	ccggcgctcag	ccacaatatc	aggaaatggt	ggaccaaaga	120
agaagaagaa	ctgtgttaat	agaggattgt	gggataaaca	gattccgacg	gatctgctgc	180
aagagatact	gtcttgccctc	ggattaaaag	ccaacataca	tgcttctctc	gtctgcaaga	240
catggcttaa	agaagctggt	tctgtcagga	agtttcagag	tcgtccttgg	cttttttatc	300
cacagagtca	gagaggagga	ccaaaagaag	gagactacgt	tctctttaac	ccatcacggt	360
ctcaaacaca	tcacctcaag	tttccagagt	taacgggcta	cagaaataaa	ttagcttggt	420
ctaaggatgg	ttgggtgctt	gtggtaaaag	ataaccccga	tgtgggtcttc	tttcttaacc	480
cgtttaccgg	ggaacgcatac	tgcttaccctc	aggtgccaca	aaattccaca	cgcgattgct	540
taactttctc	agccgctccc	acatcaacta	gttgttgctg	catatccttc	acccctcaaa	600
gttttcttta	cgcagttggt	aaagttgata	cttggcgccc	tggtgaatcc	gtatggacca	660
ctcatcactt	tgatcaaaag	cgttacgggt	aggtaatcaa	tagatgtatc	ttctccaatg	720
gtatgttcta	ttgtctcagt	accagtggcc	gcctctcggt	tttcgaccgc	tctagagaaa	780
cctggaatgt	tcttccagtg	aaaccatgtc	gggcctttcg	tcgtaaaatt	atgcttggtga	840
ggcaagtatt	catgacagag	catgaaggag	acatctttgt	tgtgactaca	cgcgcgctaa	900
acaacagaaa	actgttggcc	tttaactaa	accttcaagg	caatgtgtgg	gaagagatga	960
aagtacctaa	tggcttgaca	gtattttcaa	gtgacgctac	ctctttaaca	agagctggtc	1020
ttccagagga	ggagaggaac	attctatatt	catcgatat	cgatgatttt	gtgaaaagct	1080
ctcatccaac	tttctattat	tatgactgca	gcgcttggct	ccagccacct	catgacaatt	1140
ttaatttttg	actatcatcc	ttaagtgttt	ttgtttttga	aaaaacatgt	tttaataacct	1200
tttaagctt	ttgatcc					

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1481633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Lys	Met	Arg	Thr	Arg	Arg	Gln	Thr	Tyr	Pro	Pro	Ile	Ala	Glu	Ser	
1				5				10						15		
Leu	Thr	Ala	Arg	Ser	Ile	Val	Gln	Ala	Leu	Pro	Ala	Ser	Ala	Thr	Ile	
			20					25					30			
Ser	Gly	Asn	Gly	Gly	Pro	Lys	Lys	Lys	Asn	Cys	Val	Asn	Arg	Gly		
		35				40					45					
Leu	Trp	Asp	Lys	Gln	Ile	Pro	Thr	Asp	Leu	Leu	Gln	Glu	Ile	Leu	Ser	
	50				55						60					
Cys	Leu	Gly	Leu	Lys	Ala	Asn	Ile	His	Ala	Ser	Leu	Val	Cys	Lys	Thr	
65				70					75					80		
Trp	Leu	Lys	Glu	Ala	Val	Ser	Val	Arg	Lys	Phe	Gln	Ser	Arg	Pro	Trp	
			85					90					95			
Leu	Phe	Tyr	Pro	Gln	Ser	Gln	Arg	Gly	Gly	Pro	Lys	Glu	Gly	Asp	Tyr	
		100					105						110			
Val	Leu	Phe	Asn	Pro	Ser	Arg	Ser	Gln	Thr	His	His	Leu	Lys	Phe	Pro	
	115					120						125				
Glu	Leu	Thr	Gly	Tyr	Arg	Asn	Lys	Leu	Ala	Cys	Ala	Lys	Asp	Gly	Trp	
	130				135						140					
Leu	Leu	Val	Val	Lys	Asp	Asn	Pro	Asp	Val	Val	Phe	Phe	Leu	Asn	Pro	
145				150					155					160		
Phe	Thr	Gly	Glu	Arg	Ile	Cys	Leu	Pro	Gln	Val	Pro	Gln	Asn	Ser	Thr	
			165					170						175		

Arg Asp Cys Leu Thr Phe Ser Ala Ala Pro Thr Ser Thr Ser Cys Cys
180 185 190
Val Ile Ser Phe Thr Pro Gln Ser Phe Leu Tyr Ala Val Val Lys Val
195 200 205
Asp Thr Trp Arg Pro Gly Glu Ser Val Trp Thr Thr His His Phe Asp
210 215 220
Gln Lys Arg Tyr Gly Glu Val Ile Asn Arg Cys Ile Phe Ser Asn Gly
225 230 235 240
Met Phe Tyr Cys Leu Ser Thr Ser Gly Arg Leu Ser Phe Phe Asp Pro
245 250 255
Ser Arg Glu Thr Trp Asn Val Leu Pro Val Lys Pro Cys Arg Ala Phe
260 265 270
Arg Arg Lys Ile Met Leu Val Arg Gln Val Phe Met Thr Glu His Glu
275 280 285
Gly Asp Ile Phe Val Val Thr Thr Arg Arg Val Asn Asn Arg Lys Leu
290 295 300
Leu Ala Phe Lys Leu Asn Leu Gln Gly Asn Val Trp Glu Glu Met Lys
305 310 315 320
Val Pro Asn Gly Leu Thr Val Phe Ser Ser Asp Ala Thr Ser Leu Thr
325 330 335
Arg Ala Gly Leu Pro Glu Glu Glu Arg Asn Ile Leu Tyr Ser Ser Asp
340 345 350
Ile Asp Asp Phe Val Lys Ser Ser His Pro Thr Phe Tyr Tyr Tyr Asp
355 360 365
Cys Ser Ala Trp Leu Gln Pro Pro His Asp Asn Phe Asn Phe
370 375 380

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Arg Thr Arg Arg Gln Thr Tyr Pro Pro Ile Ala Glu Ser Leu Thr
1 5 10 15
Ala Arg Ser Ile Val Gln Ala Leu Pro Ala Ser Ala Thr Ile Ser Gly
20 25 30
Asn Gly Gly Pro Lys Lys Lys Lys Asn Cys Val Asn Arg Gly Leu Trp
35 40 45
Asp Lys Gln Ile Pro Thr Asp Leu Leu Gln Glu Ile Leu Ser Cys Leu
50 55 60
Gly Leu Lys Ala Asn Ile His Ala Ser Leu Val Cys Lys Thr Trp Leu
65 70 75 80
Lys Glu Ala Val Ser Val Arg Lys Phe Gln Ser Arg Pro Trp Leu Phe
85 90 95
Tyr Pro Gln Ser Gln Arg Gly Gly Pro Lys Glu Gly Asp Tyr Val Leu
100 105 110
Phe Asn Pro Ser Arg Ser Gln Thr His His Leu Lys Phe Pro Glu Leu
115 120 125
Thr Gly Tyr Arg Asn Lys Leu Ala Cys Ala Lys Asp Gly Trp Leu Leu
130 135 140
Val Val Lys Asp Asn Pro Asp Val Val Phe Phe Leu Asn Pro Phe Thr
145 150 155 160
Gly Glu Arg Ile Cys Leu Pro Gln Val Pro Gln Asn Ser Thr Arg Asp

				165					170					175	
Cys	Leu	Thr	Phe	Ser	Ala	Ala	Pro	Thr	Ser	Thr	Ser	Cys	Cys	Val	Ile
			180						185				190		
Ser	Phe	Thr	Pro	Gln	Ser	Phe	Leu	Tyr	Ala	Val	Val	Lys	Val	Asp	Thr
		195						200				205			
Trp	Arg	Pro	Gly	Glu	Ser	Val	Trp	Thr	Thr	His	His	Phe	Asp	Gln	Lys
	210					215					220				
Arg	Tyr	Gly	Glu	Val	Ile	Asn	Arg	Cys	Ile	Phe	Ser	Asn	Gly	Met	Phe
225					230					235					240
Tyr	Cys	Leu	Ser	Thr	Ser	Gly	Arg	Leu	Ser	Phe	Phe	Asp	Pro	Ser	Arg
			245						250				255		
Glu	Thr	Trp	Asn	Val	Leu	Pro	Val	Lys	Pro	Cys	Arg	Ala	Phe	Arg	Arg
			260					265					270		
Lys	Ile	Met	Leu	Val	Arg	Gln	Val	Phe	Met	Thr	Glu	His	Glu	Gly	Asp
	275						280					285			
Ile	Phe	Val	Val	Thr	Thr	Arg	Arg	Val	Asn	Asn	Arg	Lys	Leu	Leu	Ala
	290					295					300				
Phe	Lys	Leu	Asn	Leu	Gln	Gly	Asn	Val	Trp	Glu	Glu	Met	Lys	Val	Pro
305					310					315					320
Asn	Gly	Leu	Thr	Val	Phe	Ser	Ser	Asp	Ala	Thr	Ser	Leu	Thr	Arg	Ala
			325						330					335	
Gly	Leu	Pro	Glu	Glu	Glu	Arg	Asn	Ile	Leu	Tyr	Ser	Ser	Asp	Ile	Asp
		340						345					350		
Asp	Phe	Val	Lys	Ser	Ser	His	Pro	Thr	Phe	Tyr	Tyr	Tyr	Asp	Cys	Ser
	355						360					365			
Ala	Trp	Leu	Gln	Pro	Pro	His	Asp	Asn	Phe	Asn	Phe				
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

mtgacgcttg	gysttcttgc	accctaccgt	gggattggca	ttggtaagtc	ataaatctgc	60
tgtgccaaac	ttgaataccg	acaaaacatg	aataatgaag	aaaactgtta	gcatgttgtg	120
taattctggt	gttttcctta	cgttttaaca	catgaggcca	gctgtagtat	gtttattctg	180
tagttctcta	tttgaagtgt	ctccatttag	agattcaaac	caccaagaaa	tagtccttag	240
ggttttatgc	atatcgttgt	tttaccgaga	aactggaatt	agtgactatg	atttcctcct	300
atatcaagat	ttaagatcga	attccctgct	tttagaaaga	aaaactcgat	gtctataatt	360
tgtgtatctt	gtttttttcg	tcttttgcag	gctcaaactt	attgaatcat	gttcttgaca	420
tgtgctccaa	gcaaaacatg	tgtgagatat	acttgcatgt	gcagacaaac	aacgaagacg	480
caatcaagtt	ctacaagaag	ttcggctttg	agatcacaga	taccatacaa	aactattaca	540
tcaacattga	gccaaagagat	tgctacgttg	tcagcaagtc	ctttgctcaa	tctgaagcca	600
acaaatgatg	aaaaatacca	aacttgggga	agcatttctt	ccccagtttc	tttgttgcat	660
tcagttc						

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1481636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Arg Pro Ala Val Val Cys Leu Phe Cys Ser Ser Leu Phe Glu Val
1 5 10 15
Ser Pro Phe Arg Asp Ser Asn His Gln Glu Ile Val Leu Arg Val Leu
20 25 30
Cys Ile Ser Leu Phe Tyr Arg Glu Thr Gly Ile Ser Asp Tyr Asp Phe
35 40 45
Leu Leu Tyr Gln Asp Leu Arg Ser Asn Ser Leu Leu Leu Glu Arg Lys
50 55 60
Thr Arg Cys Leu
65

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1481637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Phe Leu Thr Cys Ala Pro Ser Lys Thr Cys Val Arg Tyr Thr Cys
1 5 10 15
Met Cys Arg Gln Thr Thr Lys Thr Gln Ser Ser Ser Thr Arg Ser Ser
20 25 30
Ala Leu Arg Ser Gln Ile Pro Tyr Lys Thr Ile Thr Ser Thr Leu Ser
35 40 45
Gln Glu Ile Ala Thr Leu Ser Ala Ser Pro Leu Leu Asn Leu Lys Pro
50 55 60
Thr Asn Asp Glu Lys Tyr Gln Thr Trp Gly Ser His Ser Ser Pro Val
65 70 75 80
Ser Leu Leu His Ser Val
85

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1481638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Cys Arg Gln Thr Thr Lys Thr Gln Ser Ser Ser Thr Arg Ser Ser
1 5 10 15
Ala Leu Arg Ser Gln Ile Pro Tyr Lys Thr Ile Thr Ser Thr Leu Ser
20 25 30
Gln Glu Ile Ala Thr Leu Ser Ala Ser Pro Leu Leu Asn Leu Lys Pro
35 40 45
Thr Asn Asp Glu Lys Tyr Gln Thr Trp Gly Ser His Ser Ser Pro Val
50 55 60
Ser Leu Leu His Ser Val

65

70

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
ctttgcgatg gtaaaatagt gttctcagat tgggctagca atgtgagttc tattcttttg 60
gtccctgttc gtgccttgag tgagaagctt gctagagggt catcatcagt cactccgctg 120
aaacaagata ttttagaggg aatgagaact gtagctttga aacttgaatt tggggttcat 180
cataaccaga tatttgagag aaccatagct gcacatttta ccgatccctt tgatgtgacc 240
acaagggtgg caaacaaatg caatgatggc actttggtct tgcaggttat gttacactcc 300
ctcgtcaagg cgaacttgat agttcttgat gtttggcttg atcttcaaga tggatttatt 360
catggacaaa atgatggaag accgacttca acgttctttc cgcttgctcg gtctccagga 420
tctagagcag cagtcgtggt cagtatatgc ctagacaaga gtatgtcatc agaagggaaa 480
gatttgcagc taccagaaag cattctgaat atcaaatatg gaatccatgg ggatagagca 540
gctggagcac acaggccagt ggatgcagat cactctgaaa ctgatactta agggagagat 600
ttggtgttca agagtgcctat tgttttgcag cgtccagtac ttgatccttg cctcacagtt 660
ggattcctcc cacttccttc tgatgggctt agggctcggga aacttatcac catgcagtgg 720
agagtggaaa ggcttaaaga tctcaaagaa agtgaagccg tggaacaaca acatgatgag 780
gtgttatatg aagtcfaatg aaattcggag aattggatga tgcgtggtag gaagagaggc 840
catgtctctc tctcagagga gcaagggttca agagtagtaa tctcgatact atgtgtcccg 900
ttagttgcgg gttatgtccg tcctcctcaa ctcggttgc caaacgtaga agaagcaaatt 960
gtaagcagca atccatcggg tcctcactta gtatgtgtct tgcctccact tctcagttct 1020
tcctactgcg tacctgtcaa gtaatagaat ctactctat attttttcca agaaaacatt 1080
ttttctgtat ttttattttg tttgcgatca aagaaatatc agagtatggg atcatcaatg 1140
atgagagtga tttttctttt gtgacgattt tattttcc
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
Leu Cys Asp Gly Lys Ile Val Phe Ser Asp Trp Ala Ser Asn Val Ser
1          5          10          15
Ser Ile Leu Trp Val Pro Val Arg Ala Leu Ser Glu Lys Leu Ala Arg
20          25          30
Gly Ser Ser Ser Val Thr Pro Leu Lys Gln Asp Ile Leu Glu Gly Met
35          40          45
Arg Thr Val Ala Leu Lys Leu Glu Phe Gly Val His His Asn Gln Ile
50          55          60
Phe Glu Arg Thr Ile Ala Ala His Phe Thr Asp Pro Phe Asp Val Thr
65          70          75          80
Thr Arg Val Ala Asn Lys Cys Asn Asp Gly Thr Leu Val Leu Gln Val
85          90          95
Met Leu His Ser Leu Val Lys Ala Asn Leu Ile Val Leu Asp Val Trp
100          105          110
```

Leu Asp Leu Gln Asp Gly Phe Ile His Gly Gln Asn Asp Gly Arg Pro
115 120 125
Thr Ser Thr Phe Phe Pro Leu Val Val Ser Pro Gly Ser Arg Ala Ala
130 135 140
Val Val Phe Ser Ile Cys Leu Asp Lys Ser Met Ser Ser Glu Gly Lys
145 150 155 160
Asp Leu Gln Leu Pro Glu Ser Ile Leu Asn Ile Lys Tyr Gly Ile His
165 170 175
Gly Asp Arg Ala Ala Gly Ala His Arg Pro Val Asp Ala Asp His Ser
180 185 190
Glu Thr Asp Thr
195

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1481641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Arg Thr Val Ala Leu Lys Leu Glu Phe Gly Val His His Asn Gln
1 5 10 15
Ile Phe Glu Arg Thr Ile Ala Ala His Phe Thr Asp Pro Phe Asp Val
20 25 30
Thr Thr Arg Val Ala Asn Lys Cys Asn Asp Gly Thr Leu Val Leu Gln
35 40 45
Val Met Leu His Ser Leu Val Lys Ala Asn Leu Ile Val Leu Asp Val
50 55 60
Trp Leu Asp Leu Gln Asp Gly Phe Ile His Gly Gln Asn Asp Gly Arg
65 70 75 80
Pro Thr Ser Thr Phe Phe Pro Leu Val Val Ser Pro Gly Ser Arg Ala
85 90 95
Ala Val Val Phe Ser Ile Cys Leu Asp Lys Ser Met Ser Ser Glu Gly
100 105 110
Lys Asp Leu Gln Leu Pro Glu Ser Ile Leu Asn Ile Lys Tyr Gly Ile
115 120 125
His Gly Asp Arg Ala Ala Gly Ala His Arg Pro Val Asp Ala Asp His
130 135 140
Ser Glu Thr Asp Thr
145

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1481642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Gln Trp Arg Val Glu Arg Leu Lys Asp Leu Lys Glu Ser Glu Ala
1 5 10 15
Val Glu Gln Gln His Asp Glu Val Leu Tyr Glu Val Asn Ala Asn Ser

```

                20                25                30
Glu Asn Trp Met Ile Ala Gly Arg Lys Arg Gly His Val Ser Leu Ser
                35                40                45
Glu Glu Gln Gly Ser Arg Val Val Ile Ser Ile Leu Cys Val Pro Leu
                50                55                60
Val Ala Gly Tyr Val Arg Pro Pro Gln Leu Gly Leu Pro Asn Val Glu
                65                70                75                80
Glu Ala Asn Val Ser Ser Asn Pro Ser Gly Pro His Leu Val Cys Val
                85                90                95
Leu Pro Pro Leu Leu Ser Ser Ser Tyr Cys Val Pro Val Lys
                100                105                110
```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

aaaaaaaaataa aaataaaaaa tcttcacgtt tcttctctct ctctctctct cgagccacca      60
aatctgaatt aggggtttttt gagaatattc atcttttgat ttcaaattct tcaccactg      120
tgtaatttca ctcgtcagga ttcacacagag gaatcatgat tacagattcg atcaccaacg      180
cttctgctac ttcagctccg agagattccg gaaagaagaa gaggaacaat aagtcggcta      240
agatgaagca gaacaagctt ggtctccgtc gtgagcaatg gctttctcaa gttgcggtga      300
gcaataagga agttaaagag gagaggagtg ttaatcgtag tcaaaagcct gatcatgaga      360
gttcagataa ggtgcgtaga gaagaggata acaatgggtg gaataatctt cttcatcatg      420
agagttttat ggagtcacct tcaaatagct ctggtgggtg tacatatctg agcactaact      480
tcagtgggag aagtagcagg agtagtagta gcagcagtgg cttttgctct ggtaataataa      540
cagaagagga aaatgtagac gatgatgatg atgggtgtgt ggatgattgg gaagctggtg      600
ctgatgcgtt agcggctgag gaagagattg agaaaaagag tcgtcctctt gagtctgtga      660
aagagcaagt gagtgttggg caatcagctt ctaatgtgtg tgatbcgtcg attagtgatg      720
catcagatgt tgtgggtgtt gaagatccaa agcaggaatg cttgagagtg tcatcaagga      780
agcagactag taatagagct tggaggctag atgatgacct tcgcccacag gggttacctt      840
atttggcgaa gcagcttagt tttccggagt tagacaagcg ttttagctct gtggcgattc      900
cgtcttcatg tcccatatgc tacgaagact tggacttgac ggattcgaat ttcctcccct      960
gtccttgttg atttcggctc tgtctgttct gccacaagac catttgcgat ggagatgggc      1020
gttgtccagg ctgcaggaaa ccctatgaac ggaatatggt caaggctgag actagtattc      1080
aaggtggttg tctaacaatt cggttggtc gttcgtctag catgttttgc aagtttttaa      1140
aggagaggtg cggttttctc aaccatgttg tcttttgaa ctcgagaact tgagctctgt      1200
tttctatgtc atctatggtt ctaagtctga aacactgttg tgatgatgta gaatgtgatg      1260
tgtgaataca taaaagggtg tacagaaaat gattcaataa catttagata gtttcaataa      1320
tgaatgctat gttctcc
```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..327
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ile Thr Asp Ser Ile Thr Asn Ala Ser Ala Thr Ser Ala Pro Arg

```

1           5           10           15
Asp Ser Gly Lys Lys Lys Arg Asn Asn Lys Ser Ala Lys Met Lys Gln
20           25           30
Asn Lys Leu Gly Leu Arg Arg Glu Gln Trp Leu Ser Gln Val Ala Val
35           40           45
Ser Asn Lys Glu Val Lys Glu Glu Arg Ser Val Asn Arg Ser Gln Lys
50           55           60
Pro Asp His Glu Ser Ser Asp Lys Val Arg Arg Glu Glu Asp Asn Asn
65           70           75           80
Gly Gly Asn Asn Leu Leu His His Glu Ser Phe Met Glu Ser Pro Ser
85           90           95
Asn Ser Ser Val Gly Gly Thr Tyr Ser Ser Thr Asn Phe Ser Gly Arg
100          105          110
Ser Ser Arg Ser Ser Ser Ser Ser Ser Gly Phe Cys Ser Gly Asn Ile
115          120          125
Thr Glu Glu Glu Asn Val Asp Asp Asp Asp Gly Cys Val Asp Asp
130          135          140
Trp Glu Ala Val Ala Asp Ala Leu Ala Ala Glu Glu Glu Ile Glu Lys
145          150          155          160
Lys Ser Arg Pro Leu Glu Ser Val Lys Glu Gln Val Ser Val Gly Gln
165          170          175
Ser Ala Ser Asn Val Cys Asp Xaa Ser Ile Ser Asp Ala Ser Asp Val
180          185          190
Val Gly Val Glu Asp Pro Lys Gln Glu Cys Leu Arg Val Ser Ser Arg
195          200          205
Lys Gln Thr Ser Asn Arg Ala Trp Arg Leu Asp Asp Asp Leu Arg Pro
210          215          220
Gln Gly Leu Pro Asn Leu Ala Lys Gln Leu Ser Phe Pro Glu Leu Asp
225          230          235          240
Lys Arg Phe Ser Ser Val Ala Ile Pro Ser Ser Cys Pro Ile Cys Tyr
245          250          255
Glu Asp Leu Asp Leu Thr Asp Ser Asn Phe Leu Pro Cys Pro Cys Gly
260          265          270
Phe Arg Leu Cys Leu Phe Cys His Lys Thr Ile Cys Asp Gly Asp Gly
275          280          285
Arg Cys Pro Gly Cys Arg Lys Pro Tyr Glu Arg Asn Met Val Lys Ala
290          295          300
Glu Thr Ser Ile Gln Gly Gly Gly Leu Thr Ile Arg Leu Ala Arg Ser
305          310          315          320
Ser Ser Met Phe Cys Lys Phe
325

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..298

(D) OTHER INFORMATION: / Ceres Seq. ID 1481649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Lys Gln Asn Lys Leu Gly Leu Arg Arg Glu Gln Trp Leu Ser Gln
1           5           10           15
Val Ala Val Ser Asn Lys Glu Val Lys Glu Glu Arg Ser Val Asn Arg
20           25           30
Ser Gln Lys Lys Pro Asp His Glu Ser Ser Asp Lys Val Arg Arg Glu Glu
35           40           45

```

Asp Asn Asn Gly Gly Asn Asn Leu Leu His His Glu Ser Phe Met Glu
50 55 60
Ser Pro Ser Asn Ser Ser Val Gly Gly Thr Tyr Ser Ser Thr Asn Phe
65 70 75 80
Ser Gly Arg Ser Ser Arg Ser Ser Ser Ser Ser Gly Phe Cys Ser
85 90 95
Gly Asn Ile Thr Glu Glu Glu Asn Val Asp Asp Asp Asp Asp Gly Cys
100 105 110
Val Asp Asp Trp Glu Ala Val Ala Asp Ala Leu Ala Ala Glu Glu Glu
115 120 125
Ile Glu Lys Lys Ser Arg Pro Leu Glu Ser Val Lys Glu Gln Val Ser
130 135 140
Val Gly Gln Ser Ala Ser Asn Val Cys Asp Xaa Ser Ile Ser Asp Ala
145 150 155 160
Ser Asp Val Val Gly Val Glu Asp Pro Lys Gln Glu Cys Leu Arg Val
165 170 175
Ser Ser Arg Lys Gln Thr Ser Asn Arg Ala Trp Arg Leu Asp Asp Asp
180 185 190
Leu Arg Pro Gln Gly Leu Pro Asn Leu Ala Lys Gln Leu Ser Phe Pro
195 200 205
Glu Leu Asp Lys Arg Phe Ser Ser Val Ala Ile Pro Ser Ser Cys Pro
210 215 220
Ile Cys Tyr Glu Asp Leu Asp Leu Thr Asp Ser Asn Phe Leu Pro Cys
225 230 235 240
Pro Cys Gly Phe Arg Leu Cys Leu Phe Cys His Lys Thr Ile Cys Asp
245 250 255
Gly Asp Gly Arg Cys Pro Gly Cys Arg Lys Pro Tyr Glu Arg Asn Met
260 265 270
Val Lys Ala Glu Thr Ser Ile Gln Gly Gly Gly Leu Thr Ile Arg Leu
275 280 285
Ala Arg Ser Ser Ser Met Phe Cys Lys Phe
290 295

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1481650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Glu Ser Pro Ser Asn Ser Ser Val Gly Gly Thr Tyr Ser Ser Thr
1 5 10 15
Asn Phe Ser Gly Arg Ser Ser Arg Ser Ser Ser Ser Ser Ser Gly Phe
20 25 30
Cys Ser Gly Asn Ile Thr Glu Glu Asn Val Asp Asp Asp Asp
35 40 45
Gly Cys Val Asp Asp Trp Glu Ala Val Ala Asp Ala Leu Ala Ala Glu
50 55 60
Glu Glu Ile Glu Lys Lys Ser Arg Pro Leu Glu Ser Val Lys Glu Gln
65 70 75 80
Val Ser Val Gly Gln Ser Ala Ser Asn Val Cys Asp Xaa Ser Ile Ser
85 90 95
Asp Ala Ser Asp Val Val Gly Val Glu Asp Pro Lys Gln Glu Cys Leu
100 105 110
Arg Val Ser Ser Arg Lys Gln Thr Ser Asn Arg Ala Trp Arg Leu Asp

115	120	125
Asp Asp Leu Arg Pro Gln Gly Leu Pro Asn Leu Ala Lys Gln Leu Ser		
130	135	140
Phe Pro Glu Leu Asp Lys Arg Phe Ser Ser Val Ala Ile Pro Ser Ser		
145	150	155
Cys Pro Ile Cys Tyr Glu Asp Leu Asp Leu Thr Asp Ser Asn Phe Leu		
165	170	175
Pro Cys Pro Cys Gly Phe Arg Leu Cys Leu Phe Cys His Lys Thr Ile		
180	185	190
Cys Asp Gly Asp Gly Arg Cys Pro Gly Cys Arg Lys Pro Tyr Glu Arg		
195	200	205
Asn Met Val Lys Ala Glu Thr Ser Ile Gln Gly Gly Gly Leu Thr Ile		
210	215	220
Arg Leu Ala Arg Ser Ser Ser Met Phe Cys Lys Phe		
225	230	235

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

amatcctmat	cgaaaaacgg	aaattagttt	acaggctgta	atTTTTcttt	caggctctct	60
ctcttttcgtc	gccgaaccag	ttccagaaag	gctgtagcga	ttcaaaattt	cacaaattaa	120
agtcttcttc	ctctcsaat	cagagattgt	ctccttctta	gctcagatct	gggagcttct	180
tgtgatagat	ttggaagaag	atgactgtga	tcgatattct	gactagagtt	gactcgatct	240
gtaagaagta	cgacaagtac	gatgtcgaca	agcagcggga	ggccaatatc	tccggcgatg	300
atgcctttgc	tcgtctctat	ggagctttcg	aaacccaaat	cgagaccgct	ctcgagaaag	360
ctgaacttgt	tacgaaggag	aaaaacaggg	ctgctgctgt	tgcaatgaat	gctgagatcc	420
gccggaccac	ggcacgattg	tcagagggaag	ttcccaagtt	gcaaagactt	gctgtcaagc	480
gggttaaggg	ccttacaacc	gaagagcttg	ctgcgagaaa	tgatttggtg	ctcgctcttc	540
cagccaggat	tgaagccata	cctgatggga	cagcagggtg	ccctaaaagc	actagtgtt	600
ggactccctc	ctcaacaaca	tctcgtcctg	atatcaaatt	tgattcagat	gggcgttttg	660
acgatgatta	ctttcaagaa	tcaaatgaat	ctagccaatt	caggcaggag	tatgagatgc	720
ggaaaataaa	acaggaacaa	ggtcttgaca	tgatctccga	agggttagat	gctttgaaga	780
acatggcttc	tgatatgaac	gaggaactgg	atagacaagt	tccactgatg	gatgaaatcg	840
acacaaaggt	ggacagagca	acctccgatc	ttaagaacac	caatgttaga	cttaaagata	900
ccgtgaacca	gctgagatct	agccggaact	tctgtatcga	tattgttttg	ttgtgtattg	960
ttctgggtat	cgctgcatac	ttatacaatg	tactgaagta	atgagatgaa	ccctacgaaa	1020
ggacccatta	gtacttatca	cccagtgcaa	tatccagtgt	gtgcttgtgt	cttactcttc	1080
ttctctgata	tttctacgag	agtttcttct	taatgtcaag	aatattcaag	tcttatcttc	1140
ctgcatcgac	ttttctccat	gttgttcgtg	tgcatagatt	tcattctgtc	aaatgtgcgt	1200
caaactaatt	gattgctgtg	tctgcggcag	tgtgctatta	ttttccagcc	aaaatatgat	1260
tttttattta	ttttaaaatc	aagccaaatt	ttaattcc			

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1481669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Thr Val Ile Asp Ile Leu Thr Arg Val Asp Ser Ile Cys Lys Lys
1 5 10 15
Tyr Asp Lys Tyr Asp Val Asp Lys Gln Arg Glu Ala Asn Ile Ser Gly
20 25 30
Asp Asp Ala Phe Ala Arg Leu Tyr Gly Ala Phe Glu Thr Gln Ile Glu
35 40 45
Thr Ala Leu Glu Lys Ala Glu Leu Val Thr Lys Glu Lys Asn Arg Ala
50 55 60
Ala Ala Val Ala Met Asn Ala Glu Ile Arg Arg Thr Lys Ala Arg Leu
65 70 75 80
Ser Glu Glu Val Pro Lys Leu Gln Arg Leu Ala Val Lys Arg Val Lys
85 90 95
Gly Leu Thr Thr Glu Glu Leu Ala Ala Arg Asn Asp Leu Val Leu Ala
100 105 110
Leu Pro Ala Arg Ile Glu Ala Ile Pro Asp Gly Thr Ala Gly Gly Pro
115 120 125
Lys Ser Thr Ser Ala Trp Thr Pro Ser Ser Thr Thr Ser Arg Pro Asp
130 135 140
Ile Lys Phe Asp Ser Asp Gly Arg Phe Asp Asp Asp Tyr Phe Gln Glu
145 150 155 160
Ser Asn Glu Ser Ser Gln Phe Arg Gln Glu Tyr Glu Met Arg Lys Ile
165 170 175
Lys Gln Glu Gln Gly Leu Asp Met Ile Ser Glu Gly Leu Asp Ala Leu
180 185 190
Lys Asn Met Ala Ser Asp Met Asn Glu Glu Leu Asp Arg Gln Val Pro
195 200 205
Leu Met Asp Glu Ile Asp Thr Lys Val Asp Arg Ala Thr Ser Asp Leu
210 215 220
Lys Asn Thr Asn Val Arg Leu Lys Asp Thr Val Asn Gln Leu Arg Ser
225 230 235 240
Ser Arg Asn Phe Cys Ile Asp Ile Val Leu Leu Cys Ile Val Leu Gly
245 250 255
Ile Ala Ala Tyr Leu Tyr Asn Val Leu Lys
260 265

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1481670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Asn Ala Glu Ile Arg Arg Thr Lys Ala Arg Leu Ser Glu Glu Val
1 5 10 15
Pro Lys Leu Gln Arg Leu Ala Val Lys Arg Val Lys Gly Leu Thr Thr
20 25 30
Glu Glu Leu Ala Ala Arg Asn Asp Leu Val Leu Ala Leu Pro Ala Arg
35 40 45
Ile Glu Ala Ile Pro Asp Gly Thr Ala Gly Gly Pro Lys Ser Thr Ser
50 55 60
Ala Trp Thr Pro Ser Ser Thr Thr Ser Arg Pro Asp Ile Lys Phe Asp
65 70 75 80
Ser Asp Gly Arg Phe Asp Asp Asp Tyr Phe Gln Glu Ser Asn Glu Ser

85 90 95
Ser Gln Phe Arg Gln Glu Tyr Glu Met Arg Lys Ile Lys Gln Glu Gln
100 105 110
Gly Leu Asp Met Ile Ser Glu Gly Leu Asp Ala Leu Lys Asn Met Ala
115 120 125
Ser Asp Met Asn Glu Glu Leu Asp Arg Gln Val Pro Leu Met Asp Glu
130 135 140
Ile Asp Thr Lys Val Asp Arg Ala Thr Ser Asp Leu Lys Asn Thr Asn
145 150 155 160
Val Arg Leu Lys Asp Thr Val Asn Gln Leu Arg Ser Ser Arg Asn Phe
165 170 175
Cys Ile Asp Ile Val Leu Leu Cys Ile Val Leu Gly Ile Ala Ala Tyr
180 185 190
Leu Tyr Asn Val Leu Lys
195

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..770
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

cytttcgacc	tctcctactt	actactactc	agctgcttct	gccttctagg	gttctttctc	60
cgttcaccct	ccgccgcacg	agttgtccag	ctccgccgca	ttcttctgtc	tcccagatca	120
ccggctttta	gcaaatccgg	ctgcttttca	ctctaattcg	taaaccactt	gtgggatttg	180
agcatctttt	acattctcca	aaatctctgc	tttctagggt	tttgtgagtt	ttgggtgggat	240
gagtagtggtg	ttcagtgatc	agatcctgat	tgataagctc	gctaagctca	atagcagtc	300
acagtctatc	gaaactctgt	cacattgggtg	tatattcaat	cggagcaaag	cagaattgat	360
cgttacgaca	tgggagaaac	agtttcacag	tacagagatg	gatcagaaag	tccctctttt	420
gtatttggtt	aatgatattc	ttcagaacag	taagcgtcaa	ggtaatgagt	ttgtgcaaga	480
gttctggaat	gttcttccta	aggctcttaa	agacattggt	tctcaaggag	atgataatgg	540
caaaagcgct	gtcgcacgtg	tgatcaagat	atgggaagaa	agaagagtgt	ttggatcacg	600
ttcaaagagt	cttaaagatg	taatgcttgg	agaagatggt	cctctgccac	ttgatatcag	660
caaaaagcgg	gsctcgcgga	tccaaatctt	caaaacggga	gtcaaaatcg	tccagaacga	720
aattaacatc	aagtgggtgt	gtgctgarar	gtagcatcac	catatcattt		

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ser Ser Val Phe Ser Asp Gln Ile Leu Ile Asp Lys Leu Ala Lys
1 5 10 15
Leu Asn Ser Ser Gln Gln Ser Ile Glu Thr Leu Ser His Trp Cys Ile
20 25 30
Phe Asn Arg Ser Lys Ala Glu Leu Ile Val Thr Thr Trp Glu Lys Gln
35 40 45
Phe His Ser Thr Glu Met Asp Gln Lys Val Pro Leu Leu Tyr Leu Ala

50	55	60
Asn Asp Ile Leu Gln	Asn Ser Lys Arg Gln Gly	Asn Glu Phe Val Gln
65	70	75
Glu Phe Trp Asn Val	Leu Pro Lys Ala Leu Lys	Asp Ile Val Ser Gln
85	90	95
Gly Asp Asp Asn Gly	Lys Ser Ala Val Ala Arg	Val Ile Lys Ile Trp
100	105	110
Glu Glu Arg Arg Val	Phe Gly Ser Arg Ser Lys	Ser Leu Lys Asp Val
115	120	125
Met Leu Gly Glu Asp	Val Pro Leu Pro Leu Asp	Ile Ser Lys Lys Arg
130	135	140
Xaa Ser Arg Ile Gln	Ile Phe Lys Thr Gly Val	Lys Ile Val Gln Asn
145	150	155
Glu Ile Asn Ile Lys	Trp Trp Cys Ala Xaa Xaa	
165	170	

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Asp Gln Lys Val	Pro Leu Leu Tyr	Leu Ala Asn Asp	Ile Leu Gln
1	5	10	15
Asn Ser Lys Arg	Gln Gly Asn Glu	Phe Val Gln Glu	Phe Trp Asn Val
20	25	30	
Leu Pro Lys Ala	Leu Lys Asp Ile	Val Ser Gln Gly	Asp Asp Asn Gly
35	40	45	
Lys Ser Ala Val	Ala Arg Val Ile	Lys Ile Trp Glu	Glu Arg Arg Val
50	55	60	
Phe Gly Ser Arg	Ser Lys Ser Leu	Lys Asp Val	Met Leu Gly Glu Asp
65	70	75	80
Val Pro Leu Pro	Leu Asp Ile Ser	Lys Lys Arg	Xaa Ser Arg Ile Gln
85	90	95	
Ile Phe Lys Thr	Gly Val Lys Ile	Val Gln Asn Glu	Ile Asn Ile Lys
100	105	110	
Trp Trp Cys Ala	Xaa Xaa		
115			

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1004
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ctcgcatcgc atcgatcctc	ccatctgcgc acccgcaagc	ctattctccg cacctcctca	60
ggtgaccggg aagatgatgc	cgttgagcca aaccgacttc	tcgccgtcgc agttcacctc	120
ctcccagaat gccgccgccg	actccaccac gccttccaag	atgcgcggcg cgtccagcac	180
catgccgctc accgtgaagc	aggctcgtcga cgcgcasagt	ctggcacggg cgagaagggc	240

```
gctccgttca tcgtcaatgg cgtcgagatg gctaacatgc gacttgtggg gatgggtcaat 300
gccaaggtgg agcggacgac cgatgtgacc ttcacgctcg acgatggcac cggccgcctc 360
gatttcatca gatgggtgaa tgatgcttca gattcttttg aaactgctgc tattcagaat 420
ggtatgtaca ttgcggtcac tggaagcctc aagggactgc aagagaggaa gcgtgctact 480
gctttctcaa tcaggcctat aaccgatttc aatgaggtta cgctgcattt cattcagtgt 540
gttcggatgc atatatagaa cattgaatta aaggctggca gtcctgcacg aatcagttct 600
tctatgggag tgtcattctc aaatggattc agtgaatcaa gcacaccgac atctttgaaa 660
tccagtcccg caccgggtgac cagcgggtca tccgatactg atctgcacac gcaggctcgt 720
aattttttta atgaaccagc gaacctcgag agtgagcatg ggggtgcacgt tgatgaagta 780
ctcaagcggg tcaaactttt gccgaagaag cagatcacgg atgctattga ttacaatatg 840
gactcggggc gtctttactc aacaattgat gaattccact acaaggcaac ttaaccgatt 900
tgaaggccag cctgctggaa atggcagagg actaagtatc acttgtacta aaccaaagtc 960
tggaatgtc atgttggtc atgaaatgca tggttggtt atgg
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1481701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
Leu Ala Ser His Arg Ser Ser His Leu Arg Thr Arg Lys Pro Ile Leu
1          5          10          15
Arg Thr Ser Ser Gly Asp Arg Glu Asp Asp Ala Val Glu Pro Asn Arg
20          25          30
Leu Leu Ala Val Ala Val His Leu Leu Pro Glu Cys Arg Arg Arg Leu
35          40          45
His His Ala Phe Gln Asp Ala Arg Arg Val Gln His His Ala Ala His
50          55          60
Arg Glu Ala Gly Arg Arg Ala Xaa Ser Gly Thr Gly Glu Lys Gly
65          70          75          80
Ala Pro Phe Ile Val Asn Gly Val Glu Met Ala Asn Ile Arg Leu Val
85          90          95
Gly Met Val Asn Ala Lys Val Glu Arg Thr Thr Asp Val Thr Phe Thr
100         105         110
Leu Asp Asp Gly Thr Gly Arg Leu Asp Phe Ile Arg Trp Val Asn Asp
115         120         125
Ala Ser Asp Ser Phe Glu Thr Ala Ala Ile Gln Asn Gly Met Tyr Ile
130         135         140
Ala Val Ile Gly Ser Leu Lys Gly Leu Gln Glu Arg Lys Arg Ala Thr
145         150         155         160
Ala Phe Ser Ile Arg Pro Ile Thr Asp Phe Asn Glu Val Thr Leu His
165         170         175
Phe Ile Gln Cys Val Arg Met His Ile Glu Asn Ile Glu Leu Lys Ala
180         185         190
Gly Ser Pro Ala Arg Ile Ser Ser Ser Met Gly Val Ser Phe Ser Asn
195         200         205
Gly Phe Ser Glu Ser Ser Thr Pro Thr Ser Leu Lys Ser Ser Pro Ala
210         215         220
Pro Val Thr Ser Gly Ser Ser Asp Thr Asp Leu His Thr Gln Val Leu
225         230         235         240
Asn Phe Phe Asn Glu Pro Ala Asn Leu Glu Ser Glu His Gly Val His
245         250         255
Val Asp Glu Val Leu Lys Arg Phe Lys Leu Leu Pro Lys Lys Gln Ile
260         265         270
```

Thr Asp Ala Ile Asp Tyr Asn Met Asp Ser Gly Arg Leu Tyr Ser Thr
275 280 285
Ile Asp Glu Phe His Tyr Lys Ala Thr
290 295

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1481702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Asn Ile Arg Leu Val Gly Met Val Asn Ala Lys Val Glu Arg
1 5 10 15
Thr Thr Asp Val Thr Phe Thr Leu Asp Asp Gly Thr Gly Arg Leu Asp
20 25 30
Phe Ile Arg Trp Val Asn Asp Ala Ser Asp Ser Phe Glu Thr Ala Ala
35 40 45
Ile Gln Asn Gly Met Tyr Ile Ala Val Ile Gly Ser Leu Lys Gly Leu
50 55 60
Gln Glu Arg Lys Arg Ala Thr Ala Phe Ser Ile Arg Pro Ile Thr Asp
65 70 75 80
Phe Asn Glu Val Thr Leu His Phe Ile Gln Cys Val Arg Met His Ile
85 90 95
Glu Asn Ile Glu Leu Lys Ala Gly Ser Pro Ala Arg Ile Ser Ser Ser
100 105 110
Met Gly Val Ser Phe Ser Asn Gly Phe Ser Glu Ser Ser Thr Pro Thr
115 120 125
Ser Leu Lys Ser Ser Pro Ala Pro Val Thr Ser Gly Ser Ser Asp Thr
130 135 140
Asp Leu His Thr Gln Val Leu Asn Phe Phe Asn Glu Pro Ala Asn Leu
145 150 155 160
Glu Ser Glu His Gly Val His Val Asp Glu Val Leu Lys Arg Phe Lys
165 170 175
Leu Leu Pro Lys Lys Gln Ile Thr Asp Ala Ile Asp Tyr Asn Met Asp
180 185 190
Ser Gly Arg Leu Tyr Ser Thr Ile Asp Glu Phe His Tyr Lys Ala Thr
195 200 205

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1481703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Val Asn Ala Lys Val Glu Arg Thr Thr Asp Val Thr Phe Thr Leu
1 5 10 15
Asp Asp Gly Thr Gly Arg Leu Asp Phe Ile Arg Trp Val Asn Asp Ala

20 25 30
Ser Asp Ser Phe Glu Thr Ala Ala Ile Gln Asn Gly Met Tyr Ile Ala
35 40 45
Val Ile Gly Ser Leu Lys Gly Leu Gln Glu Arg Lys Arg Ala Thr Ala
50 55 60
Phe Ser Ile Arg Pro Ile Thr Asp Phe Asn Glu Val Thr Leu His Phe
65 70 75 80
Ile Gln Cys Val Arg Met His Ile Glu Asn Ile Glu Leu Lys Ala Gly
85 90 95
Ser Pro Ala Arg Ile Ser Ser Ser Met Gly Val Ser Phe Ser Asn Gly
100 105 110
Phe Ser Glu Ser Ser Thr Pro Thr Ser Leu Lys Ser Ser Pro Ala Pro
115 120 125
Val Thr Ser Gly Ser Ser Asp Thr Asp Leu His Thr Gln Val Leu Asn
130 135 140
Phe Phe Asn Glu Pro Ala Asn Leu Glu Ser Glu His Gly Val His Val
145 150 155 160
Asp Glu Val Leu Lys Arg Phe Lys Leu Leu Pro Lys Lys Gln Ile Thr
165 170 175
Asp Ala Ile Asp Tyr Asn Met Asp Ser Gly Arg Leu Tyr Ser Thr Ile
180 185 190
Asp Glu Phe His Tyr Lys Ala Thr
195 200

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

atcattactc	cactccacat	tcgacaaaat	atatcttaga	caagttaagt	ttaacgataa	60
tggattcaag	atatgttacc	ctatgcattt	tcttagtact	tgccttacat	ggagatacta	120
ctttggcaga	aacttgcagg	cagtatgttg	aagggcagcc	attttgcttt	aaagcaatgt	180
gcaaggcaaa	ttgttttatg	gagggaaaat	tctctgatgg	ttcttatgta	aagggttaca	240
gatgtgaatc	aggtggattc	cactcggtgt	gtgtttgcct	tttgtgcaaa	aattagttat	300
ctaaagacaa	gcggatatat	cttcttatgt	tcctatccat	tatttaggat	tatagtccaa	360
ataattatac	aatagcttag	ttaaatagtt	ttttatttat	agacaaatgt	agcactagtt	420
aactagttgt	gatttttttaa	atttctcagc	tataaatcag	gaaatatttt	ttaacacttc	480
aataatatat	ctttgttcgc					

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ser Leu Leu His Ser Thr Phe Asp Lys Ile Tyr Leu Arg Gln Val Lys
1 5 10 15
Phe Asn Asp Asn Gly Phe Lys Ile Cys Tyr Pro Met His Phe Leu Ser

20 25 30
Thr Cys Leu Thr Trp Arg Tyr Tyr Phe Gly Arg Asn Leu Gln Ala Val
35 40 45
Cys

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1481706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

His Tyr Ser Thr Pro His Ser Thr Lys Tyr Ile Leu Asp Lys Leu Ser
1 5 10 15
Leu Thr Ile Met Asp Ser Arg Tyr Val Thr Leu Cys Ile Phe Leu Val
20 25 30
Leu Ala Leu His Gly Asp Thr Thr Leu Ala Glu Thr Cys Arg Gln Tyr
35 40 45
Val Glu Gly Gln Pro Phe Cys Phe Lys Ala Met Cys Lys Ala Asn Cys
50 55 60
Phe Met Glu Gly Lys Phe Ser Asp Gly Ser Tyr Val Lys Gly Tyr Arg
65 70 75 80
Cys Glu Ser Gly Gly Phe His Ser Val Cys Val Cys Leu Leu Cys Lys
85 90 95
Asn

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1481707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Asp Ser Arg Tyr Val Thr Leu Cys Ile Phe Leu Val Leu Ala Leu
1 5 10 15
His Gly Asp Thr Thr Leu Ala Glu Thr Cys Arg Gln Tyr Val Glu Gly
20 25 30
Gln Pro Phe Cys Phe Lys Ala Met Cys Lys Ala Asn Cys Phe Met Glu
35 40 45
Gly Lys Phe Ser Asp Gly Ser Tyr Val Lys Gly Tyr Arg Cys Glu Ser
50 55 60
Gly Gly Phe His Ser Val Cys Val Cys Leu Leu Cys Lys Asn
65 70 75

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..916

(D) OTHER INFORMATION: / Ceres Seq. ID 1481716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

aattttctgag	caccaaacca	accaagccaa	tcttacgact	gccttgccctt	tggcattgtct	60
ctaatttcga	cagcttcgat	actcctcctc	cacgcctgcw	ccctgctcgc	cgccgcaaga	120
gtccccgacc	cggtagaaca	tggcgacgtg	aacacggcga	tgcttaccaa	cggtcgggcc	180
tggcgacgc	cgctgtcccc	tgacagcagc	agcaacggca	acttcgagac	gtacttctgc	240
ttcctctgct	cgggccgcga	cccgtgtctc	attcaccact	gccccatcta	ctgggacgag	300
tgccacctca	tctgcgacga	tgacatgtcc	accgccactc	ctactccacc	tgctgttgca	360
gtgtcgtcgt	cgctcgtcgtc	ccmgccccgt	ccccatggtg	caggtgcagg	gcgatgatga	420
ctgtacgtc	atgaagctct	acatgtccgg	ccgctacgtc	atcgtcgaac	accggccatg	480
caaatacatc	gcctgggtgct	tcctcacntg	cggcgscggg	gagctggcgg	cgcccgaccg	540
gaaagccgtc	acggccactg	cgatccaggg	gacctctctg	cctgcccagc	tatgcggcac	600
gcaggcggtc	aatgctccac	cattagcagg	cgctcgtcgtc	ccagcagcag	cagcagcagc	660
tggtggtgct	ggtgcgcacc	gacggcgcta	gctgcctagc	tacttatccg	cgaactaagg	720
gttaatttta	gacataaaac	ctgagaggag	gattcaaggg	attaaaatct	ctttcttatt	780
ccaaagaaat	tttagccact	cgaatcctct	ctgattttct	ggctcctaaa	ttagccctaa	840
tattaaagga	ccaacagatg	ccaaacttaa	accatcgatc	tctacaagat	aactaatatt	900
ttgatttcca	aacttt					

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1481717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met	Ser	Leu	Ile	Ser	Thr	Ala	Ser	Ile	Leu	Leu	Leu	His	Ala	Cys	Xaa
1			5						10					15	
Leu	Leu	Ala	Ala	Ala	Arg	Val	Pro	Asp	Pro	Val	Glu	His	Gly	Asp	Val
			20						25				30		
Asn	Thr	Ala	Met	Leu	Thr	Asn	Gly	Ser	Ala	Ser	Ala	Thr	Pro	Ser	Ser
			35				40					45			
Pro	Asp	Ser	Ser	Ser	Asn	Gly	Asn	Phe	Glu	Thr	Tyr	Phe	Cys	Phe	Leu
			50			55					60				
Cys	Ser	Gly	Arg	Asp	Pro	Leu	Leu	Ile	His	His	Cys	Pro	Ile	Tyr	Trp
65				70					75					80	
Asp	Glu	Cys	His	Leu	Ile	Cys	Asp	Asp	Asp	Met	Ser	Thr	Ala	Thr	Pro
			85						90					95	
Thr	Pro	Pro	Ala	Val	Ala	Val	Ser	Ser	Ser	Ser	Ser	Ser	Xaa	Pro	Arg
			100					105					110		
Pro	His	Gly	Ala	Gly	Ala	Gly	Arg								
			115				120								

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1481718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
Met Thr Cys Pro Pro Pro Leu Leu Leu His Leu Leu Leu Gln Cys Arg
1      5      10      15
Arg Arg Arg Arg Pro Xaa Pro Val Pro Met Val Gln Val Gln Gly Asp
      20      25      30
Asp Asp Cys Tyr Val Met Lys Leu Tyr Met Ser Gly Arg Tyr Val Ile
      35      40      45
Val Glu His Arg Pro Cys Lys Tyr Ile Ala Trp Cys Phe Leu Xaa Cys
      50      55      60
Gly Xaa Gly Glu Leu Ala Ala Ala Asp Arg Lys Ala Val Thr Ala Thr
65      70      75      80
Ala Ile Gln Gly Thr Ser Leu Pro Ala Glu Leu Cys Gly Thr Gln Ala
      85      90      95
Val Asn Ala Pro Pro Leu Ala Gly Val Val Val Pro Ala Ala Ala Ala
      100      105      110
Ala Ala Gly Gly Ala Gly Ala His Arg Arg Arg
      115      120
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1481719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
Met Val Gln Val Gln Gly Asp Asp Asp Cys Tyr Val Met Lys Leu Tyr
1      5      10      15
Met Ser Gly Arg Tyr Val Ile Val Glu His Arg Pro Cys Lys Tyr Ile
      20      25      30
Ala Trp Cys Phe Leu Xaa Cys Gly Xaa Gly Glu Leu Ala Ala Ala Asp
      35      40      45
Arg Lys Ala Val Thr Ala Thr Ala Ile Gln Gly Thr Ser Leu Pro Ala
      50      55      60
Glu Leu Cys Gly Thr Gln Ala Val Asn Ala Pro Pro Leu Ala Gly Val
65      70      75      80
Val Val Pro Ala Ala Ala Ala Ala Ala Gly Gly Ala Gly Ala His Arg
      85      90      95
Arg Arg
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..553

(D) OTHER INFORMATION: / Ceres Seq. ID 1481728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
aaatcgcggt cactgctccg aagtcggaac cttcatcac atcgtctcgt ttccgatttc      60
cccaaattca ggccacaggc gctacaggac ccaggcacca ctcggtcggc ggccaccgcg      120
```

tcgccccgcc	tgctcgattg	gggtcgcggtg	tgcgatagga	agtattgtgt	tgtgtttgca	180
acgtgatagc	ttgtactggg	aacaaagggtc	aagatgggag	ccttggacct	acaccttgac	240
tttgcttctg	ctcaacatgg	acaagccaag	ttaaaggaat	atgccaagag	ctctctgttg	300
tctgatggaa	actacaatac	agacaagatc	aatgggtcaa	accctgatga	ctatgagaaa	360
tttgagaaag	ggataatgca	ctatgggtgt	ccacattata	gaaggagatg	ccgcataaga	420
gctccttgct	gcaatgaaat	ttttgattgc	cgacactgcc	acaatgaaac	taagaattcc	480
atataaattg	ataaaatgaa	gaggcatgaa	cttccacgcc	atgaagtgca	gcaggttgta	540
tgctcattgt	gtg					

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Lys	Ser	Arg	Ser	Leu	Leu	Arg	Ser	Pro	Asn	Leu	His	Thr	His	Arg	Leu
1				5					10					15	
Val	Ser	Asp	Phe	Pro	Lys	Phe	Arg	Pro	Gln	Ala	Leu	Gln	Asp	Pro	Gly
			20					25					30		
Thr	Thr	Arg	Ser	Ala	Ala	Thr	Ala	Ser	Pro	Arg	Leu	Leu	Asp	Trp	Gly
		35					40					45			
Arg	Val	Cys	Asp	Arg	Lys	Tyr	Cys	Val	Val	Phe	Ala	Thr			
50					55						60				

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Asn	Arg	Gly	His	Cys	Ser	Glu	Val	Arg	Thr	Phe	Ile	His	Ile	Val	Ser
1				5					10					15	
Phe	Pro	Ile	Ser	Pro	Asn	Ser	Gly	His	Arg	Arg	Tyr	Arg	Thr	Gln	Ala
			20					25					30		
Pro	Leu	Gly	Arg	Arg	Pro	Pro	Arg	Arg	Pro	Ala	Cys	Ser	Ile	Gly	Val
		35					40					45			
Ala	Cys	Ala	Ile	Gly	Ser	Ile	Val	Leu	Cys	Leu	Gln	Arg	Asp	Ser	Leu
50					55					60					
Tyr	Trp	Glu	Gln	Arg	Ser	Arg	Trp	Ala	Pro	Trp	Thr	Tyr	Thr	Leu	Thr
65				70					75					80	
Leu	Leu	Leu	Leu	Asn	Met	Asp	Lys	Pro	Ser						
			85					90							

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1481731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met	Gly	Ala	Leu	Asp	Leu	His	Leu	Asp	Phe	Ala	Ser	Ala	Gln	His	Gly
1			5					10					15		
Gln	Ala	Lys	Leu	Lys	Glu	Tyr	Ala	Lys	Ser	Ser	Leu	Leu	Ser	Asp	Gly
			20					25					30		
Asn	Tyr	Asn	Thr	Asp	Lys	Ile	Asn	Gly	Ser	Asn	Pro	Asp	Asp	Tyr	Glu
			35				40					45			
Lys	Phe	Glu	Lys	Gly	Ile	Met	His	Tyr	Gly	Cys	Pro	His	Tyr	Arg	Arg
			50			55				60					
Arg	Cys	Arg	Ile	Arg	Ala	Pro	Cys	Cys	Asn	Glu	Ile	Phe	Asp	Cys	Arg
65					70				75					80	
His	Cys	His	Asn	Glu	Thr	Lys	Asn	Ser	Ile	Lys	Ile	Asp	Lys	Met	Lys
			85					90					95		
Arg	His	Glu	Leu	Pro	Arg	His	Glu	Val	Gln	Gln	Val	Val	Cys	Ser	Leu
			100					105					110		

Cys

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..709

(D) OTHER INFORMATION: / Ceres Seq. ID 1481732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

atattcttctg	tgcctgggcg	ttcccagggtg	ccatgcgagt	agatcggcaa	ctactccatc	60
ctcctctctcc	tacctggcca	togtgcagca	gccgtgctga	gcctctgctg	ccctctctct	120
ggccactcgc	gtgagcccct	gctggtcggc	tgtccggaca	cgacggctat	ggccgagccc	180
agcgcaagt	catcctccag	gactgagccc	ctgtgcagcc	actaccgccg	gcaggcctcg	240
gtgtccggtt	gtgcttcgac	aagtcacgcg	cctccgacaa	acctcgcgcc	cgtcgtgttc	300
ttgcctctac	gtcaatcgac	acgcatagaa	tgcgatccat	ctccaagctt	cgagggatcg	360
aagatcaagc	gttggcgacc	atgtgatcaa	gctctctgag	ttctatgagg	ctgaagatcc	420
tgagcatctg	tttgggtgaag	attgcctttg	gtgcaatcta	tgctcaggta	aagagggcgt	480
cgaggcggat	ctccaggagt	tccaggacgt	cgacgggttc	gaggattagg	ctagcgacct	540
ccccagtcga	gctgcctgtg	gtgggttggt	tacgttggtc	acgtttcgat	tctgtgtact	600
ttgatttata	ttatgtaaat	ggttctagtt	tgtaatatata	ttacttactc	tttattgtaa	660
ttcgaagcat	tgtgctatga	tgagtcattt	atgtaatcgc	cgtgtacgc		

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1481733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Phe	Leu	Arg	Ala	Trp	Ala	Phe	Pro	Gly	Ala	Met	Arg	Val	Asp	Arg	Gln
1			5					10					15		

Leu Leu His Pro Pro Leu Pro Thr Trp Pro Ser Cys Ser Ser Arg Ala
20 25 30
Glu Pro Leu Leu Pro Ser Leu Trp Pro Leu Ala
35 40

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1481734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ala Glu Pro Ser Ala Lys Ser Ser Ser Arg Thr Glu Pro Leu Cys
1 5 10 15
Ser His Tyr Arg Arg Gln Ala Ser Val Ser Gly Cys Ala Ser Thr Ser
20 25 30
His Ala Pro Pro Thr Asn Leu Ala Pro Val Val Phe Leu Pro Leu Arg
35 40 45
Gln Ser Thr Arg Ile Glu Cys Asp Pro Ser Pro Ser Phe Glu Gly Ser
50 55 60
Lys Ile Lys Arg Trp Arg Pro Cys Asp Gln Ala Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1481735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Arg Leu Lys Ile Leu Ser Ile Cys Leu Val Lys Ile Ala Phe Gly
1 5 10 15
Ala Ile Tyr Ala Gln Val Lys Arg Ala Ser Arg Arg Ile Ser Arg Ser
20 25 30
Ser Arg Thr Ser Thr Gly Ser Arg Ile Arg Leu Ala Thr Ser Pro Ser
35 40 45
Gln Leu Pro Val Val Gly Cys Leu Arg Trp Leu Arg Phe Asp Ser Val
50 55 60
Tyr Phe Asp Leu Tyr Tyr Val Asn Gly Ser Ser Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 951 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..951

(D) OTHER INFORMATION: / Ceres Seq. ID 1481740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

attacacaaa	tgtgcgccgc	catgttctcc	aatctcttcg	ccaagtttga	ctacggacga	60
tcgtctccac	cgaagacgcc	acacgatgac	ggccgccgta	gccacatgtc	tgatctttcc	120
ctagaaaagac	agcctcgacg	gtcgtccgtc	tccgtccgca	tgaggcgcc	cgtggatgat	180
gacgacgtca	ctgcgccgcc	cgtagccgag	gtgatgagca	cggaccatgg	cggccacgag	240
gagtcgtctc	caccgaagac	gccacacgat	gacggctgcc	gtagccacat	gtctgatctt	300
tccctagaaa	gacagcctcg	acagtcgtcc	gtctcggtcc	gcatggaggc	gcccgtggat	360
gacgacgacg	tcactkcggc	gcccgtagcc	gaggtgatga	gcatggacca	tggcggccac	420
gaggagtgcg	cgacgggtccc	gtgcctcgcg	ttcgcgtccg	agcacgggta	cagcatcttc	480
tccctagcct	acatgcgcgd	tgttcatcga	cggcgccscac	ggkttcamag	tcaccgccga	540
cccagwggga	gcgaaagcga	aaccgcgkt	acgtgattct	tgccaaycgg	ctaacacmcc	600
catktggacg	tctggccgtc	gtgtttgacg	tccgcttctc	cgaccttdgg	aggccagagc	660
scwtggggcg	gctaaagcta	aacmccggcg	aggttgascc	aatktggggc	cagccgcact	720
ggatcatgcc	trgggataga	tcggatcgtc	gtcaaggata	twtcaactag	tacagtttat	780
tgtaggtagt	tmcattagtt	tacatactct	ggctgtcagg	cmctatttct	acgtaaagtt	840
ttttttggca	ttrgggaaa	atattmcgga	tctataagat	atthtgrgtt	ttaaaagcta	900
ctgataaatc	tacatgtacg	ttgcaatgcg	aaataaactg	tgtctatgtt	t	

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile	Thr	Gln	Met	Cys	Ala	Ala	Met	Phe	Ser	Asn	Leu	Phe	Ala	Lys	Phe
1			5					10						15	
Asp	Tyr	Gly	Arg	Ser	Ser	Pro	Pro	Lys	Thr	Pro	His	Asp	Asp	Gly	Arg
			20					25						30	
Arg	Ser	His	Met	Ser	Asp	Leu	Ser	Leu	Glu	Arg	Gln	Pro	Arg	Arg	Ser
		35					40					45			
Ser	Val	Ser	Val	Arg	Met	Glu	Ala	Pro	Val	Asp	Asp	Asp	Asp	Val	Thr
	50					55				60					
Ala	Ala	Pro	Val	Ala	Glu	Val	Met	Ser	Thr	Asp	His	Gly	Gly	His	Glu
65				70					75					80	
Glu	Ser	Ser	Pro	Pro	Lys	Thr	Pro	His	Asp	Asp	Gly	Cys	Arg	Ser	His
			85					90						95	
Met	Ser	Asp	Leu	Ser	Leu	Glu	Arg	Gln	Pro	Arg	Gln	Ser	Ser	Val	Ser
			100					105					110		
Val	Arg	Met	Glu	Ala	Pro	Val	Asp	Asp	Asp	Asp	Val	Thr	Xaa	Ala	Pro
		115					120					125			
Val	Ala	Glu	Val	Met	Ser	Met	Asp	His	Gly	Gly	His	Glu	Glu	Ser	Pro
	130					135					140				
Thr	Val	Pro	Cys	Leu	Ala	Phe	Ala	Ser	Glu	His	Gly	Tyr	Ser	Ile	Phe
145				150					155					160	
Ser	Leu	Ala	Tyr	Met	Arg	Xaa	Val	His	Arg	Arg	Arg	Xaa	Arg	Xaa	Xaa
			165					170						175	
Ser	His	Arg	Arg	Pro	Xaa	Gly	Ser	Glu	Ser	Glu	Thr	Ala	Xaa	Thr	
			180				185						190		

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1481742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Met	Cys	Ala	Ala	Met	Phe	Ser	Asn	Leu	Phe	Ala	Lys	Phe	Asp	Tyr	Gly	
1				5					10					15		
Arg	Ser	Ser	Pro	Pro	Lys	Thr	Pro	His	Asp	Asp	Gly	Arg	Arg	Ser	His	
			20					25					30			
Met	Ser	Asp	Leu	Ser	Leu	Glu	Arg	Gln	Pro	Arg	Arg	Ser	Ser	Val	Ser	
		35				40					45					
Val	Arg	Met	Glu	Ala	Pro	Val	Asp	Asp	Asp	Asp	Val	Thr	Ala	Ala	Pro	
		50				55					60					
Val	Ala	Glu	Val	Met	Ser	Thr	Asp	His	Gly	Gly	His	Glu	Glu	Ser	Ser	
65					70				75						80	
Pro	Pro	Lys	Thr	Pro	His	Asp	Asp	Gly	Cys	Arg	Ser	His	Met	Ser	Asp	
				85				90						95		
Leu	Ser	Leu	Glu	Arg	Gln	Pro	Arg	Gln	Ser	Ser	Val	Ser	Val	Arg	Met	
			100					105					110			
Glu	Ala	Pro	Val	Asp	Asp	Asp	Asp	Val	Thr	Xaa	Ala	Pro	Val	Ala	Glu	
		115					120					125				
Val	Met	Ser	Met	Asp	His	Gly	Gly	His	Glu	Glu	Ser	Pro	Thr	Val	Pro	
		130				135					140					
Cys	Leu	Ala	Phe	Ala	Ser	Glu	His	Gly	Tyr	Ser	Ile	Phe	Ser	Leu	Ala	
145					150				155						160	
Tyr	Met	Arg	Xaa	Val	His	Arg	Arg	Arg	Xaa	Arg	Xaa	Xaa	Ser	His	Arg	
				165					170					175		
Arg	Pro	Xaa	Gly	Ser	Glu	Ser	Glu	Thr	Ala	Xaa	Thr					
			180					185								

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1481743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Phe	Ser	Asn	Leu	Phe	Ala	Lys	Phe	Asp	Tyr	Gly	Arg	Ser	Ser	Pro	
1				5				10						15		
Pro	Lys	Thr	Pro	His	Asp	Asp	Gly	Arg	Arg	Ser	His	Met	Ser	Asp	Leu	
			20					25					30			
Ser	Leu	Glu	Arg	Gln	Pro	Arg	Arg	Ser	Ser	Val	Ser	Val	Arg	Met	Glu	
		35					40					45				
Ala	Pro	Val	Asp	Asp	Asp	Asp	Val	Thr	Ala	Ala	Pro	Val	Ala	Glu	Val	
		50				55					60					
Met	Ser	Thr	Asp	His	Gly	Gly	His	Glu	Glu	Ser	Pro	Pro	Lys	Thr		
65					70				75					80		
Pro	His	Asp	Asp	Gly	Cys	Arg	Ser	His	Met	Ser	Asp	Leu	Ser	Leu	Glu	
				85				90						95		
Arg	Gln	Pro	Arg	Gln	Ser	Ser	Val	Ser	Val	Arg	Met	Glu	Ala	Pro	Val	
			100					105					110			
Asp	Asp	Asp	Asp	Val	Thr	Xaa	Ala	Pro	Val	Ala	Glu	Val	Met	Ser	Met	
		115					120					125				
Asp	His	Gly	Gly	His	Glu	Glu	Ser	Pro	Thr	Val	Pro	Cys	Leu	Ala	Phe	

130 135 140
Ala Ser Glu His Gly Tyr Ser Ile Phe Ser Leu Ala Tyr Met Arg Xaa
145 150 155 160
Val His Arg Arg Arg Xaa Arg Xaa Xaa Ser His Arg Arg Pro Xaa Gly
165 170 175
Ser Glu Ser Glu Thr Ala Xaa Thr
180

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

agttctaaac cctaaacctg acgcccgcac ggccgcccgc gttcgccaca tcgtgcgccg	60
ccgcctctcc acggccgccc ccatactgc accgggtccc actccggcct ccatactcaa	120
cccgctctcg ccgagcactc ccctcacctc gcgacataag acccgactcg ccatactccct	180
cctcaagtct tccccgcccgc ctccccccga ccagatcctc tccatttgcc gcgcccgcga	240
ctgacccccg agacacacat cgaccgcac gcgctgtcgc tagccgcac aaagctctcc	300
tccgctccgg acaccctccg tgacctcgcc tccacmgtcc tcaccccgcg cmamgcaccc	360
cacgcmatcg cgctcttcgg ccaggcacam ctctccccg acgssatctc cactttccag	420
tcctccccct cc	

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Val Leu Asn Pro Lys Pro Asp Ala Ala Met Ala Ala Val Arg His	
1 5 10 15	
Ile Val Arg Arg Arg Leu Ser Thr Ala Ala Ile Thr Ala Pro Val	
20 25 30	
Pro Thr Pro Ala Ser Ile Leu Asn Pro Ser Ser Pro Ser Thr Pro Leu	
35 40 45	
Thr Ser Arg His Lys Thr Arg Leu Ala Ile Ser Leu Leu Lys Ser Ser	
50 55 60	
Pro Pro Pro Pro Pro Asp Gln Ile Leu Ser Ile Cys Arg Ala Ala His	
65 70 75 80	

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1481746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ala Ala Ala Val Arg His Ile Val Arg Arg Arg Leu Ser Thr Ala
1 5 10 15
Ala Ala Ile Thr Ala Pro Val Pro Thr Pro Ala Ser Ile Leu Asn Pro
20 25 30
Ser Ser Pro Ser Thr Pro Leu Thr Ser Arg His Lys Thr Arg Leu Ala
35 40 45
Ile Ser Leu Leu Lys Ser Ser Pro Pro Pro Pro Asp Gln Ile Leu
50 55 60
Ser Ile Cys Arg Ala Ala His
65 70

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 557 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..557

(D) OTHER INFORMATION: / Ceres Seq. ID 1481747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

agactccggc cacagccgag acgagactag cagcagccgc ttgctcagat cggcagcttc 60
ggcggcggcg gagatggcga ttcggtactg gccgatggcc ggagcagccg ttgggttccg 120
cctcgctcctg gttctcttcg gcggggatct ccaccttgcc tctcgccctg aggtctccac 180
ccccctcacc tcccttcgcc gcctggcgga aggctactgg ctgaagcaag cgtccgtgtc 240
accgtactcc ggttctatgt atcacggttc cccattgctc ctgtctgttc ttggtccatt 300
aactagtagc aggccgtgacg gacatcatgc tcatatttac tgcagtttga tttttgtggc 360
tgtagatttt ctagcagcca tgctcatccg agcgactggg catgaactcg aaatggcacg 420
gaacagaagt ttgaagtcac ttgacctcac aaaggcagtw aaggatacag ttaatgtaag 480
cgctggagat gttgcttctc tcatatattt gtggaaccct tgggcaatag tcacttgtgt 540
gggatcatgt acatcac

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1481748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Asp Ser Gly His Ser Arg Asp Glu Thr Ser Ser Ser Arg Leu Leu Arg
1 5 10 15
Ser Ala Ala Ser Ala Ala Ala Glu Met Ala Ile Arg Tyr Trp Pro Met
20 25 30
Ala Gly Ala Ala Val Gly Phe Arg Leu Val Leu Val Leu Phe Gly Gly
35 40 45
Asp Leu His Leu Ala Ser Arg Pro Glu Val Ser Thr Pro Leu Thr Ser
50 55 60
Leu Arg Arg Leu Ala Glu Gly Tyr Trp Leu Lys Gln Ala Ser Val Ser
65 70 75 80
Pro Tyr Ser Gly Ser Met Tyr His Gly Ser Pro Leu Leu Leu Ser Val

				85					90					95		
Leu	Gly	Pro	Leu	Thr	Ser	Ser	Arg	Pro	Asp	Gly	His	His	Ala	His	Ile	
			100					105					110			
Tyr	Cys	Ser	Leu	Ile	Phe	Val	Ala	Val	Asp	Phe	Leu	Ala	Ala	Met	Leu	
		115					120					125				
Ile	Arg	Ala	Thr	Gly	His	Glu	Leu	Glu	Met	Ala	Arg	Asn	Arg	Ser	Leu	
	130					135					140					
Lys	Ser	Leu	Asp	Leu	Thr	Lys	Ala	Xaa	Lys	Asp	Thr	Val	Asn	Val	Ser	
145					150					155					160	
Ala	Gly	Asp	Val	Ala	Ser	Leu	Ile	Tyr	Leu	Trp	Asn	Pro	Trp	Ala	Ile	
			165						170					175		
Val	Thr	Cys	Val	Gly	Ser	Cys	Thr	Ser								
		180					185									

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1481749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met	Ala	Ile	Arg	Tyr	Trp	Pro	Met	Ala	Gly	Ala	Ala	Val	Gly	Phe	Arg	
1				5					10					15		
Leu	Val	Leu	Val	Leu	Phe	Gly	Gly	Asp	Leu	His	Leu	Ala	Ser	Arg	Pro	
			20					25					30			
Glu	Val	Ser	Thr	Pro	Leu	Thr	Ser	Leu	Arg	Arg	Leu	Ala	Glu	Gly	Tyr	
		35					40					45				
Trp	Leu	Lys	Gln	Ala	Ser	Val	Ser	Pro	Tyr	Ser	Gly	Ser	Met	Tyr	His	
	50					55					60					
Gly	Ser	Pro	Leu	Leu	Leu	Ser	Val	Leu	Gly	Pro	Leu	Thr	Ser	Ser	Arg	
65					70					75					80	
Pro	Asp	Gly	His	His	Ala	His	Ile	Tyr	Cys	Ser	Leu	Ile	Phe	Val	Ala	
				85					90					95		
Val	Asp	Phe	Leu	Ala	Ala	Met	Leu	Ile	Arg	Ala	Thr	Gly	His	Glu	Leu	
			100						105				110			
Glu	Met	Ala	Arg	Asn	Arg	Ser	Leu	Lys	Ser	Leu	Asp	Leu	Thr	Lys	Ala	
		115					120					125				
Xaa	Lys	Asp	Thr	Val	Asn	Val	Ser	Ala	Gly	Asp	Val	Ala	Ser	Leu	Ile	
	130						135					140				
Tyr	Leu	Trp	Asn	Pro	Trp	Ala	Ile	Val	Thr	Cys	Val	Gly	Ser	Cys	Thr	
145					150					155					160	
Ser																

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1481750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Met Ala Gly Ala Ala Val Gly Phe Arg Leu Val Leu Val Leu Phe Gly
1 5 10 15
Gly Asp Leu His Leu Ala Ser Arg Pro Glu Val Ser Thr Pro Leu Thr
20 25 30
Ser Leu Arg Arg Leu Ala Glu Gly Tyr Trp Leu Lys Gln Ala Ser Val
35 40 45
Ser Pro Tyr Ser Gly Ser Met Tyr His Gly Ser Pro Leu Leu Leu Ser
50 55 60
Val Leu Gly Pro Leu Thr Ser Ser Arg Pro Asp Gly His His Ala His
65 70 75 80
Ile Tyr Cys Ser Leu Ile Phe Val Ala Val Asp Phe Leu Ala Ala Met
85 90 95
Leu Ile Arg Ala Thr Gly His Glu Leu Glu Met Ala Arg Asn Arg Ser
100 105 110
Leu Lys Ser Leu Asp Leu Thr Lys Ala Xaa Lys Asp Thr Val Asn Val
115 120 125
Ser Ala Gly Asp Val Ala Ser Leu Ile Tyr Leu Trp Asn Pro Trp Ala
130 135 140
Ile Val Thr Cys Val Gly Ser Cys Thr Ser
145 150

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

acaagcaagt ggccaccttt gagtggatgt tggaagaaat agcagccaca agcaagtagt	60
cacctgtgtc atcttattcc gatcctagsc cctcccattc ccaawkcctc gstitcctcct	120
cccttctcta gttctctgat cctcagcact tagcatcaag cttagsacac cggcgagatg	180
gcctccamct ccamcttcct gtccamcctc gccagcaggt ccgcggcagc cgatagcctg	240
ygcamgccgt gccgtccttc gccaagatcg tcaggttctt gcccgcgcar gcgcagatca	300
gccgcavggn cmgcgcggcg gtgctgccca cgccgarggc ggcggtgtcg ggcacgagaa	360
ggcgccgtcg agcaagcacg	

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met Ala Ser Xaa Ser Xaa Phe Leu Ser Xaa Leu Ala Ser Arg Ser Ala
1 5 10 15
Ala Ala Asp Ser Leu Xaa Xaa Pro Cys Arg Pro Ser Pro Arg Ser Ser
20 25 30
Gly Ser Cys Pro Arg Xaa Arg Arg Ser Ala Ala Xaa Xaa Ala Arg Arg
35 40 45
Cys Cys Pro Arg Arg Xaa Arg Arg Cys Arg Ala Arg Glu Gly Ala Val
50 55 60

Glu Gln Ala

65

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ctgttcttcc	acctgctggc	tgwcctggc	tccctgccc	cccaaacc	cccgcctgc	60
cgtccccgca	gccgcagcct	gctctcggt	cccgcgcgc	tctaccgcgt	cctgcggctg	120
cggtgttgcg	tcacctcggg	ttcgccctaa	cttccacaat	cctgcgcgtc	ctggtgctcc	180
gccgcccctc	cctttgtact	cgcgctggag	ctgcagatcc	accgcgacct	ggcgaccaat	240
tcctcctccc	gctgaagaat	tggcgacctt	ggcctccgcm	cccgcggcgc	gaggagtcaa	300
ctgtggtagc	aaccaccgcg	gaggctgcaa	gcttcggtaa	gggaggaaag	ttgacttgtt	360
ggaagccggt	ccagggccgc	gatgacgtcg	acagccgcgc	ggcgtcgtcg	tcggcggcga	420
agagcgagtc	ctacctgcgg	gccgacaaga	tcgacctcga	gagcctggac	atccagctgg	480

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Cys	Ser	Ser	Thr	Cys	Trp	Leu	Xaa	Leu	Pro	Pro	Leu	Arg	Pro	Lys	Pro
1				5					10					15	
Thr	Arg	Leu	Ala	Val	Pro	Ala	Ala	Ala	Ala	Cys	Ser	Arg	Leu	Pro	Pro
			20					25					30		
Pro	Ser	Thr	Ala	Ser	Cys	Gly	Cys	Gly	Val	Ala	Ser	Pro	Arg	Val	Arg
			35				40					45			
Leu	Asn	Phe	His	Asn	Pro	Arg	Arg	Pro	Gly	Ala	Pro	Pro	Pro	Leu	Pro
			50			55					60				
Leu	Tyr	Ser	Arg	Trp	Ser	Cys	Arg	Ser	Thr	Ala	Thr	Trp	Arg	Pro	Ile
65					70					75				80	
Pro	Pro	Pro	Ala	Glu	Glu	Leu	Ala	Thr	Leu	Ala	Ser	Xaa	Pro	Ala	Ala
			85					90					95		
Arg	Gly	Val	Asn	Cys	Gly	Ser	Asn	His	Arg	Gly	Gly	Cys	Lys	Leu	Arg
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1481766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
Val Leu Pro Pro Ala Gly Cys Xaa Cys Leu Pro Cys Ala Pro Asn Pro
1      5      10      15
Pro Ala Ser Pro Ser Pro Gln Pro Gln Pro Ala Leu Gly Ser Arg Arg
20      25      30
Arg Leu Pro Arg Pro Ala Ala Ala Val Leu Arg His Leu Gly Phe Ala
35      40      45
Leu Thr Ser Thr Ile Leu Ala Val Leu Val Leu Arg Arg Pro Ser Leu
50      55      60
Cys Thr Arg Ala Gly Ala Ala Asp Pro Pro Arg Pro Gly Asp Gln Phe
65      70      75      80
Leu Leu Pro Leu Lys Asn Trp Arg Pro Trp Pro Pro Xaa Pro Arg Arg
85      90      95
Glu Glu Ser Thr Val Val Ala Thr Thr Ala Glu Ala Ala Ser Phe Gly
100     105     110
Lys Gly Gly Lys Leu Thr Cys Trp Lys Pro Val Gln Gly Arg Asp Asp
115     120     125
Val Asp Ser Arg Arg Ala Ser Ser Ser Ala Ala Lys Ser Glu Ser Tyr
130     135     140
Leu Arg Ala Asp Lys Ile Asp Leu Glu Ser Leu Asp Ile Gln Leu Glu
145     150     155     160
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1481770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
ggactcacga agcagcacac tctgcactct cggcaacaac tgacggccgg aggaagaagg      60
cgcagacgac aagcagaagc ttgtgccatc gatcaatggc ggcggtgaca aagatctacg      120
tcgtgtacta ctgcacgtac gghcacgtgg cgargctggc ggaggagatc aagaagggcg      180
ccgactccgt ggacggcgctc gaggcaacca tctggcargw agcggaracg ctgccggavg      240
argcgctggc gaagatgcrc gcaccggcga ggagcgagga gcaccgggtg atctcgggca      300
arcagctggg ggacgcrnac ggcacccctgt tcggcttccc rgcrccggttc ggcacgatgg      360
crgcgcagat gaaggc
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1481771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
Thr His Glu Ala Ala His Ser Ala Leu Ser Ala Thr Thr Asp Gly Arg
1      5      10      15
```

Arg Lys Lys Ala Gln Thr Thr Ser Arg Ser Leu Cys His Arg Ser Met
20 25 30
Ala Ala Val Thr Lys Ile Tyr Val Val Tyr Tyr Ser Thr Tyr Xaa His
35 40 45
Val Ala Xaa Leu Ala Glu Glu Ile Lys Lys Gly Ala Asp Ser Val Asp
50 55 60
Gly Val Glu Ala Thr Ile Trp Xaa Xaa Ala Xaa Thr Leu Pro Xaa Xaa
65 70 75 80
Ala Leu Ala Lys Met Xaa Ala Pro Ala Arg Ser Glu Glu His Pro Val
85 90 95
Ile Ser Gly Xaa Gln Leu Val Asp Xaa Asp Gly Ile Leu Phe Gly Phe
100 105 110
Xaa Xaa Arg Phe Gly Met Met Xaa Ala Gln Met Lys
115 120

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Ala Ala Val Thr Lys Ile Tyr Val Val Tyr Tyr Ser Thr Tyr Xaa
1 5 10 15
His Val Ala Xaa Leu Ala Glu Glu Ile Lys Lys Gly Ala Asp Ser Val
20 25 30
Asp Gly Val Glu Ala Thr Ile Trp Xaa Xaa Ala Xaa Thr Leu Pro Xaa
35 40 45
Xaa Ala Leu Ala Lys Met Xaa Ala Pro Ala Arg Ser Glu Glu His Pro
50 55 60
Val Ile Ser Gly Xaa Gln Leu Val Asp Xaa Asp Gly Ile Leu Phe Gly
65 70 75 80
Phe Xaa Xaa Arg Phe Gly Met Met Xaa Ala Gln Met Lys
85 90

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..448
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

attgagtata ggtttgctct cctacacttt tttgagaaag acattgaagg atgacatagt	60
tgttccaatg cttgatttta agatccaaga tggggacatt gtaccgttgg tgtatgggtc	120
acaggggtgat tgggatagta gtctgaagat agtacttgat tgggtcccctt tttcttcgaa	180
ggaagaactt ctgcagcagt ttcaggatgt tggtagtcat ggaactaaag tggtagtgta	240
caatttatgg atgaatgatg atggcctttt ggaacttgac tttgaggatg atgatgagga	300
catattactt agagatcaag gtagcgcaag tsvggggggt ctcaaagagt cagaaagaaa	360
ttgttaagca acacatatcc cacaggtcca gakttttcat tgcgagctta tacctccatc	420
ctttacctca ggaagtttga taatttcc	

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..121
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481776
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:
Leu Ser Ile Gly Leu Leu Ser Tyr Thr Phe Leu Arg Lys Thr Leu Lys
1 5 10 15
Asp Asp Ile Val Val Pro Met Leu Asp Phe Lys Ile Gln Asp Gly Asp
 20 25 30
Ile Val Pro Leu Val Tyr Gly Ser Gln Gly Asp Trp Asp Ser Ser Leu
 35 40 45
Lys Ile Val Leu Asp Trp Ser Pro Phe Ser Ser Lys Glu Glu Leu Leu
 50 55 60
Gln Gln Phe Gln Asp Val Gly Ser His Gly Thr Lys Val Val Val Tyr
65 70 75 80
Asn Leu Trp Met Asn Asp Asp Gly Leu Leu Glu Leu Asp Phe Glu Asp
 85 90 95
Asp Asp Glu Asp Ile Leu Leu Arg Asp Gln Gly Ser Ala Ser Xaa Gly
 100 105 110
Val Leu Lys Glu Ser Glu Arg Asn Cys
 115 120
(2) INFORMATION FOR SEQ ID NO:158:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..99
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481777
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:
Met Leu Asp Phe Lys Ile Gln Asp Gly Asp Ile Val Pro Leu Val Tyr
1 5 10 15
Gly Ser Gln Gly Asp Trp Asp Ser Ser Leu Lys Ile Val Leu Asp Trp
 20 25 30
Ser Pro Phe Ser Ser Lys Glu Glu Leu Leu Gln Gln Phe Gln Asp Val
 35 40 45
Gly Ser His Gly Thr Lys Val Val Val Tyr Asn Leu Trp Met Asn Asp
 50 55 60
Asp Gly Leu Leu Glu Leu Asp Phe Glu Asp Asp Asp Glu Asp Ile Leu
65 70 75 80
Leu Arg Asp Gln Gly Ser Ala Ser Xaa Gly Val Leu Lys Glu Ser Glu
 85 90 95
Arg Asn Cys

(2) INFORMATION FOR SEQ ID NO:159:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..61
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481778
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:
Met Met Met Ala Phe Trp Asn Leu Thr Leu Arg Met Met Met Arg Thr
1 5 10 15
Tyr Tyr Leu Glu Ile Lys Val Ala Gln Xaa Xaa Gly Phe Ser Lys Ser
 20 25 30
Gln Lys Glu Ile Val Lys Gln His Ile Ser His Arg Leu Arg Xaa Phe
 35 40 45
Ile Ala Ser Leu Tyr Leu His Pro Leu Pro Gln Glu Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..657
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
attatggatt agcgctgca taacagacca ccagggaatt ccgctctcac ctcatgggg      60
tcctgggtggg cgaataagca ccaagccctc cgcttgatc grccatcgtg cgcgtccctt    120
gctcgcgctcg agagatttcc aacgccgagc tagcgcacag ggaagggaga gaaaagtgag    180
tgccaccgcg gggacgaggg aaactcgact caccacctat cgctccttgg agttgtgtcc    240
tggggattct ccgggcttgg aggaggaagg ttgaagcagc tcttccgggg attcgtgttc    300
aacgttgttg gaattcctcg ccaccaggaa ctaccctgcc gtggaccgcg ggtccgctg    360
gccaagactg tcctcgctgc tagccttgac gagcaagcca cacatgatcg agtgcttcag    420
taggtggaga ctgctgagca ggagctcatt gaagcccccc acaggagaag aacatgtgg    480
tcaagaggag ccacacaatg aggagtcca cttgatctag gtgtcgtttc ccagttgact    540
ttatggcgcc aaggatggac atttgctcgt tttatattat tattttgtaa gacttccgct    600
atgtaataag tactctgatt atattgtgac atttatctct atacactctg ttattgt
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Leu Trp Ile Ser Ala Cys Ile Thr Asp His Gln Gly Ile Pro Leu Ser
1 5 10 15
Pro His Trp Gly Pro Gly Gly Arg Ile Ser Thr Lys Pro Ser Ala Trp
 20 25 30
Ile Xaa His Arg Ala Arg Pro Leu Leu Ala Ser Arg Asp Phe Gln Arg
 35 40 45
Arg Ala Ser Ala Gln Gly Arg Glu Arg Lys Val Ser Ala Thr Ala Gly
50 55 60
Thr Arg Glu Thr Arg Leu Thr Thr Tyr Arg Ser Leu Glu Leu Cys Pro
65 70 75 80

Gly Asp Ser Pro Gly Leu Glu Glu Glu Gly
85 90

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..413
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ctgctcgtc	tctccctctc	gtcgttttct	ttcctggtcg	cgccgccctt	catcaggtct	60
cctccgcctt	agccggtgaa	gagcgaccag	gcccaataaa	taatcaccat	ggctcatcaa	120
aagcgtgaag	gcagctacgc	cgatgatgat	agtacatcca	agcgcatcaa	aggcaccgac	180
actgcttctg	aaacggggga	cagtgtagag	tctagtgttt	cacagcaa	ggatgctgaa	240
gctaggagga	cctgccaaaa	ggaaagcgaa	caccatcgga	caaatgcgtt	tcagatgggg	300
aatgcgctgc	aaactctaag	gttttggggt	aagcagaaga	kggtattgac	tgttgctcag	360
gctgatcgcg	cggacgacaa	gggttgacag	cacactatgg	aggacgcctg	ggk	

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Met	Ala	His	Gln	Lys	Arg	Glu	Gly	Ser	Tyr	Ala	Asp	Asp	Asp	Ser	Thr
1				5					10					15	
Ser	Lys	Arg	Ile	Lys	Gly	Thr	Asp	Thr	Ala	Ser	Glu	Thr	Gly	Asp	Ser
			20					25					30		
Val	Glu	Ser	Ser	Val	Ser	Gln	Gln	Met	Asp	Ala	Glu	Ala	Arg	Arg	Thr
			35				40					45			
Cys	Gln	Lys	Glu	Ser	Glu	His	His	Arg	Thr	Asn	Ala	Phe	Gln	Met	Gly
			50				55				60				
Asn	Ala	Leu	Gln	Thr	Leu	Arg	Phe	Trp	Gly	Lys	Gln	Lys	Xaa	Val	Leu
65					70					75				80	
Thr	Val	Val	Glu	Ala	Asp	Ala	Ala	Asp	Asp	Lys	Gly	Cys	Arg	His	Thr
				85				90						95	
Met	Glu	Asp	Ala	Trp											
				100											

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Asp Ala Glu Ala Arg Arg Thr Cys Gln Lys Glu Ser Glu His His
1 5 10 15
Arg Thr Asn Ala Phe Gln Met Gly Asn Ala Leu Gln Thr Leu Arg Phe
20 25 30
Trp Gly Lys Gln Lys Xaa Val Leu Thr Val Val Glu Ala Asp Ala Ala
35 40 45
Asp Asp Lys Gly Cys Arg His Thr Met Glu Asp Ala Trp
50 55 60

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..460
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

atcaaggaac agtgcaaac agaagaaacc tccgtcatca gcgacctctc cccaacggcg	60
ccgacgatgg cgcaacagca gacgcagcta accactggct cgggcacacct ggatgccgtc	120
ccgctcttcg tcgtcatcct cctcgcgcc cagtcctgg ccctcgtgtt ctggatgtac	180
aagctggctt ccgagaagca accaccccg aggaagacac agtgacggcg ccgatctacg	240
ccatcggcga gtccttcgct agcctcttta tcggttccat tttcatgtga accagtaccc	300
tccagaacat tcaggccgct aattattcag agatatccat atagtctttc aatttgtttt	360
atttatactt attgcatttt gggtattgtt tgataacaac ttagcgatat tctatgaatc	420
actatccggt tgggtgataa ataatgttc ctagttttag	

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Ile Lys Glu Gln Cys Lys Leu Glu Glu Thr Ser Val Ile Ser Asp Leu
1 5 10 15
Ser Pro Thr Ala Pro Thr Met Ala Gln Gln Thr Gln Leu Thr Thr
20 25 30
Gly Ser Gly Ile Leu Asp Ala Val Pro Leu Phe Val Val Ile Leu Leu
35 40 45
Ala Ala His Val Leu Ala Leu Val Phe Trp Met Tyr Lys Leu Ala Ser
50 55 60
Glu Lys Gln Pro Pro Arg Arg Lys Thr Gln
65 70

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1481794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Gln Gly Thr Val Gln Thr Arg Arg Asn Leu Arg His Gln Arg Pro Leu
1 5 10 15
Pro Asn Gly Ala Asp Asp Gly Ala Thr Ala Asp Ala Ala Asn His Trp
20 25 30
Leu Gly His Pro Gly Cys Arg Pro Ala Leu Arg Arg His Pro Pro Arg
35 40 45
Gly Pro Arg Pro Gly Pro Arg Val Leu Asp Val Gln Ala Gly Phe Arg
50 55 60
Glu Ala Thr Thr Pro Glu Glu Asp Thr Val Thr Ala Pro Ile Tyr Ala
65 70 75 80
Ile Gly Glu Ser Phe Ala Ser Leu Phe Ile Gly Ser Ile Phe Met
85 90 95

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1481795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ala Gln Gln Gln Thr Gln Leu Thr Thr Gly Ser Gly Ile Leu Asp
1 5 10 15
Ala Val Pro Leu Phe Val Val Ile Leu Leu Ala Ala His Val Leu Ala
20 25 30
Leu Val Phe Trp Met Tyr Lys Leu Ala Ser Glu Lys Gln Pro Pro Arg
35 40 45
Arg Lys Thr Gln
50

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..761

(D) OTHER INFORMATION: / Ceres Seq. ID 1481796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

aggacaacga	gacgtctgam	ggcgtgargc	tgagaccaa	ggagaacaga	nacggarang	60
agcdcrccg	cccgggcgcc	ggagcctgga	gggtagggga	agagaagaga	agaggcgatg	120
gcgtcaatcg	ggtcctccaa	catcggattc	cagctgctga	agaagtctgg	ttggaaggag	180
ggcactggcc	tttgagcgca	ggagcagggg	aggttggaa	ctgtagagac	tcgtgttaag	240
aataacaagc	gtggtatagg	ttctaaagaa	ccaaaaccac	aacctaaagg	tgaggatgac	300
attgaaacac	atcctcaaaa	gccaagcag	gaaatgcaat	caaagaaaag	ggcaaaatta	360
gctgcaaaga	ggataagaaa	actgcaagaa	gaggagaagc	gcttgaaaga	gaaggaattc	420
gragatggct	tttttcaggg	aatttttggc	ctgataatgt	ggtaaggcag	aaacttcaac	480
acttgacaat	gtagctgctg	acttttgsct	gatatagtgg	atgtataggc	ttgcaaaacg	540
cttggcctac	aaaatgttac	cccatcatt	ccgtggatga	tttcacacat	gatttgtggc	600
tagggttggc	acaaagctgt	tcatccatgt	agtggacaaa	tctagtgtag	aattgcccac	660
gctatgtgat	cttgtaattt	ttatacatta	taaatcttgt	ttttttttgt	tcataataact	720

gtgctcaata ttttgccttg ccaatgcaaa tattttaaattc t

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1481797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Asp	Asn	Glu	Thr	Ser	Xaa	Gly	Val	Xaa	Leu	Arg	Pro	Lys	Glu	Asn	Arg
1				5					10					15	
Xaa	Gly	Xaa	Glu	Xaa	Xaa	Gly	Pro	Gly	Ala	Gly	Ala	Trp	Arg	Val	Gly
			20					25					30		
Glu	Glu	Lys	Arg	Arg	Gly	Asp	Gly	Val	Asn	Arg	Val	Leu	Gln	His	Arg
			35				40					45			
Ile	Pro	Ala	Ala	Glu	Glu	Val	Trp	Leu	Glu	Gly	Gly	His	Trp	Pro	Xaa
			50				55					60			
Ser	Ala	Gly	Ala	Gly	Lys	Val	Gly	Thr	Cys	Arg	Asp	Ser	Cys		
65					70				75						

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1481798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Met	Ala	Ser	Ile	Gly	Ser	Ser	Asn	Ile	Gly	Phe	Gln	Leu	Leu	Lys	Lys
1				5					10					15	
Ser	Gly	Trp	Lys	Glu	Gly	Thr	Gly	Leu	Xaa	Ala	Gln	Glu	Gln	Gly	Arg
			20					25					30		
Leu	Glu	Pro	Val	Glu	Thr	Arg	Val	Lys	Asn	Asn	Lys	Arg	Gly	Ile	Gly
			35				40					45			
Ser	Lys	Glu	Pro	Lys	Pro	Gln	Pro	Lys	Val	Glu	Asp	Asp	Ile	Glu	Thr
			50				55				60				
His	Pro	Gln	Lys	Pro	Lys	Gln	Glu	Met	Gln	Ser	Lys	Lys	Arg	Ala	Lys
65					70				75					80	
Leu	Ala	Ala	Lys	Arg	Ile	Arg	Lys	Leu	Gln	Glu	Glu	Glu	Lys	Arg	Leu
			85						90					95	
Lys	Glu	Lys	Glu	Phe	Xaa	Asp	Gly	Phe	Phe	Gln	Gly	Ile	Phe	Gly	Leu
			100					105						110	
Ile	Met	Trp													

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..712

(D) OTHER INFORMATION: / Ceres Seq. ID 1481799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

gtttatcttg	gacaaaggaa	ctaagtgaat	ggactatggt	tacttgagta	gattgaagag	60
tggttatggt	tctaaaacaa	atatagtgtg	ctaatttgca	agatgctacc	attatgacat	120
tgtctgctac	tgaaatctgc	ttgtcacgcc	agaaatagac	atgctttatt	tttgttttct	180
atccttgta	atttttccgg	caattgaaat	tgttactgtg	tcaattctta	cagtttgcat	240
agtttggtga	atgtactttt	actttttacc	tagtacaatg	ctaattgtaga	atactgtaac	300
cagtttgcac	ttgcaggttc	tcttctcaga	catcaatgct	tatgagggtg	agcttggtac	360
tgatgaagag	aagcactgct	tctgccgtga	gtcagacttg	ttagctgtag	ttgaatgaat	420
tttaccatga	aaatttcgga	cttacctggg	aatgctccaa	cggcatgaac	ttatcttgcc	480
cccactttgt	tgtatgccat	ttgaacgttc	gttaattcag	cttctagatg	attgttagtt	540
accgttgatt	tttggtcgcc	ataaactgga	attatgttaa	tgcccatttt	ctttacagag	600
gctcttgctc	acgtttggaa	tacgaaactg	tgctgaaccg	aacttgaaat	gtttacattg	660
cccactctgat	gtttctgctt	ctgaacattc	tttaggcaac	atcctaatta	tt	

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..794

(D) OTHER INFORMATION: / Ceres Seq. ID 1481800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

atgcattctt	ctagtcctag	cgcagctcc	tcatcttctt	gcgcgcgctc	cttctctgtc	60
tcccatggcc	gagcgtcttc	cctgctcttc	tctcctttat	ctccctctcc	atgccggcgc	120
ttccctagct	cgttttccca	tctccctgct	ccttcccatg	gtgcgcaggg	cgctctcccc	180
tgcactccct	ccctagctcc	ccaccgctcg	ccttccctct	cttccctagc	gcccgmttcc	240
agctcgggtc	gcactcgccg	tccctgcccc	tcgctgtttt	tgtggccagc	cgagctcgcc	300
cagccccctg	cctctccacc	tcatacaacg	cctcagccat	ggatgtcgaa	tccccctctc	360
ttagtgccct	tctttgcagc	ccctgcgtcg	cogtgcattg	aagggtgttt	gtctaaatgc	420
tcaagaggag	tgctgtgtcg	tggacagccc	ttttggcgtc	gtcgggtgtt	tgatgttttg	480
cgcattccgt	ctacgacacc	gtcgaccctc	agtgatattt	cgttcttgct	ttgtcgtttt	540
atcgatcgac	gtctatttgc	taatgtgaag	tgtgtgtatg	tgccatgtgt	tgttgaggag	600
cgacatctgt	ggaatctggg	tgaagaagaa	acagagcacg	tccgacgctt	actagctgct	660
gggtgaaagga	ttgaatcggc	tatcatggtc	gtttagtgtc	gatcgagtca	accttagctg	720
tggttaagcta	ccattatttc	tgctatttag	ccgatgtatg	agttagatgg	ataaaatagt	780
tacgatgatt	ttcc					

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1481801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met	His	Leu	Pro	Ser	Pro	Ser	Arg	Ser	Ser	Ser	Ser	Ser	Cys	Ala	Arg
1			5						10					15	
Ser	Phe	Ser	Val	Ser	His	Gly	Arg	Ala	Ser	Ser	Leu	Leu	Leu	Ser	Pro
			20					25					30		
Leu	Ser	Pro	Ser	Pro	Cys	Arg	Arg	Phe	Pro	Ser	Ser	Phe	Ser	His	Leu

35 40 45
Pro Ala Pro Ser His Gly Ala Gln Gly Val Leu Pro Ser Thr Pro Ser
50 55 60
Leu Ala Pro His Arg Ser Pro Ser Ser Pro Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1481802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Met His Leu Pro Ser Pro Ser Arg Ser Ser Ser Ser Cys Ala Arg
1 5 10 15
Ser Phe Ser Val Ser His Gly Arg Ala Ser Ser Leu Leu Leu Ser Pro
20 25 30
Leu Ser Pro Ser Pro Cys Arg Arg Phe Pro Ser Ser Phe Ser His Leu
35 40 45
Pro Ala Pro Ser His Gly Ala Gln Gly Val Leu Pro Ser Thr Pro Ser
50 55 60
Leu Ala Pro His Arg Ser Pro Ser Ser Pro Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1481803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Cys Ile Phe Leu Val Leu Ala Ala Ala Pro His Leu Pro Ala Arg Ala
1 5 10 15
Pro Ser Leu Ser Pro Met Ala Glu Arg Pro Pro Cys Ser Ser Leu Leu
20 25 30
Tyr Leu Pro Leu His Ala Gly Ala Ser Leu Ala Arg Phe Pro Ile Ser
35 40 45
Leu Leu Leu Pro Met Val Arg Arg Ala Ser Ser Pro Arg Leu Pro Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1481808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

atataa	acaa	gcctat	gtta	gcctgt	ctacg	cactgt	gttc	gtgcat	gttt	tcattt	gacc	60
ttgttt	ccat	gatgct	tcga	cgtgtt	acgc	gtgctc	gtgc	ttcttg	ctgt	gtcatc	actg	120
gtccac	attt	tcttgt	ggaa	agtgtt	ccct	tgtacg	agct	tatgaa	acca	gtgtgc	acaa	180
gcgacg	gacg	gatttg	tacc	atccag	naac	gnatag	tgan	tcggtt	tttac	taactc	ctg	

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1481809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Ile	Asn	Lys	Pro	Met	Leu	Ala	Cys	Tyr	Ala	Leu	Cys	Ser	Cys	Met	Phe
1				5					10					15	
Ser	Phe	Asp	Leu	Val	Ser	Met	Met	Leu	Arg	Arg	Val	Thr	Arg	Ala	Arg
			20					25					30		
Ala	Ser	Cys	Cys	Val	Ile	Thr	Gly	Pro	His	Phe	Leu	Val	Glu	Ser	Val
		35					40					45			
Pro	Leu	Tyr	Glu	Leu	Met	Lys	Pro	Val	Cys	Thr	Ser	Asp	Gly	Arg	Ile
	50					55					60				
Cys	Thr	Ile	Gln	Xaa	Xaa	Ile	Val	Xaa	Pro	Phe	Tyr				
65				70					75						

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1481810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Met	Leu	Ala	Cys	Tyr	Ala	Leu	Cys	Ser	Cys	Met	Phe	Ser	Phe	Asp	Leu
1				5					10					15	
Val	Ser	Met	Met	Leu	Arg	Arg	Val	Thr	Arg	Ala	Arg	Ala	Ser	Cys	Cys
			20					25					30		
Val	Ile	Thr	Gly	Pro	His	Phe	Leu	Val	Glu	Ser	Val	Pro	Leu	Tyr	Glu
		35					40					45			
Leu	Met	Lys	Pro	Val	Cys	Thr	Ser	Asp	Gly	Arg	Ile	Cys	Thr	Ile	Gln
	50					55					60				
Xaa	Xaa	Ile	Val	Xaa	Pro	Phe	Tyr								
65				70											

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids -

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1481811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Met	Phe	Ser	Phe	Asp	Leu	Val	Ser	Met	Met	Leu	Arg	Arg	Val	Thr	Arg
1				5				10					15		
Ala	Arg	Ala	Ser	Cys	Cys	Val	Ile	Thr	Gly	Pro	His	Phe	Leu	Val	Glu
			20					25					30		
Ser	Val	Pro	Leu	Tyr	Glu	Leu	Met	Lys	Pro	Val	Cys	Thr	Ser	Asp	Gly
		35					40					45			
Arg	Ile	Cys	Thr	Ile	Gln	Xaa	Xaa	Ile	Val	Xaa	Pro	Phe	Tyr		
50					55					60					

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1481815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

gatggaatca	atttcctcga	tcatttttagc	tgacagcaata	tgaatcatga	tccatcaatt	60
gctgcagaaa	gtaagcaaaa	caatgaagat	gaaccttttaa	gggaaatgaa	gaataaaaaag	120
aagaaatgga	agcaaggtac	tagtagcatt	gaaccaaaatg	acattctaga	atctttttccc	180
tcagagaaaag	ctagcttaac	tggtcatttt	ggtaccagca	aagctattgt	gccatctgtt	240
gcaaaagaaa	gcatgaacat	agaaaatgag	aatgtgaatg	acggcaagga	gaagaagaga	300
aagggaagaa	ctaatatgga	agtacctact	gctgaaaagg	acaattctaa	ttgtgataat	360
caaggaattg	atattagtac	ccaagaatca	cttaktkctt	ttgtacaaaa	tgaaggrtg	420
ggtcaggaaa	atg					

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1481816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Asp	Gly	Ile	Asn	Phe	Leu	Asp	His	Phe	Ser	Cys	Ser	Asn	Met	Asn	His
1			5					10				15			
Asp	Pro	Ser	Ile	Ala	Ala	Glu	Ser	Lys	Gln	Asn	Asn	Glu	Asp	Glu	Pro
			20					25				30			
Leu	Arg	Glu	Met	Lys	Asn	Lys	Lys	Lys	Lys	Trp	Lys	Gln	Gly	Thr	Ser
		35				40					45				
Ser	Ile	Glu	Pro	Asn	Asp	Ile	Leu	Glu	Ser	Phe	Pro	Ser	Glu	Lys	Ala
	50				55				60						
Ser	Leu	Thr	Gly	His	Phe	Gly	Thr	Ser	Lys	Ala	Ile	Val	Pro	Ser	Val
65				70					75					80	
Ala	Lys	Glu	Ser	Met	Asn	Ile	Glu	Asn	Glu	Asn	Val	Asn	Asp	Gly	Lys
			85					90						95	
Glu	Lys	Lys	Arg	Lys	Gly	Lys	Ala	Asn	Met	Glu	Val	Pro	Thr	Ala	Glu
			100					105					110		
Lys	Asp	Asn	Ser	Asn	Cys	Asp	Asn	Gln	Gly	Ile	Asp	Ile	Ser	Thr	Gln
		115					120					125			

Glu Ser Leu Xaa Xaa Phe Val Gln Asn Glu Arg Xaa Gly Gln Glu Asn
130 135 140

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1481817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Met Asn His Asp Pro Ser Ile Ala Ala Glu Ser Lys Gln Asn Asn Glu
1 5 10 15
Asp Glu Pro Leu Arg Glu Met Lys Asn Lys Lys Lys Lys Trp Lys Gln
20 25 30
Gly Thr Ser Ser Ile Glu Pro Asn Asp Ile Leu Glu Ser Phe Pro Ser
35 40 45
Glu Lys Ala Ser Leu Thr Gly His Phe Gly Thr Ser Lys Ala Ile Val
50 55 60
Pro Ser Val Ala Lys Glu Ser Met Asn Ile Glu Asn Glu Asn Val Asn
65 70 75 80
Asp Gly Lys Glu Lys Lys Arg Lys Gly Lys Ala Asn Met Glu Val Pro
85 90 95
Thr Ala Glu Lys Asp Asn Ser Asn Cys Asp Asn Gln Gly Ile Asp Ile
100 105 110
Ser Thr Gln Glu Ser Leu Xaa Xaa Phe Val Gln Asn Glu Arg Xaa Gly
115 120 125
Gln Glu Asn
130

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1481818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Lys Asn Lys Lys Lys Lys Trp Lys Gln Gly Thr Ser Ser Ile Glu
1 5 10 15
Pro Asn Asp Ile Leu Glu Ser Phe Pro Ser Glu Lys Ala Ser Leu Thr
20 25 30
Gly His Phe Gly Thr Ser Lys Ala Ile Val Pro Ser Val Ala Lys Glu
35 40 45
Ser Met Asn Ile Glu Asn Glu Asn Val Asn Asp Gly Lys Glu Lys Lys
50 55 60
Arg Lys Gly Lys Ala Asn Met Glu Val Pro Thr Ala Glu Lys Asp Asn
65 70 75 80
Ser Asn Cys Asp Asn Gln Gly Ile Asp Ile Ser Thr Gln Glu Ser Leu
85 90 95
Xaa Xaa Phe Val Gln Asn Glu Arg Xaa Gly Gln Glu Asn

100 105
(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

anrgggaggg	ctgcggttg	ggaagagaga	gatagaagag	aatcagggta	atgcagatgg	60
gatcgatgga	attcgtagcg	ccggcggttg	aggagctttt	gccggaactt	tccctcgagg	120
agcagccacg	gttgacagaa	caatcccgcg	agcgtgaccg	catccggaag	cgacgtaaca	180
agcactctcc	tcctccccgt	ccgtcggtga	tctcggtaca	gtacgtgatg	gatatgggat	240
cgatgggaat	ggatttcgtg	gcgcggcggt	tggaggagct	gctgccggat	ctttcccgcg	300
aggagcagct	acgggttgcaa	aacaaatccc	gcgggcgtga	ccgcatctcg	aagccacgta	360
acaagcacgc	tcctcgtccc	cgtccgtcgc	cgttctcgga	atgggacggc	aacatcttca	420
aaattcccca	ggtcctccac	gctctcgsc	actacaatgc	caggcaccct	ggtggcgag	480
tcgatgttgt	gaagc					

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met	Gln	Met	Gly	Ser	Met	Glu	Phe	Val	Ala	Pro	Ala	Leu	Glu	Glu	Leu	
1				5				10					15			
Leu	Pro	Glu	Leu	Ser	Leu	Glu	Glu	Gln	Pro	Arg	Leu	Gln	Asn	Gln	Ser	
				20				25					30			
Arg	Glu	Arg	Asp	Arg	Ile	Arg	Lys	Arg	Arg	Asn	Lys	His	Ser	Pro	Pro	
				35				40					45			
Pro	Arg	Pro	Ser	Leu	Ile	Ser	Val	Gln	Tyr	Val	Met	Asp	Met	Gly	Ser	
				50				55				60				
Met	Gly	Met	Asp	Phe	Val	Ala	Pro	Ala	Leu	Glu	Glu	Leu	Leu	Pro	Asp	
65				70				75						80		
Leu	Ser	Arg	Glu	Glu	Gln	Leu	Arg	Leu	Gln	Asn	Lys	Ser	Arg	Gly	Arg	
				85				90						95		
Asp	Arg	Ile	Ser	Lys	Pro	Arg	Asn	Lys	His	Ala	Pro	Arg	Pro	Arg	Pro	
				100				105					110			
Ser	Pro	Phe	Ser	Glu	Trp	Asp	Gly	Asn	Ile	Phe	Lys	Ile	Pro	Gln	Val	
				115				120					125			
Leu	His	Ala	Leu	Xaa	His	Tyr	Asn	Ala	Arg	His	Pro	Gly	Gly	Glu	Phe	
				130				135					140			
Asp	Val	Val	Lys													
145																

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..146
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481821
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Gly Ser Met Glu Phe Val Ala Pro Ala Leu Glu Glu Leu Leu Pro
1 5 10 15
Glu Leu Ser Leu Glu Glu Gln Pro Arg Leu Gln Asn Gln Ser Arg Glu
 20 25 30
Arg Asp Arg Ile Arg Lys Arg Arg Asn Lys His Ser Pro Pro Pro Arg
 35 40 45
Pro Ser Leu Ile Ser Val Gln Tyr Val Met Asp Met Gly Ser Met Gly
 50 55 60
Met Asp Phe Val Ala Pro Ala Leu Glu Glu Leu Leu Pro Asp Leu Ser
65 70 75 80
Arg Glu Glu Gln Leu Arg Leu Gln Asn Lys Ser Arg Gly Arg Asp Arg
 85 90 95
Ile Ser Lys Pro Arg Asn Lys His Ala Pro Arg Pro Arg Pro Ser Pro
 100 105 110
Phe Ser Glu Trp Asp Gly Asn Ile Phe Lys Ile Pro Gln Val Leu His
 115 120 125
Ala Leu Xaa His Tyr Asn Ala Arg His Pro Gly Gly Glu Phe Asp Val
130 135 140
Val Lys
145

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..143
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met Glu Phe Val Ala Pro Ala Leu Glu Glu Leu Leu Pro Glu Leu Ser
1 5 10 15
Leu Glu Glu Gln Pro Arg Leu Gln Asn Gln Ser Arg Glu Arg Asp Arg
 20 25 30
Ile Arg Lys Arg Arg Asn Lys His Ser Pro Pro Pro Arg Pro Ser Leu
 35 40 45
Ile Ser Val Gln Tyr Val Met Asp Met Gly Ser Met Gly Met Asp Phe
 50 55 60
Val Ala Pro Ala Leu Glu Glu Leu Leu Pro Asp Leu Ser Arg Glu Glu
65 70 75 80
Gln Leu Arg Leu Gln Asn Lys Ser Arg Gly Arg Asp Arg Ile Ser Lys
 85 90 95
Pro Arg Asn Lys His Ala Pro Arg Pro Arg Pro Ser Pro Phe Ser Glu
 100 105 110
Trp Asp Gly Asn Ile Phe Lys Ile Pro Gln Val Leu His Ala Leu Xaa
 115 120 125
His Tyr Asn Ala Arg His Pro Gly Gly Glu Phe Asp Val Val Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1481823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

agtccccact	ctcgtcccg	ctccctccaa	agtccaaacc	ctaccacccc	acttccccac	60
caccactaca	tggcgggcg	gctcgctcc	tcccgctact	gctggagccg	cccgtcgctg	120
ccgccccaac	cgaccgcgg	cgccgctcc	gtcactagct	gcgcgctctc	cggacgagag	180
aaaagaaact	cctttagctg	gagagagtgt	gcaatttctg	ttgcattgtc	agttggacta	240
atcactggtg	caccaacgtt	tggaccaccg	gcctatgctt	cttctcttga	acctgttctt	300
ccagatgtgt	ctgttcttat	ctctggacct	cccattaaag	atccaggtgc	tttattgaga	360
tatgctttac	caatagataa	taaagctatt	cggatgaagt	caaaagccgc	tggaggatat	420
cactgasagc	ctcaaggttg	stggkgttag	aggcttggat	tcagttgaaa	gaaaatgtca	480
gasaagcatc	gaaagcackg					

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1481824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Ser	Pro	His	Ser	Arg	Pro	Arg	Ser	Leu	Gln	Ser	Pro	Asn	Pro	Thr	Thr
1				5				10						15	
Pro	Leu	Pro	His	His	Tyr	Met	Ala	Ala	Ala	Leu	Ala	Ser	Ser	Arg	
			20				25					30			
Tyr	Cys	Trp	Ser	Arg	Pro	Ser	Leu	Pro	Pro	Gln	Pro	Thr	Arg	Gly	Arg
		35					40					45			
Arg	Ser	Val	Thr	Ser	Cys	Ala	Leu	Ser	Gly	Arg	Glu	Lys	Arg	Asn	Ser
		50				55					60				
Phe	Ser	Trp	Arg	Glu	Cys	Ala	Ile	Ser	Val	Ala	Leu	Ser	Val	Gly	Leu
65					70				75					80	
Ile	Thr	Gly	Ala	Pro	Thr	Phe	Gly	Pro	Pro	Ala	Tyr	Ala	Ser	Ser	Leu
			85					90						95	
Glu	Pro	Val	Leu	Pro	Asp	Val	Ser	Val	Leu	Ile	Ser	Gly	Pro	Pro	Ile
		100						105					110		
Lys	Asp	Pro	Gly	Ala	Leu	Leu	Arg	Tyr	Ala	Leu	Pro	Ile	Asp	Asn	Lys
		115					120					125			
Ala	Ile	Arg													
		130													

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1481825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```
Val Pro Thr Leu Val Pro Ala Pro Ser Lys Val Gln Thr Leu Pro Pro
1          5          10          15
His Phe Pro Thr Thr Thr Thr Trp Arg Arg Arg Ser Pro Pro Pro Ala
20          25          30
Thr Ala Gly Ala Ala Arg Arg Cys Arg Pro Asn Arg Pro Ala Ala Ala
35          40          45
Ala Pro Ser Leu Ala Ala Arg Ser Pro Asp Glu Arg Lys Glu Thr Pro
50          55          60
Leu Ala Gly Glu Ser Val Gln Phe Leu Leu His Cys Gln Leu Asp
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1481826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```
Met Ala Ala Ala Leu Ala Ser Ser Arg Tyr Cys Trp Ser Arg Pro Ser
1          5          10          15
Leu Pro Pro Gln Pro Thr Arg Gly Arg Ser Val Thr Ser Cys Ala
20          25          30
Leu Ser Gly Arg Glu Lys Arg Asn Ser Phe Ser Trp Arg Glu Cys Ala
35          40          45
Ile Ser Val Ala Leu Ser Val Gly Leu Ile Thr Gly Ala Pro Thr Phe
50          55          60
Gly Pro Pro Ala Tyr Ala Ser Ser Leu Glu Pro Val Leu Pro Asp Val
65          70          75          80
Ser Val Leu Ile Ser Gly Pro Pro Ile Lys Asp Pro Gly Ala Leu Leu
85          90          95
Arg Tyr Ala Leu Pro Ile Asp Asn Lys Ala Ile Arg
100          105
```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1481827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```
gaaggcacac tgccggcgct ctatcttccg ctctctctcc tactcgcgct cggcaaggcg      60
gcgggcgsst caggctcggg ctacggcgctc acggcatccc ctccgcctct cgccagtcgc      120
ctcgcgccat cgctccggg caccacggcc ggtgactctg ctaaaaatgg tgttcctttc      180
aaatgaagac gcctggatcc atgatgaaga catcatggat gatgttgatt cagatgttga      240
agaatcagac tcagaagggtg attcagggtga agaagctcag gctaagcctg cagacaaagc      300
gatatacaac aaggaggcta ttcttgaaaa acttgaagac atagcctggc ccaagaatgt      360
ggactggatg cacaaactca ctggtgagca tgatcaaggg gagaaagttg atgtgaacga      420
tgatcttgcc cgcgaacttg cgttttacac ccaagctttg gatggcacia ggcaggcctt      480
tgagaagctg cagtcgatga aggtccggtt cctcagacca acagattact acgctgagat      540
```

```
ggtgaagact gatgcacaca tgcacaagat caaggggagg ttgttgtcag agaagaagag      600
gattgaggaa gctgaggagc ggaggaaggc tagggagtcc aggaagaaag caaaggaggt      660
tcaggctgag aagaagaagg agagggctaa gcagaagaag gagcagattg agtcagtcaa      720
gaagtggaga aagcagagac aacaaggggg attcaccaag ggaaatgatg atgtgccaga      780
ccttaatttt gaaggagaag aaggatttaa acaatcaaag aaaaagaggc ccggtgtttc      840
tcctggtgac aggtctggtg gtcttgccctt ctcttc
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1481828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
Lys Ala His Cys Arg Arg Ser Ile Phe Arg Ser Leu Ser Tyr Ser Arg
1      5      10      15
Ser Ala Arg Arg Arg Arg Xaa Gln Ala Arg Ala Thr Ala Ser Arg His
20      25      30
Pro Leu Arg Leu Ser Pro Val Ala Ser Arg His Arg Leu Arg Ser His
35      40      45
Arg Pro Val Thr Leu Leu Lys Met Val Phe Leu Ser Asn Glu Asp Ala
50      55      60
Trp Ile His Asp Glu Asp Ile Met Asp Asp Val Asp Ser Asp Val Glu
65      70      75      80
Glu Ser Asp Ser Glu Gly Asp Ser Gly Glu Glu Ala Gln Ala Lys Pro
85      90      95
Ala Asp Lys Ala Ile Tyr Asn Lys Glu Ala Ile Leu Glu Lys Leu Glu
100     105     110
Asp Ile Ala Trp Pro Lys Asn Val Asp Trp Met His Lys Leu Thr Val
115     120     125
Glu His Asp Gln Gly Glu Lys Val Asp Val Asn Asp Asp Leu Ala Arg
130     135     140
Glu Leu Ala Phe Tyr Thr Gln Ala Leu Asp Gly Thr Arg Gln Ala Phe
145     150     155     160
Glu Lys Leu Gln Ser Met Lys Val Arg Phe Leu Arg Pro Thr Asp Tyr
165     170     175
Tyr Ala Glu Met Val Lys Thr Asp Ala His Met His Lys Ile Lys Gly
180     185     190
Arg Leu Leu Ser Glu Lys Lys Arg Ile Glu Glu Ala Glu Glu Arg Arg
195     200     205
Lys Ala Arg Glu Ser Arg Lys Lys Ala Lys Glu Val Gln Ala Glu Lys
210     215     220
Lys Lys Glu Arg Ala Lys Gln Lys Lys Glu Gln Ile Glu Ser Val Lys
225     230     235     240
Lys Trp Arg Lys Gln Arg Gln Gln Gly Gly Phe Thr Lys Gly Asn Asp
245     250     255
Asp Val Pro Asp Leu Asn Phe Glu Gly Glu Glu Gly Phe Lys Gln Ser
260     265     270
Lys Lys Lys Arg Pro Gly Val Ser Pro Gly Asp Arg Ser Gly Gly Leu
275     280     285
Ala Phe Ser
290
```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..236
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
Met Val Phe Leu Ser Asn Glu Asp Ala Trp Ile His Asp Glu Asp Ile
1          5          10          15
Met Asp Asp Val Asp Ser Asp Val Glu Glu Ser Asp Ser Glu Gly Asp
20          25          30
Ser Gly Glu Glu Ala Gln Ala Lys Pro Ala Asp Lys Ala Ile Tyr Asn
35          40          45
Lys Glu Ala Ile Leu Glu Lys Leu Glu Asp Ile Ala Trp Pro Lys Asn
50          55          60
Val Asp Trp Met His Lys Leu Thr Val Glu His Asp Gln Gly Glu Lys
65          70          75          80
Val Asp Val Asn Asp Asp Leu Ala Arg Glu Leu Ala Phe Tyr Thr Gln
85          90          95
Ala Leu Asp Gly Thr Arg Gln Ala Phe Glu Lys Leu Gln Ser Met Lys
100         105         110
Val Arg Phe Leu Arg Pro Thr Asp Tyr Tyr Ala Glu Met Val Lys Thr
115         120         125
Asp Ala His Met His Lys Ile Lys Gly Arg Leu Leu Ser Glu Lys Lys
130         135         140
Arg Ile Glu Glu Ala Glu Glu Arg Arg Lys Ala Arg Glu Ser Arg Lys
145         150         155         160
Lys Ala Lys Glu Val Gln Ala Glu Lys Lys Lys Glu Arg Ala Lys Gln
165         170         175
Lys Lys Glu Gln Ile Glu Ser Val Lys Lys Trp Arg Lys Gln Arg Gln
180         185         190
Gln Gly Gly Phe Thr Lys Gly Asn Asp Asp Val Pro Asp Leu Asn Phe
195         200         205
Glu Gly Glu Glu Gly Phe Lys Gln Ser Lys Lys Lys Arg Pro Gly Val
210         215         220
Ser Pro Gly Asp Arg Ser Gly Gly Leu Ala Phe Ser
225         230         235
```

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..220
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```
Met Asp Asp Val Asp Ser Asp Val Glu Glu Ser Asp Ser Glu Gly Asp
1          5          10          15
Ser Gly Glu Glu Ala Gln Ala Lys Pro Ala Asp Lys Ala Ile Tyr Asn
20          25          30
Lys Glu Ala Ile Leu Glu Lys Leu Glu Asp Ile Ala Trp Pro Lys Asn
35          40          45
Val Asp Trp Met His Lys Leu Thr Val Glu His Asp Gln Gly Glu Lys
50          55          60
```

Val Asp Val Asn Asp Asp Leu Ala Arg Glu Leu Ala Phe Tyr Thr Gln
65 70 75 80
Ala Leu Asp Gly Thr Arg Gln Ala Phe Glu Lys Leu Gln Ser Met Lys
85 90 95
Val Arg Phe Leu Arg Pro Thr Asp Tyr Tyr Ala Glu Met Val Lys Thr
100 105 110
Asp Ala His Met His Lys Ile Lys Gly Arg Leu Leu Ser Glu Lys Lys
115 120 125
Arg Ile Glu Glu Ala Glu Glu Arg Arg Lys Ala Arg Glu Ser Arg Lys
130 135 140
Lys Ala Lys Glu Val Gln Ala Glu Lys Lys Lys Glu Arg Ala Lys Gln
145 150 155 160
Lys Lys Glu Gln Ile Glu Ser Val Lys Lys Trp Arg Lys Gln Arg Gln
165 170 175
Gln Gly Gly Phe Thr Lys Gly Asn Asp Asp Val Pro Asp Leu Asn Phe
180 185 190
Glu Gly Glu Glu Gly Phe Lys Gln Ser Lys Lys Lys Arg Pro Gly Val
195 200 205
Ser Pro Gly Asp Arg Ser Gly Gly Leu Ala Phe Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..530
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

aagctcgtct cgcaccagaa acccgcggaat caatcccga tcccgatcga ccggcgggcgc	60
gggaggcgat gccggacaag gcggtggacg acgtcatgga ggccgcgggtg gggggcccact	120
tcagcggcct ccgcctcgag gcgctgcgcc tctccacctc tgcgccctct tccccttct	180
cctccccgcg cgcgcggcg cacacgcact ccaacggagc cgtctacgcc aacggcacca	240
ccgagcttcc ctctcctgcc gctgcccggc agccattcgt catcggggtt tctggaggga	300
cggcgctcggg gaagacgacg gtgtgcgaca tgatcatcca gcagctgcac gaccaccgtg	360
tcgtgctcgt taaccaggat tcgtttttacc gtggccttac tgctgaagag tctgcacacg	420
cacaagacta taattttgat caccctgatg catttgatac agagcaactt ctagaatgca	480
tggggcagct gaaatgtgct caacctgtaa atgttcctat atatgatttc	

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala Arg Leu Ala Pro Glu Thr Arg Glu Ser Ile Pro Asn Pro Asp Arg
1 5 10 15
Pro Ala Ala Arg Glu Ala Met Pro Asp Lys Ala Val Asp Asp Val Met
20 25 30
Glu Ala Ala Val Gly Ala His Phe Ser Gly Leu Arg Leu Glu Ala Leu
35 40 45

```

Arg Leu Ser Thr Ser Ala Pro Ser Ser Pro Ser Ser Ser Pro Ala Ala
 50          55          60
Ala Ala His Thr His Ser Asn Gly Ala Val Tyr Ala Asn Gly Thr Thr
65          70          75          80
Glu Leu Pro Ser Pro Ala Ala Ala Arg Gln Pro Phe Val Ile Gly Val
      85          90          95
Ser Gly Gly Thr Ala Ser Gly Lys Thr Thr Val Cys Asp Met Ile Ile
      100          105          110
Gln Gln Leu His Asp His Arg Val Val Leu Val Asn Gln Asp Ser Phe
      115          120          125
Tyr Arg Gly Leu Thr Ala Glu Glu Ser Ala His Ala Gln Asp Tyr Asn
      130          135          140
Phe Asp His Pro Asp Ala Phe Asp Thr Glu Gln Leu Leu Glu Cys Met
145          150          155          160
Gly Gln Leu Lys Cys Ala Gln Pro Val Asn Val Pro Ile Tyr Asp Phe
      165          170          175

```

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1481833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

Met Pro Asp Lys Ala Val Asp Asp Val Met Glu Ala Ala Val Gly Ala
1      5      10      15
His Phe Ser Gly Leu Arg Leu Glu Ala Leu Arg Leu Ser Thr Ser Ala
      20      25      30
Pro Ser Ser Pro Ser Ser Ser Pro Ala Ala Ala His Thr His Ser
      35      40      45
Asn Gly Ala Val Tyr Ala Asn Gly Thr Thr Glu Leu Pro Ser Pro Ala
50      55      60
Ala Ala Arg Gln Pro Phe Val Ile Gly Val Ser Gly Gly Thr Ala Ser
65      70      75      80
Gly Lys Thr Thr Val Cys Asp Met Ile Ile Gln Gln Leu His Asp His
      85      90      95
Arg Val Val Leu Val Asn Gln Asp Ser Phe Tyr Arg Gly Leu Thr Ala
      100      105      110
Glu Glu Ser Ala His Ala Gln Asp Tyr Asn Phe Asp His Pro Asp Ala
      115      120      125
Phe Asp Thr Glu Gln Leu Leu Glu Cys Met Gly Gln Leu Lys Cys Ala
      130      135      140
Gln Pro Val Asn Val Pro Ile Tyr Asp Phe
145      150

```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1481834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
Met Glu Ala Ala Val Gly Ala His Phe Ser Gly Leu Arg Leu Glu Ala
1          5          10          15
Leu Arg Leu Ser Thr Ser Ala Pro Ser Ser Pro Ser Ser Ser Pro Ala
20          25          30
Ala Ala Ala His Thr His Ser Asn Gly Ala Val Tyr Ala Asn Gly Thr
35          40          45
Thr Glu Leu Pro Ser Pro Ala Ala Arg Gln Pro Phe Val Ile Gly
50          55          60
Val Ser Gly Gly Thr Ala Ser Gly Lys Thr Thr Val Cys Asp Met Ile
65          70          75          80
Ile Gln Gln Leu His Asp His Arg Val Val Leu Val Asn Gln Asp Ser
85          90          95
Phe Tyr Arg Gly Leu Thr Ala Glu Glu Ser Ala His Ala Gln Asp Tyr
100         105         110
Asn Phe Asp His Pro Asp Ala Phe Asp Thr Glu Gln Leu Leu Glu Cys
115         120         125
Met Gly Gln Leu Lys Cys Ala Gln Pro Val Asn Val Pro Ile Tyr Asp
130         135         140
Phe
145
```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1087 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1087

(D) OTHER INFORMATION: / Ceres Seq. ID 1481839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
aatcaagctg actcgggttg tccgccgtgt tacctgccag ctcaaggaac gattccaagc 60
tcgatattctg ctgtttcaga tcataatccg gtcctaaatcc gtaactcagg ttctgaaact 120
cgtccccatt tccaaatcct atacactcca ccgggaaact cggctgactt aactcgctct 180
cactctgaga gacaacgcag accttcttgc ccggaggctg atcgggtgat cgtggcgatg 240
acggcggagg agtataatta ggaggaggag gatggtgcag atctgggaag ttgagcttgg 300
ctttatcacc acggatctgc ttggccgcaa catcataagc catggcagct tcctccgccg 360
tgttgaacgt accaagccaa actctaacac cttttcgtgg atctcgaatc tcagccgccc 420
attttcccca tggacgctta cgtatccctc tataaacatt cttcctcttc ctccgtttcc 480
ccggctctgt gcctgctcc ttcttctactg cctcctcttt cacgttaact tcaaaatttt 540
caccggattc cccaaagttc aaaatttaca attttaaccc cacacagata attaaataat 600
cctgataaat tacattacca aaaccacaaa tatttttttt ttatcatctt ccgtaagttc 660
cagaaatatt attttacctt ttgtctaaaa aggttagaaa aaactatatg tttgtgtttt 720
tgaatgattt tgtatttttg tttatgattm ataggagagt acataccttg gttggtggga 780
tgaggttttg aggtggaata gaaaccccag aagtcgctcg cggcggaagc atcgagctct 840
gaccagagtt cctcagccgt gagtttacgg cccttggcct tggtgacgag aggggcataa 900
tcggaaataa tagcaccgcc acacattttc tctgtttgtt gctgtgggtt tctttcaaga 960
gaaagtttcc tacggtggag ctgaaatgcc tttataggcg caaaataaat gttttatggt 1020
aataaagtgt gagtgaatg aattacttta tattagaata ataattctaa tagttttatg 1080
ttccttg
```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Asn	Gln	Ala	Asp	Ser	Val	Ala	Pro	Pro	Cys	Tyr	Arg	Pro	Ala	Gln	Gly
1				5					10					15	
Thr	Ile	Pro	Ser	Ser	Ile	Ser	Ala	Val	Ser	Asp	His	Asn	Pro	Ala	Gln
			20					25					30		
Ile	Arg	Asn	Ser	Gly	Ser	Glu	Thr	Arg	Pro	His	Phe	Gln	Ile	Leu	Tyr
		35				40					45				
Thr	Pro	Pro	Gly	Asn	Ser	Ala	Asp	Leu	Thr	Arg	Ser	His	Ser	Glu	Arg
	50				55					60					
Gln	Arg	Arg	Pro	Ser	Ser	Pro	Glu	Ala	Asp	Arg	Leu	Ile	Val	Ala	Met
65				70					75						80
Thr	Ala	Glu	Glu	Tyr	Asn										
					85										

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ile	Lys	Leu	Thr	Arg	Leu	Leu	Arg	Arg	Val	Thr	Val	Gln	Leu	Lys	Glu
1				5					10					15	
Arg	Phe	Gln	Ala	Arg	Tyr	Leu	Leu	Phe	Gln	Ile	Ile	Ile	Arg	Leu	Lys
		20						25					30		
Ser	Val	Thr	Gln	Val	Leu	Lys	Leu	Val	Pro	Ile	Ser	Lys	Ser	Tyr	Thr
		35				40						45			
Leu	His	Arg	Glu	Thr	Arg	Leu	Thr								
	50				55										

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met	Val	Gln	Ile	Trp	Glu	Val	Glu	Leu	Gly	Phe	Ile	Thr	Thr	Asp	Leu
1				5					10					15	
Leu	Gly	Arg	Asn	Ile	Ile	Ser	His	Gly	Ser	Phe	Leu	Arg	Arg	Val	Glu
		20						25					30		
Arg	Thr	Lys	Pro	Asn	Ser	Asn	Thr	Phe	Ser	Trp	Ile	Ser	Asn	Leu	Ser
		35					40					45			
Arg	Pro	Phe	Ser	Pro	Trp	Thr	Leu	Thr	Tyr	Pro	Ser	Ile	Asn	Ile	Leu
	50					55						60			

Pro Leu Pro Pro Phe Pro Arg Leu Cys Cys Leu Leu Leu Leu His Cys
65 70 75 80
Leu Leu Phe His Val Asn Phe Lys Ile Phe Thr Gly Phe Pro Lys Val
85 90 95
Gln Asn Leu Gln Phe
100

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

gaggtttctt	gggaacagga	tcgcttctac	agatatttca	cccatgtcaa	gtttaacagt	60
gagaagggtg	tcgcgcgaag	atatacaact	ggttcagaat	ctaattgaac	gatgcctcca	120
gctttacatg	aaccagaaag	aagttgttga	cactcttcta	gaacaggcta	agatcgaacc	180
tggttttaca	gaactagttt	ggcagaagct	tgaagaagag	aaccgcgaat	ttttcaaggc	240
atattatctg	aggctcatgg	tgaagcacca	gataatggaa	tataacgaac	tgcttgagca	300
gcagataaac	cacatgcgcc	agatgcaccc	aactgcaggg	gcttctgttc	gaaacaggaa	360
tggttctcat	gttccaccaa	tgaatcagca	acaattactc	tatgaacgca	aggaaccaga	420
tcaatcctct	cctaattctgt	caagtccata	cctcaatgga	ggctcagcaa	ttaacacaaa	480
tataccttct	tatgtggact	tttcatccca	ttctagaaga	gttgatcctt	caccaaactc	540
gctctccttg	caggccacaa	atatgccttt	gatgcaagga	atgatcaagt	ctgagactgc	600
atatcaaaac	tgtgctccat	acatgtatgg	tggtgaagca	cagtccacag	ttggagatgt	660
caccatcgca	tctttcagca	atgattccag	caaccaatcc	ctgaatgatc	ctcttgtcga	720
tccagatgct	cctacatttg	gctcgttagg	acaaattcct	cagaacttca	gcctctctga	780
tctgacagct	gatttttccc	agagttcaga	tattctggag	agctacgagg	gatcaccggt	840
cctattggct	gatgctgaaa	atttcctgga	ctctagcgaa	agggtagaac	atcaaggaga	900
ccacgaaaga	ttgaggacca	tatcatcagg	cttcagttac	gaaaacttcc	gaagcaatta	960
ggtttattac	acatggaaact	tcgtagtcat	gcttttacgt	ctgcaactac	ttgcaggatt	1020
taatcccatt	atcagtgtac	atagatatcc	ttacctttcg	aaagacaatt	ttgggggttc	1080
gggtgattac	taatattatt	attctcaagt	gtagagaaaat	ttgggttttta	gtaataaata	1140
tttaagaacc	tggtgatttt					

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Arg	Phe	Leu	Gly	Asn	Arg	Ile	Ala	Ser	Thr	Asp	Ile	Ser	Pro	Met	Ser
1				5					10					15	
Ser	Leu	Thr	Val	Arg	Arg	Val	Ser	Arg	Glu	Asp	Ile	Gln	Leu	Val	Gln
			20					25					30		
Asn	Leu	Ile	Glu	Arg	Cys	Leu	Gln	Leu	Tyr	Met	Asn	Gln	Lys	Glu	Val
		35					40					45			
Val	Asp	Thr	Leu	Leu	Glu	Gln	Ala	Lys	Ile	Glu	Pro	Gly	Phe	Thr	Glu
	50					55					60				
Leu	Val	Trp	Gln	Lys	Leu	Glu	Glu	Glu	Asn	Arg	Glu	Phe	Phe	Lys	Ala

65				70					75				80
Tyr	Tyr	Leu	Arg	Leu	Met	Val	Lys	His	Gln	Ile	Met	Glu	Tyr
				85					90				95
Leu	Leu	Glu	Gln	Gln	Ile	Asn	His	Met	Arg	Gln	Met	His	Pro
			100					105				110	
Gly	Ala	Ser	Val	Arg	Asn	Arg	Asn	Gly	Ser	His	Val	Pro	Pro
		115				120					125		Met
Gln	Gln	Gln	Leu	Leu	Tyr	Glu	Arg	Lys	Glu	Pro	Asp	Gln	Ser
		130				135					140		Ser
Asn	Leu	Ser	Ser	Pro	Tyr	Leu	Asn	Gly	Gly	Ser	Ala	Ile	Asn
145					150					155			Thr
Ile	Pro	Ser	Tyr	Val	Asp	Phe	Ser	Ser	His	Ser	Arg	Arg	Val
				165					170				Asp
Ser	Pro	Asn	Ser	Leu	Ser	Leu	Gln	Ala	Thr	Asn	Met	Pro	Leu
			180					185					Met
Gly	Met	Ile	Lys	Ser	Glu	Thr	Ala	Tyr	Gln	Asn	Cys	Ala	Pro
		195					200					205	Tyr
Tyr	Gly	Gly	Glu	Ala	Gln	Ser	Thr	Val	Gly	Asp	Val	Thr	Ile
		210				215					220		Ala
Phe	Ser	Asn	Asp	Ser	Ser	Asn	Gln	Ser	Leu	Asn	Asp	Pro	Leu
225					230					235			Val
Pro	Asp	Ala	Pro	Thr	Phe	Gly	Ser	Leu	Gly	Gln	Ile	Pro	Gln
				245					250				Asn
Ser	Leu	Ser	Asp	Leu	Thr	Ala	Asp	Phe	Ser	Gln	Ser	Ser	Asp
			260				265						Ile
Glu	Ser	Tyr	Glu	Gly	Ser	Pro	Phe	Leu	Leu	Ala	Asp	Ala	Glu
		275				280						285	Asn
Leu	Asp	Ser	Ser	Glu	Arg	Val	Glu	His	Gln	Gly	Asp	His	Glu
		290				295					300		Arg
Arg	Thr	Ile	Ser	Ser	Gly	Phe	Ser	Tyr	Glu	Asn	Phe	Arg	Ser
305					310					315			Asn

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1481849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met	Ser	Ser	Leu	Thr	Val	Arg	Arg	Val	Ser	Arg	Glu	Asp	Ile	Gln	Leu
1			5					10						15	
Val	Gln	Asn	Leu	Ile	Glu	Arg	Cys	Leu	Gln	Leu	Tyr	Met	Asn	Gln	Lys
			20					25					30		
Glu	Val	Val	Asp	Thr	Leu	Leu	Glu	Gln	Ala	Lys	Ile	Glu	Pro	Gly	Phe
			35				40					45			
Thr	Glu	Leu	Val	Trp	Gln	Lys	Leu	Glu	Glu	Glu	Asn	Arg	Glu	Phe	Phe
			50			55					60				
Lys	Ala	Tyr	Tyr	Leu	Arg	Leu	Met	Val	Lys	His	Gln	Ile	Met	Glu	Tyr
65				70					75					80	
Asn	Glu	Leu	Leu	Glu	Gln	Gln	Ile	Asn	His	Met	Arg	Gln	Met	His	Pro
			85					90					95		
Thr	Ala	Gly	Ala	Ser	Val	Arg	Asn	Arg	Asn	Gly	Ser	His	Val	Pro	Pro
			100				105					110			
Met	Asn	Gln	Gln	Leu	Leu	Tyr	Glu	Arg	Lys	Glu	Pro	Asp	Gln	Ser	
			115				120					125			

Ser Pro Asn Leu Ser Ser Pro Tyr Leu Asn Gly Gly Ser Ala Ile Asn
130 135 140
Thr Asn Ile Pro Ser Tyr Val Asp Phe Ser Ser His Ser Arg Arg Val
145 150 155 160
Asp Pro Ser Pro Asn Ser Leu Ser Leu Gln Ala Thr Asn Met Pro Leu
165 170 175
Met Gln Gly Met Ile Lys Ser Glu Thr Ala Tyr Gln Asn Cys Ala Pro
180 185 190
Tyr Met Tyr Gly Gly Glu Ala Gln Ser Thr Val Gly Asp Val Thr Ile
195 200 205
Ala Ser Phe Ser Asn Asp Ser Ser Asn Gln Ser Leu Asn Asp Pro Leu
210 215 220
Val Asp Pro Asp Ala Pro Thr Phe Gly Ser Leu Gly Gln Ile Pro Gln
225 230 235 240
Asn Phe Ser Leu Ser Asp Leu Thr Ala Asp Phe Ser Gln Ser Ser Asp
245 250 255
Ile Leu Glu Ser Tyr Glu Gly Ser Pro Phe Leu Leu Ala Asp Ala Glu
260 265 270
Asn Phe Leu Asp Ser Ser Glu Arg Val Glu His Gln Gly Asp His Glu
275 280 285
Arg Leu Arg Thr Ile Ser Ser Gly Phe Ser Tyr Glu Asn Phe Arg Ser
290 295 300
Asn
305

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..277

(D) OTHER INFORMATION: / Ceres Seq. ID 1481850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Asn Gln Lys Glu Val Val Asp Thr Leu Leu Glu Gln Ala Lys Ile
1 5 10 15
Glu Pro Gly Phe Thr Glu Leu Val Trp Gln Lys Leu Glu Glu Glu Asn
20 25 30
Arg Glu Phe Phe Lys Ala Tyr Tyr Leu Arg Leu Met Val Lys His Gln
35 40 45
Ile Met Glu Tyr Asn Glu Leu Leu Glu Gln Gln Ile Asn His Met Arg
50 55 60
Gln Met His Pro Thr Ala Gly Ala Ser Val Arg Asn Arg Asn Gly Ser
65 70 75 80
His Val Pro Pro Met Asn Gln Gln Gln Leu Leu Tyr Glu Arg Lys Glu
85 90 95
Pro Asp Gln Ser Ser Pro Asn Leu Ser Ser Pro Tyr Leu Asn Gly Gly
100 105 110
Ser Ala Ile Asn Thr Asn Ile Pro Ser Tyr Val Asp Phe Ser Ser His
115 120 125
Ser Arg Arg Val Asp Pro Ser Pro Asn Ser Leu Ser Leu Gln Ala Thr
130 135 140
Asn Met Pro Leu Met Gln Gly Met Ile Lys Ser Glu Thr Ala Tyr Gln
145 150 155 160
Asn Cys Ala Pro Tyr Met Tyr Gly Gly Glu Ala Gln Ser Thr Val Gly
165 170 175
Asp Val Thr Ile Ala Ser Phe Ser Asn Asp Ser Ser Asn Gln Ser Leu

180	185	190
Asn Asp Pro Leu Val Asp Pro Asp Ala Pro Thr Phe Gly Ser Leu Gly		
195	200	205
Gln Ile Pro Gln Asn Phe Ser Leu Ser Asp Leu Thr Ala Asp Phe Ser		
210	215	220
Gln Ser Ser Asp Ile Leu Glu Ser Tyr Glu Gly Ser Pro Phe Leu Leu		
225	230	235
Ala Asp Ala Glu Asn Phe Leu Asp Ser Ser Glu Arg Val Glu His Gln		
245	250	255
Gly Asp His Glu Arg Leu Arg Thr Ile Ser Ser Gly Phe Ser Tyr Glu		
260	265	270
Asn Phe Arg Ser Asn		
275		

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..806
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

cagcttaaca	cttgatgagg	ttcaaaatca	cttggggagt	tctggtaaag	ctctgggaag	60
catgaacctt	gatgagcttt	tgaagagtgt	ctgttctgtt	gaagctaata	agccatcgtc	120
tatggctgtc	aatgggtggag	cagctgctca	ggagggtcct	tctcgccagg	ggagtttgac	180
tttgccctcg	gatctcagca	aaaagactgt	tgatgaggtt	tggaaagaca	ttcagcagaa	240
taagaatgga	ggtagtgtc	atgagaggag	ggataagcag	cctacacttg	gggaaatgac	300
gcttgaagac	ctgttggtga	aagcaggagt	ggtcactgag	actatccctg	gttcgaacca	360
tgatggtcct	gttggtggtg	gtagtgtctg	ttcaggtgct	ggtttagggc	aaaacattac	420
tcaagttggc	ccatggattc	aatatcatca	gctcccatca	atgccacagc	ctcaagcatt	480
tatgccctat	ccggtttcag	atatgcaagc	aatggtgtct	cagtcttctt	tgatgggtgg	540
tttgtcagat	acacaaactc	ctggaaggaa	gagggtagct	tcaggagaag	ttgtagagaa	600
gactgtgaca	ccattgcttg	catagtgcga	acaggtaaaag	gtccactcaa	caattgggct	660
actcacctca	gtgatccact	ccacaccacc	atcatcgata	ccttctcctc	atcttaaaat	720
cattatcatg	tgagattcta	tttghtaactt	atgtaaaaac	agagctatga	tgatactgaa	780
tcgacttttg	gcttttgctt	gtttgg				

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..207
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Ser Leu Thr Leu Asp Glu Val Gln Asn His Leu Gly Ser Ser Gly Lys		
1	5	10
Ala Leu Gly Ser Met Asn Leu Asp Glu Leu Leu Lys Ser Val Cys Ser		
20	25	30
Val Glu Ala Asn Gln Pro Ser Ser Met Ala Val Asn Gly Gly Ala Ala		
35	40	45
Ala Gln Glu Gly Leu Ser Arg Gln Gly Ser Leu Thr Leu Pro Arg Asp		
50	55	60

Leu Ser Lys Lys Thr Val Asp Glu Val Trp Lys Asp Ile Gln Gln Asn
65 70 75 80
Lys Asn Gly Gly Ser Ala His Glu Arg Arg Asp Lys Gln Pro Thr Leu
85 90 95
Gly Glu Met Thr Leu Glu Asp Leu Leu Leu Lys Ala Gly Val Val Thr
100 105 110
Glu Thr Ile Pro Gly Ser Asn His Asp Gly Pro Val Gly Gly Ser
115 120 125
Ala Gly Ser Gly Ala Gly Leu Gly Gln Asn Ile Thr Gln Val Gly Pro
130 135 140
Trp Ile Gln Tyr His Gln Leu Pro Ser Met Pro Gln Pro Gln Ala Phe
145 150 155 160
Met Pro Tyr Pro Val Ser Asp Met Gln Ala Met Val Ser Gln Ser Ser
165 170 175
Leu Met Gly Gly Leu Ser Asp Thr Gln Thr Pro Gly Arg Lys Arg Val
180 185 190
Ala Ser Gly Glu Val Val Glu Lys Thr Val Thr Pro Leu Leu Ala
195 200 205

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Met Asn Leu Asp Glu Leu Leu Lys Ser Val Cys Ser Val Glu Ala Asn
1 5 10 15
Gln Pro Ser Ser Met Ala Val Asn Gly Gly Ala Ala Ala Gln Glu Gly
20 25 30
Leu Ser Arg Gln Gly Ser Leu Thr Leu Pro Arg Asp Leu Ser Lys Lys
35 40 45
Thr Val Asp Glu Val Trp Lys Asp Ile Gln Gln Asn Lys Asn Gly Gly
50 55 60
Ser Ala His Glu Arg Arg Asp Lys Gln Pro Thr Leu Gly Glu Met Thr
65 70 75 80
Leu Glu Asp Leu Leu Lys Ala Gly Val Val Thr Glu Thr Ile Pro
85 90 95
Gly Ser Asn His Asp Gly Pro Val Gly Gly Gly Ser Ala Gly Ser Gly
100 105 110
Ala Gly Leu Gly Gln Asn Ile Thr Gln Val Gly Pro Trp Ile Gln Tyr
115 120 125
His Gln Leu Pro Ser Met Pro Gln Pro Gln Ala Phe Met Pro Tyr Pro
130 135 140
Val Ser Asp Met Gln Ala Met Val Ser Gln Ser Ser Leu Met Gly Gly
145 150 155 160
Leu Ser Asp Thr Gln Thr Pro Gly Arg Lys Arg Val Ala Ser Gly Glu
165 170 175
Val Val Glu Lys Thr Val Thr Pro Leu Leu Ala
180 185

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..167
(D) OTHER INFORMATION: / Ceres Seq. ID 1481854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```
Met Ala Val Asn Gly Gly Ala Ala Ala Gln Glu Gly Leu Ser Arg Gln
1      5      10      15
Gly Ser Leu Thr Leu Pro Arg Asp Leu Ser Lys Lys Thr Val Asp Glu
20     25     30
Val Trp Lys Asp Ile Gln Gln Asn Lys Asn Gly Gly Ser Ala His Glu
35     40     45
Arg Arg Asp Lys Gln Pro Thr Leu Gly Glu Met Thr Leu Glu Asp Leu
50     55     60
Leu Leu Lys Ala Gly Val Val Thr Glu Thr Ile Pro Gly Ser Asn His
65     70     75     80
Asp Gly Pro Val Gly Gly Gly Ser Ala Gly Ser Gly Ala Gly Leu Gly
85     90     95
Gln Asn Ile Thr Gln Val Gly Pro Trp Ile Gln Tyr His Gln Leu Pro
100    105    110
Ser Met Pro Gln Pro Gln Ala Phe Met Pro Tyr Pro Val Ser Asp Met
115    120    125
Gln Ala Met Val Ser Gln Ser Ser Leu Met Gly Gly Leu Ser Asp Thr
130    135    140
Gln Thr Pro Gly Arg Lys Arg Val Ala Ser Gly Glu Val Val Glu Lys
145    150    155    160
Thr Val Thr Pro Leu Leu Ala
165
```

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..391
(D) OTHER INFORMATION: / Ceres Seq. ID 1481859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
acatatgctg tccgtcaccg cgcgcgcctc ctgccccttc ttcacccttt cctcccggac      60
ccggcgtctc cgtgcccgtg cgttccttct ccggcctgcg gtctcctcca ccggccaccg      120
ctgcctcgca attgggcaag gcaatcagac cgctcccatc aaccgccctg accgcgcgag      180
gaagatcaaa cgcggaggcc gtccgtccct cccgcgttat cgtgatgcca ggccctgcgcg      240
cagccgagca ggacgcgcgtc tcgctgggtgc ggcgcgtcgc ccgsgctctc aaccgccgct      300
tcaccgacat cgtcgcactg ctcttcagcc acaagggcgc tggatcgctc ggcgcgmgtcg      360
cggggttcgc matcgccgtc gtgttcgcgt g
```

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1481860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
His Met Leu Ser Val Thr Ala Arg Ala Ser Leu Pro Phe Phe Thr Leu
1          5          10          15
Ser Ser Arg Thr Arg Arg Leu Arg Ala Arg Ala Xaa Leu Leu Arg Pro
          20          25          30
Ala Val Ser Ser Thr Gly His Arg Cys Leu Ala Ile Gly Gln Gly Asn
          35          40          45
Gln Thr Ala Pro Ile Asn Arg Pro Asp Arg Ala Arg Lys Ile Lys Arg
          50          55          60
Gly Gly Arg Pro Ser Leu Pro Arg Tyr Arg Asp Ala Arg Pro Arg Arg
65          70          75          80
Ser Arg Ala Gly Arg Arg Leu Ala Gly Ala Ala Arg Arg Pro Xaa Ser
          85          90          95
Gln Pro Pro Leu His Arg His Arg Arg Thr Ala Leu Gln Pro Gln Gly
          100          105          110
Arg Trp Ile Ala Arg Arg Xaa Arg Gly Val Arg Xaa Arg Arg Arg Val
          115          120          125
Arg Val
          130
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
Ile Cys Cys Pro Ser Pro Arg Ala Pro Pro Cys Pro Ser Ser Pro Phe
1          5          10          15
Pro Pro Gly Pro Gly Val Ser Val Pro Val Arg Xaa Phe Ser Gly Leu
          20          25          30
Arg Ser Pro Pro Pro Ala Thr Ala Ala Ser Gln Leu Gly Lys Ala Ile
          35          40          45
Arg Pro Leu Pro Ser Thr Ala Leu Thr Ala Arg Gly Arg Ser Asn Ala
          50          55          60
Glu Ala Val Arg Pro Ser Arg Val Ile Val Met Pro Gly Leu Ala Ala
65          70          75          80
Ala Glu Gln Asp Ala Val Ser Leu Val Arg Arg Val Ala Xaa Ala Leu
          85          90          95
Asn Arg Arg Phe Thr Asp Ile Val Ala Leu Leu Phe Ser His Lys Gly
          100          105          110
Ala Gly Ser Leu Gly Xaa Val Ala Gly Phe Xaa Ile Ala Val Val Phe
          115          120          125
Ala
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1481862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Leu Ser Val Thr Ala Arg Ala Ser Leu Pro Phe Phe Thr Leu Ser
1 5 10 15
Ser Arg Thr Arg Arg Leu Arg Ala Arg Ala Xaa Leu Leu Arg Pro Ala
20 25 30
Val Ser Ser Thr Gly His Arg Cys Leu Ala Ile Gly Gln Gly Asn Gln
35 40 45
Thr Ala Pro Ile Asn Arg Pro Asp Arg Ala Arg Lys Ile Lys Arg Gly
50 55 60
Gly Arg Pro Ser Leu Pro Arg Tyr Arg Asp Ala Arg Pro Arg Arg Ser
65 70 75 80
Arg Ala Gly Arg Arg Leu Ala Gly Ala Ala Arg Arg Pro Xaa Ser Gln
85 90 95
Pro Pro Leu His Arg His Arg Arg Thr Ala Leu Gln Pro Gln Gly Arg
100 105 110
Trp Ile Ala Arg Arg Xaa Arg Gly Val Arg Xaa Arg Arg Val Arg
115 120 125
Val

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..589
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

agcagccgct cccgactttt accttcctac ctggtgctgt agcatccgcc gcctcccgca 60
gaaccggaag atggcgctcgt cggcgtcgac cctcgaaatc gaggcccgcg acgtgggttaa 120
gatagtgtg cagttctgca aggagaattc gctgcagcag acgttccaga cgctgcaaaa 180
cgagtgccag gtctccctca acactggtga cagcatcgac accttcattg ccgacatcaa 240
cgccgggcgt tgggatgctg tgcttcccca ggctgcacag ctcaagctgc cagcaagaa 300
gctcaggagc ctctatgagc agattgtgtt ggagatggct gagctccgtg agcttgacac 360
ggcccggtgcc atcctccgcc agacgcaggt catgggtgtt atgaagcagg agcagcctga 420
rcggtacctc cgccttgagc acctccttgt ccgcacatac ttgacccca atgaggccta 480
ccaagaatcb accaaggaga agcggcgagc actgattgct caagctgttg ctttcagaag 540
tctcagtagt acsgccatct cgtcttatgg cactgattgg tcaggcttg

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ala Ala Ala Pro Asp Phe Tyr Leu Pro Thr Trp Cys Cys Ser Ile Arg
1 5 10 15
Arg Leu Pro Gln Asn Pro Lys Met Ala Ser Ser Ala Ser Thr Leu Glu
20 25 30
Ile Glu Ala Arg Asp Val Val Lys Ile Val Leu Gln Phe Cys Lys Glu

35	40	45
Asn Ser Leu Gln Gln Thr Phe Gln Thr Leu Gln Asn Glu Cys Gln Val		
50	55	60
Ser Leu Asn Thr Val Asp Ser Ile Asp Thr Phe Ile Ala Asp Ile Asn		
65	70	75
Ala Gly Arg Trp Asp Ala Val Leu Pro Gln Val Ala Gln Leu Lys Leu		
85	90	95
Pro Arg Lys Lys Leu Glu Asp Leu Tyr Glu Gln Ile Val Leu Glu Met		
100	105	110
Ala Glu Leu Arg Glu Leu Asp Thr Ala Arg Ala Ile Leu Arg Gln Thr		
115	120	125
Gln Val Met Gly Val Met Lys Gln Glu Gln Pro Xaa Arg Tyr Leu Arg		
130	135	140
Leu Glu His Leu Leu Val Arg Thr Tyr Phe Asp Pro Asn Glu Ala Tyr		
145	150	155
Gln Glu Xaa Thr Lys Glu Lys Arg Arg Ala Leu Ile Ala Gln Ala Val		
165	170	175
Ala Phe Arg Ser Leu Ser Ser Xaa Ala Ile Ser Ser Tyr Gly Thr Asp		
180	185	190
Trp Ser Gly Leu		
195		

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1481865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ala Ser Ser Ala Ser Thr Leu Glu Ile Glu Ala Arg Asp Val Val		
1	5	10
Lys Ile Val Leu Gln Phe Cys Lys Glu Asn Ser Leu Gln Gln Thr Phe		
20	25	30
Gln Thr Leu Gln Asn Glu Cys Gln Val Ser Leu Asn Thr Val Asp Ser		
35	40	45
Ile Asp Thr Phe Ile Ala Asp Ile Asn Ala Gly Arg Trp Asp Ala Val		
50	55	60
Leu Pro Gln Val Ala Gln Leu Lys Leu Pro Arg Lys Lys Leu Glu Asp		
65	70	75
Leu Tyr Glu Gln Ile Val Leu Glu Met Ala Glu Leu Arg Glu Leu Asp		
85	90	95
Thr Ala Arg Ala Ile Leu Arg Gln Thr Gln Val Met Gly Val Met Lys		
100	105	110
Gln Glu Gln Pro Xaa Arg Tyr Leu Arg Leu Glu His Leu Leu Val Arg		
115	120	125
Thr Tyr Phe Asp Pro Asn Glu Ala Tyr Gln Glu Xaa Thr Lys Glu Lys		
130	135	140
Arg Arg Ala Leu Ile Ala Gln Ala Val Ala Phe Arg Ser Leu Ser Ser		
145	150	155
Xaa Ala Ile Ser Ser Tyr Gly Thr Asp Trp Ser Gly Leu		
165	170	

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 554 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..554
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

agaatttgat	ttgcaaaaac	aaactaagt	gtggcaaaga	gcatccaaa	tatgccaaat	60
tatagtcaaa	aacaatttg	tcttcaatt	cattgatttt	gcacttctt	tggtgctttt	120
tgatgtgttg	gcataaatca	ccaaaaagg	ggagattata	aggcaaagt	gcccttgggc	180
cattttctaaa	atgttttgg	gattaagtgc	ccaacacgt	tgaataagt	cttatggggc	240
aaataaagt	agaagtga	atcaaggcac	aatgtatgt	tctagactta	gtacatcggt	300
ttttgaaggc	taatgtgtt	tctctaagt	cttgaaacag	tgataaaa	gaagaaaagg	360
attgcaaaag	agttggctat	gtgcagcaaa	ctccagttcg	gcttggcaca	ccgaactgtc	420
cgggtggtgca	ccggactgtc	cgggtgcgcca	rgctggtctc	cggtgaaatg	gccactctcg	480
ggactcaaca	acgcgtatg	ctaaaaatca	ccggaccgtc	cggtgagtca	tctacgacga	540
actcattgct	ctcg					

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..44
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481874
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Glu	Phe	Asp	Leu	Gln	Lys	Gln	Thr	Lys	Trp	Trp	Gln	Arg	Ala	Ile	Gln
1				5				10						15	
Ile	Cys	Gln	Ile	Ile	Val	Lys	Asn	Asn	Leu	Val	Phe	Asn	Cys	Ile	Asp
		20					25						30		
Phe	Ala	Leu	Leu	Val	Leu	Leu	Phe	Asp	Val	Leu	Ala				
		35					40								

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..41
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481875
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	Cys	Ser	Lys	Leu	Gln	Phe	Gly	Leu	Ala	His	Arg	Thr	Val	Arg	Trp
1				5				10						15	
Cys	Thr	Gly	Leu	Ser	Gly	Ala	Pro	Xaa	Trp	Ser	Pro	Val	Lys	Trp	Pro
		20					25						30		
Leu	Ser	Gly	Leu	Asn	Asn	Ala	Tyr	Gly							
		35					40								

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..478
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

gcattgcact	mnngggagcg	tgcgcrgtag	gagtggatcg	gaggagcatg	trgaggctaa	60
agattggava	aggaggaggg	ccatggatgc	agacggcgag	cgacttccat	ggccggcagg	120
tttrggagta	cgacccggac	gccggcaccg	acgaggagcg	cacaaggtgg	agcagcttcg	180
ccgggcgttc	acagagaacc	gcttccgaag	agggaatcgc	aggacctcct	aatgcgtatg	240
cagttcgctg	gacaaaaata	tgtrcatgcv	gatctdcctg	crgccaccaa	gatagangag	300
gatggcgacg	agggtccgct	gacggaggag	aggttgamgg	aatcgctgar	gcgagcdctg	360
ggtttrcatg	ctgctctcca	agctgaagat	ggccactggc	cgcctggtga	ttacagtvvg	420
gttatgtacc	tcattgccgtt	ctggattttc	gcactgcaca	tcacaggcac	ggtcgtatg	

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..127
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ile	Ala	Xaa	Xaa	Gly	Ala	Cys	Xaa	Val	Gly	Val	Asp	Arg	Arg	Ser	Met	
1				5					10					15		
Xaa	Arg	Leu	Lys	Ile	Gly	Xaa	Gly	Gly	Gly	Pro	Trp	Met	Gln	Thr	Ala	
			20						25				30			
Ser	Asp	Phe	His	Gly	Arg	Gln	Val	Xaa	Glu	Tyr	Asp	Pro	Asp	Ala	Gly	
		35				40					45					
Thr	Asp	Glu	Glu	Arg	Thr	Arg	Trp	Ser	Ser	Phe	Ala	Gly	Arg	Ser	Gln	
	50					55					60					
Arg	Thr	Ala	Ser	Glu	Glu	Gly	Ile	Ala	Gly	Pro	Pro	Asn	Ala	Tyr	Ala	
65					70				75					80		
Val	Arg	Trp	Thr	Lys	Ile	Cys	Xaa	Cys	Xaa	Ser	Xaa	Cys	Xaa	His	Gln	
				85					90					95		
Asp	Arg	Xaa	Gly	Trp	Arg	Arg	Gly	Ala	Ala	Asp	Gly	Gly	Glu	Val	Xaa	
			100					105					110			
Gly	Ile	Ala	Xaa	Ala	Ser	Xaa	Gly	Xaa	His	Gly	Cys	Ser	Pro	Ser		
			115				120					125				

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..112
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met	Xaa	Arg	Leu	Lys	Ile	Gly	Xaa	Gly	Gly	Gly	Pro	Trp	Met	Gln	Thr	
1				5					10					15		
Ala	Ser	Asp	Phe	His	Gly	Arg	Gln	Val	Xaa	Glu	Tyr	Asp	Pro	Asp	Ala	
			20					25					30			

Gly Thr Asp Glu Glu Arg Thr Arg Trp Ser Ser Phe Ala Gly Arg Ser
35 40 45
Gln Arg Thr Ala Ser Glu Glu Gly Ile Ala Gly Pro Pro Asn Ala Tyr
50 55 60
Ala Val Arg Trp Thr Lys Ile Cys Xaa Cys Xaa Ser Xaa Cys Xaa His
65 70 75 80
Gln Asp Arg Xaa Gly Trp Arg Arg Gly Ala Ala Asp Gly Gly Glu Val
85 90 95
Xaa Gly Ile Ala Xaa Ala Ser Xaa Gly Xaa His Gly Cys Ser Pro Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Ala Gly Arg Phe Xaa Ser Thr Thr Arg Thr Pro Ala Pro Thr Arg
1 5 10 15
Ser Ala Gln Gly Gly Ala Ala Ser Pro Gly Val His Arg Glu Pro Leu
20 25 30
Pro Lys Arg Glu Ser Gln Asp Leu Leu Met Arg Met Gln Phe Ala Gly
35 40 45
Gln Lys Tyr Xaa His Xaa Asp Xaa Pro Xaa Ala Thr Lys Ile Xaa Glu
50 55 60
Asp Gly Asp Glu Val Pro Leu Thr Glu Glu Arg Leu Xaa Glu Ser Leu
65 70 75 80
Xaa Arg Xaa Leu Gly Xaa Met Ala Ala Leu Gln Ala Glu Asp Gly His
85 90 95
Trp Pro Pro Gly Asp Tyr Ser Xaa Val Met Tyr Leu Met Pro Phe Trp
100 105 110
Ile Phe Ala Leu His Ile Thr Gly Thr Val Asp
115 120

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..545
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

atagccttar cccggcgcgga gaagaaatcg tatectcgcc agctcttcac caacagattc 60
gtctcctcgc ctccgcccggg ttctgaccag aacgcccgcg ccagcccacc agtaattcct 120
ccgggcactg gtctccacct cctctgggat caccacccaa gaaaaggggtg cgcggcgcat 180
aggcgaccac tgagatttta ttctctatat aacatttggc tgtaagtgga ttataatctc 240
tataactctt aaataagtgc aaatatctca atgtcaagtg tttcaaattc tattgctgtg 300
ggtcttccaa gctatgggct atatctagag acaaggtttc tcacgcagac ctataggaac 360
ttcgcacaga aatcctctta caagtattcc agaatccgtg cagtgcaggg aaatggtggg 420

cgtcgaaggc tgggtgacat aatccgaatc attccagaac tctcaaggga ctattttaaa 480
agtcgatcga ggcgagctct ttttggtggc atctcgttgc ttggcggctt ttacgttgca 540
cagac

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1481894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Ile	Ala	Leu	Xaa	Arg	Arg	Glu	Lys	Lys	Ser	Tyr	Pro	Arg	Gln	Leu	Phe
1			5						10					15	
Thr	Asn	Arg	Phe	Val	Ser	Ser	Pro	Pro	Gly	Phe	Asp	Gln	Asn	Ala	
		20						25				30			
Ala	Ala	Ser	Pro	Pro	Val	Ile	Pro	Pro	Gly	Thr	Gly	Leu	His	Leu	Leu
		35					40					45			
Trp	Asp	His	His	Pro	Arg	Lys	Gly	Cys	Ala	Ala	His	Arg	Arg	Pro	Leu
	50					55					60				
Arg	Phe	Tyr	Ser	Leu	Tyr	Asn	Ile	Trp	Leu						
65						70									

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1481895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Ser	Leu	Xaa	Pro	Ala	Arg	Glu	Glu	Ile	Val	Ser	Ser	Pro	Ala	Leu	His
1			5						10					15	
Gln	Gln	Ile	Arg	Leu	Leu	Ala	Ser	Ala	Gly	Phe	Arg	Pro	Glu	Arg	Arg
		20						25				30			
Arg	Gln	Pro	Thr	Ser	Asn	Ser	Ser	Gly	His	Trp	Ser	Pro	Pro	Pro	Leu
		35				40						45			
Gly	Ser	Pro	Pro	Lys	Lys	Arg	Val	Arg	Gly	Ala					
	50					55									

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1481896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met	Ser	Ser	Val	Ser	Asn	Ser	Ile	Ala	Val	Gly	Leu	Pro	Ser	Tyr	Gly
1			5						10					15	

Leu Tyr Leu Glu Thr Arg Phe Leu Thr Gln Thr Tyr Arg Asn Phe Ala
20 25 30
Gln Lys Ser Ser Tyr Lys Tyr Ser Arg Ile Arg Ala Val Gln Gly Asn
35 40 45
Gly Gly Arg Arg Arg Leu Val Asp Ile Ile Arg Ile Ile Pro Glu Leu
50 55 60
Ser Arg Asp Tyr Phe Lys Ser Arg Ser Arg Arg Ala Leu Phe Gly Gly
65 70 75 80
Ile Ser Leu Leu Gly Gly Phe Tyr Val Ala Gln
85 90

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

tatgtggaaa ccatagctat tgggggcgaa gggcttatga gcgtcatttc aaggaatggc	60
gtcatcagca tgggatgcga tgccttgscat tcccccaata ctaagaattt caatgaaatt	120
acatccatcg aggaggcgaa agcgctcttg gagaaaattc aagcacgaca aggggtgaat	180
aagtggcggc cagacctaga ggaagagtat gaagatcagg aaggcaacat ctacaacaag	240
aagacctaca ctgacctgca gcgtcaaggc ctgatctagg gctcctgctg gttaaagttg	300
tcgggatttg ttcagaactt atctcatgta gttgtaactc tgaaaaatatt ggcccatctg	360
gcatacattt tatgtaataa catgattctc c	

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Tyr Val Glu Thr Ile Ala Ile Gly Gly Glu Gly Leu Met Ser Val Ile
1 5 10 15
Ser Arg Asn Gly Val Ile Ser Met Gly Cys Asp Ala Leu Xaa Phe Pro
20 25 30
Asn Thr Lys Asn Phe Asn Glu Ile Thr Ser Ile Glu Glu Ala Lys Ala
35 40 45
Leu Trp Glu Lys Ile Gln Ala Arg Gln Gly Val Asn Lys Trp Arg Pro
50 55 60
Asp Leu Glu Glu Glu Tyr Glu Asp Gln Glu Gly Asn Ile Tyr Asn Lys
65 70 75 80
Lys Thr Tyr Thr Asp Leu Gln Arg Gln Gly Leu Ile
85 90

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1481899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Met	Ser	Val	Ile	Ser	Arg	Asn	Gly	Val	Ile	Ser	Met	Gly	Cys	Asp	Ala
1				5				10						15	
Leu	Xaa	Phe	Pro	Asn	Thr	Lys	Asn	Phe	Asn	Glu	Ile	Thr	Ser	Ile	Glu
			20					25					30		
Glu	Ala	Lys	Ala	Leu	Trp	Glu	Lys	Ile	Gln	Ala	Arg	Gln	Gly	Val	Asn
		35					40					45			
Lys	Trp	Arg	Pro	Asp	Leu	Glu	Glu	Glu	Tyr	Glu	Asp	Gln	Glu	Gly	Asn
	50					55				60					
Ile	Tyr	Asn	Lys	Lys	Thr	Tyr	Thr	Asp	Leu	Gln	Arg	Gln	Gly	Leu	Ile
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1481900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met	Gly	Cys	Asp	Ala	Leu	Xaa	Phe	Pro	Asn	Thr	Lys	Asn	Phe	Asn	Glu
1				5				10						15	
Ile	Thr	Ser	Ile	Glu	Glu	Ala	Lys	Ala	Leu	Trp	Glu	Lys	Ile	Gln	Ala
			20					25					30		
Arg	Gln	Gly	Val	Asn	Lys	Trp	Arg	Pro	Asp	Leu	Glu	Glu	Glu	Tyr	Glu
		35				40					45				
Asp	Gln	Glu	Gly	Asn	Ile	Tyr	Asn	Lys	Lys	Thr	Tyr	Thr	Asp	Leu	Gln
	50					55				60					
Arg	Gln	Gly	Leu	Ile											
65															

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..722

(D) OTHER INFORMATION: / Ceres Seq. ID 1481901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

aatttattct	caaaccttat	gagtgagatc	tctcttaatc	attctctctt	tcttctctcc	60
tctgtgatgt	gaggtttcga	agatcccttct	ctgattccctc	atcaaactca	gatcagtagc	120
ggacccaagt	catttccttta	gagagatata	tggcagaggt	gaaggatcaa	ttagagatta	180
agttccggct	taacgatggg	tctgatatcg	gtcctaaatt	gtttcctgat	gctactaccg	240
ttgctacatt	gaaagaaacc	gttggtgctc	agtggccaag	agataaggag	aacggggccaa	300
agacagtga	agatgttaaa	ctgataagcg	cgggtagaat	attggagaac	aacaaaacgg	360
ttggagattg	caggagtccc	gtcggcaatt	tctcaggtgc	tgtcaccaca	atgcatgtta	420

taattcaaca tcaagttact gaaaaagaaa agaagaagaa gaagcctaaa ggtgatctga 480
aacagaacaa atgtgtctgt ttatgttttg gagctcgttg ttaacaattg tgcaagacaa 540
gtagagagag ttaaaaaagc ttgggagatt cacattctgt tcttgagcct tcttcaatac 600
cttttgcctt tggtccttgt aattcttttt tctgacatga catgacatga ttggcttttt 660
gatcgcttga gggttggttt ctattgtatt tcggattcgc aacaccgtgg aaattattag 720
gt

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Ala Glu Val Asp Gln Leu Glu Ile Lys Phe Arg Leu Asn Asp
1 5 10 15
Gly Ser Asp Ile Gly Pro Lys Leu Phe Pro Asp Ala Thr Thr Val Ala
20 25 30
Thr Leu Lys Glu Thr Val Val Ala Gln Trp Pro Arg Asp Lys Glu Asn
35 40 45
Gly Pro Lys Thr Val Lys Asp Val Lys Leu Ile Ser Ala Gly Arg Ile
50 55 60
Leu Glu Asn Asn Lys Thr Val Gly Asp Cys Arg Ser Pro Val Gly Asn
65 70 75 80
Phe Ser Gly Ala Val Thr Thr Met His Val Ile Ile Gln His Gln Val
85 90 95
Thr Glu Lys Glu Lys Lys Lys Lys Lys Pro Lys Gly Asp Leu Lys Gln
100 105 110
Asn Lys Cys Val Cys Leu Cys Phe Gly Ala Arg Cys
115 120

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..647
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

cccccttta ctacacactt cttctttttt cttcagaaag aaagaaagac agagagagag 60
agagaagatg gtgttaggaa agcgtcatgg atcactgac aagagaacaa ctagcatgaa 120
gatgatcaca ctcgatacac ccacgatcta tgacgcacat cagccgtccg atcatctaac 180
ctttcatcaa caccctcaca atccgatggg ggtgatggct agtaactacg atgatttctt 240
gaagacttgk agtctctgca atcgaagtct ctgccatcat cgtgacattt acatgtatag 300
agggaacaac gcatttttga gcttagaata cagggagaag caaattaagc tggacgagaa 360
aaaagcgaag accggcttcg taacatcgaa gaaaccaatt cgtatttagt tgatcatcta 420
tgatctaata tgataacgat agtttttctt tatgagtaaa atgaatatgt tttkcgctwt 480
cgtgtacaag aatgatgaaa ataaagagag aaaaaatgag actaaatgag tgtagtgatc 540
atatagtaat gggacttcat aagcatgatt tgatttgttc gtgtgatttg tttctttgtg 600
atgtgtaata tgtaatgtaa tatcaatggt gatgtatatt caggtgg

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

```
Pro Pro Leu Leu His Thr Ser Ser Phe Phe Arg Lys Lys Glu Arg
1          5          10          15
Gln Arg Glu Arg Glu Lys Met Val Leu Gly Lys Arg His Gly Ser Leu
          20          25          30
Ile Lys Arg Thr Thr Ser Met Lys Met Ile Thr Leu Asp Thr Pro Thr
          35          40          45
Ile Tyr Asp Ala Ser Gln Pro Ser Asp His Leu Thr Phe His Gln His
          50          55          60
Pro His Asn Pro Met Val Val Met Ala Ser Asn Tyr Asp Asp Phe Leu
          65          70          75          80
Lys Thr Xaa Ser Leu Cys Asn Arg Ser Leu Cys His His Arg Asp Ile
          85          90          95
Tyr Met Tyr Arg Gly Asn Asn Ala Phe Cys Ser Leu Glu Cys Arg Glu
          100         105         110
Lys Gln Ile Lys Leu Asp Glu Lys Lys Ala Lys Thr Gly Phe Val Thr
          115         120         125
Ser Lys Lys Pro Ile Arg Ile
          130         135
```

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```
Met Val Leu Gly Lys Arg His Gly Ser Leu Ile Lys Arg Thr Thr Ser
1          5          10          15
Met Lys Met Ile Thr Leu Asp Thr Pro Thr Ile Tyr Asp Ala Ser Gln
          20          25          30
Pro Ser Asp His Leu Thr Phe His Gln His Pro His Asn Pro Met Val
          35          40          45
Val Met Ala Ser Asn Tyr Asp Asp Phe Leu Lys Thr Xaa Ser Leu Cys
          50          55          60
Asn Arg Ser Leu Cys His His Arg Asp Ile Tyr Met Tyr Arg Gly Asn
          65          70          75          80
Asn Ala Phe Cys Ser Leu Glu Cys Arg Glu Lys Gln Ile Lys Leu Asp
          85          90          95
Glu Lys Lys Ala Lys Thr Gly Phe Val Thr Ser Lys Lys Pro Ile Arg
          100         105         110
Ile
```

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1481906
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:
Met Lys Met Ile Thr Leu Asp Thr Pro Thr Ile Tyr Asp Ala Ser Gln
1 5 10 15
Pro Ser Asp His Leu Thr Phe His Gln His Pro His Asn Pro Met Val
20 25 30
Val Met Ala Ser Asn Tyr Asp Asp Phe Leu Lys Thr Xaa Ser Leu Cys
35 40 45
Asn Arg Ser Leu Cys His His Arg Asp Ile Tyr Met Tyr Arg Gly Asn
50 55 60
Asn Ala Phe Cys Ser Leu Glu Cys Arg Glu Lys Gln Ile Lys Leu Asp
65 70 75 80
Glu Lys Lys Ala Lys Thr Gly Phe Val Thr Ser Lys Lys Pro Ile Arg
85 90 95
Ile

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..800
(D) OTHER INFORMATION: / Ceres Seq. ID 1481907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

acttttcatta gtttccaatt taacaaatca aaatcagaag aagaagaaga tgaccagctc	60
tgatcctcaa tctcacaacg tcttcgtcta cggtagcatt ctagaaccgc cgcgcgcgc	120
cgtgatcctt gatcgcacag ccgatacagt cccgcgcggt ctccatggct agtacgctct	180
ctcaccctct cgatgatcgt ttattcaatc ggagattaac aaaagattta tgggttttta	240
acagtcacag atataaactc aaaggacttc catatccatg tattgtttct tctgattctg	300
gaaaagtcaa cggaaagggt ataactggag tgtctgatgc tgagttaa attttcgatg	360
tgattgaagg taatgattat gagagagtaa ctggtgaagt tgtaagaatg gataattctg	420
agaaggtgaa agttgaaact tatgtttggg ttaataaaga tgatcctaga atgtatggag	480
aatgggattt cgaggaatgg agagtgggtc acgcggagaa attcgtggag acttttagaa	540
aaatgttgga atggaacaag aatccaaatg ggaagagcat ggaggaggct gtaggatcat	600
tattatcgtc aggggattaa ttcttgatga gcttggttaa tcttagcaga agagagtaag	660
tgagtaagta aagagtgggt tttgaataat gtgttggttg aacttgaaac agagtcttct	720
atgtgatttt gtttgtgttg ttatggatat cttgttgga ctttttctga tttcagttgg	780
aaacaggtgc gtttgcgggc	

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1481908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met Ala Ser Thr Leu Ser His Pro Leu Asp Asp Arg Leu Phe Asn Arg
1 5 10 15
Arg Leu Thr Lys Asp Leu Trp Val Phe Asn Ser His Arg Tyr Lys Leu
20 25 30
Lys Gly Leu Pro Tyr Pro Cys Ile Val Ser Ser Asp Ser Gly Lys Val
35 40 45
Asn Gly Lys Val Ile Thr Gly Val Ser Asp Ala Glu Leu Asn Asn Phe
50 55 60
Asp Val Ile Glu Gly Asn Asp Tyr Glu Arg Val Thr Val Glu Val Val
65 70 75 80
Arg Met Asp Asn Ser Glu Lys Val Lys Val Glu Thr Tyr Val Trp Val
85 90 95
Asn Lys Asp Asp Pro Arg Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp
100 105 110
Arg Val Val His Ala Glu Lys Phe Val Glu Thr Phe Arg Lys Met Leu
115 120 125
Glu Trp Asn Lys Asn Pro Asn Gly Lys Ser Met Glu Glu Ala Val Gly
130 135 140
Ser Leu Leu Ser Ser Gly Asp
145 150

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1481913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

aactcagtcg tctcaatgcc gtgtaacaac ttcatcgtct ttttcagttc aacaacttca 60
tcgtcttttt cagttcaacc tccgacatct ctctctctcca ggtgattgat cccatcgaag 120
ggtctatgga agagaacaac aacgccggga gcgattccga ctctaattcc gtcgaagatt 180
cacaagacta ttacgaaccg atctcagccg tcgatttata taactccaac gacgatgaag 240
aagacagtta tcttccgatac ggtggagatg gtctctctaa cggccattgt atgattccgg 300
atgcagaggt aggaatctct tctattagta taaacgataa cacagacagc gaagaagaga 360
cagagacgga gactggaccg gagatccgta gagcgtttga ggaggacgaa cggcggagaa 420
ggtcgccggt agtggaggag aatgccggtta gggttatgga ggcaatgcga gccatctcat 480
tccctggaac ggctcctgat tgggcctccg atgttaatga ggatcgttgg attgatcagc 540
tgcgaaagatt gagaaccact tctcaataag ctttctccaa tctcगतagt tgttttcgtt 600
taagatcttt ctcaatgttg ttcaatgtga cttcttttaa acattcaata taaaaccag 660
agaatttcac cactc

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1481914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Glu Glu Asn Asn Asn Ala Gly Ser Asp Ser Asp Ser Asn Ser Val

1 5 10 15
Glu Asp Ser Gln Asp Tyr Tyr Glu Pro Ile Ser Ala Val Asp Leu Tyr
20 25 30
Asn Ser Asn Asp Asp Glu Glu Asp Ser Tyr Leu Pro Ile Gly Gly Asp
35 40 45
Gly Leu Ser Asn Gly His Cys Met Ile Pro Asp Ala Glu Val Gly Ile
50 55 60
Ser Ser Ile Ser Ile Asn Asp Asn Thr Asp Ser Glu Glu Glu Thr Glu
65 70 75 80
Thr Glu Thr Gly Pro Glu Ile Arg Arg Ala Phe Glu Glu Asp Glu Arg
85 90 95
Arg Arg Arg Ser Pro Leu Val Glu Glu Asn Ala Val Arg Val Met Glu
100 105 110
Ala Met Arg Ala Ile Ser Phe Pro Gly Thr Ala Pro Asp Trp Ala Ser
115 120 125
Asp Val Asn Glu Asp Arg Trp Ile Asp Gln Leu Arg Arg Leu Arg Thr
130 135 140
Thr Ser Gln
145

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met Ile Pro Asp Ala Glu Val Gly Ile Ser Ser Ile Ser Ile Asn Asp
1 5 10 15
Asn Thr Asp Ser Glu Glu Glu Thr Glu Thr Glu Thr Gly Pro Glu Ile
20 25 30
Arg Arg Ala Phe Glu Glu Asp Glu Arg Arg Arg Arg Ser Pro Leu Val
35 40 45
Glu Glu Asn Ala Val Arg Val Met Glu Ala Met Arg Ala Ile Ser Phe
50 55 60
Pro Gly Thr Ala Pro Asp Trp Ala Ser Asp Val Asn Glu Asp Arg Trp
65 70 75 80
Ile Asp Gln Leu Arg Arg Leu Arg Thr Thr Ser Gln
85 90

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

acgatttttta tctgatttga caccaaagta tcttttagcc ttaattcggt acgttgtaaa 60
gaaactgata caatcccttc tattcggatt atatagaccc aatatgtaca gatccgcgag 120
ctggaaccgt gtgacggagg attactcggg gccttggtcc gcaccaaagg gattatggaa 180
gggcttagac gaagacgagg ccggctccat acgatccac tggccaaaag atgactaaga 240

aagagaagtc	acgtaccaag	tttgctgaaa	acgccgttca	cataatccct	tttgtccttc	300
ttgtttgtgc	tctcgtcctt	tggttcttct	ctaattccaga	tgtagatgtt	gggggtgaaag	360
gggacttcat	tgcggctagg	attgaaggat	taacgatcga	aggagacatt	gacaatgaca	420
gcgacggamc	tcagaccgga	ttcttaggag	ccgccacaga	ggtcggacat	tcaaaaaata	480
aactaaaacg	cgaggctaata	aaacgcaatc	ggaggataca	agcttcaagg	aaagtgatga	540
aaggttttta	ttaatcacct	ttttgtttga	taaattgttta	cgagataaac	tttcaaaaacg	600
aattattctt	ttttttcttt	ctattttgat	tgcgcatgtt	agttgatcag	gagatgtgtt	660
tctttggtta	aacttttata	tttagttctt	cacattatct	tcaagatcca	caagaactac	720
tttcactct						

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Arg	Phe	Leu	Ser	Asp	Leu	Thr	Pro	Lys	Tyr	Leu	Leu	Ala	Leu	Ile	Arg
1				5					10					15	
Tyr	Val	Val	Lys	Lys	Leu	Ile	Gln	Ser	Leu	Leu	Phe	Gly	Leu	Tyr	Arg
			20					25				30			
Pro	Asn	Met	Tyr	Arg	Ser	Ala	Ser	Trp	Asn	Arg	Val	Thr	Glu	Asp	Tyr
		35					40				45				
Ser	Val	Pro	Trp	Ser	Ala	Pro	Lys	Gly	Leu	Trp	Lys	Gly	Leu	Asp	Glu
	50				55				60						
Asp	Glu	Ala	Gly	Ser	Ile	Arg	Ser	His	Trp	Pro	Lys	Asp	Asp		
65				70					75						

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met	Thr	Lys	Lys	Glu	Lys	Ser	Arg	Thr	Lys	Phe	Ala	Glu	Asn	Ala	Val
1				5					10					15	
His	Ile	Ile	Pro	Phe	Val	Leu	Leu	Ala	Cys	Ala	Leu	Val	Leu	Trp	Phe
			20					25				30			
Phe	Ser	Asn	Pro	Asp	Val	Asp	Val	Gly	Val	Lys	Gly	Asp	Phe	Ile	Ala
		35				40					45				
Ala	Arg	Ile	Glu	Gly	Leu	Thr	Ile	Glu	Gly	Asp	Ile	Asp	Asn	Asp	Ser
	50				55				60						
Asp	Gly	Xaa	Gln	Thr	Gly	Phe	Leu	Gly	Ala	Ala	Thr	Glu	Val	Gly	His
65			70					75						80	
Ser	Lys	Asn	Lys	Leu	Lys	Arg	Glu	Ala	Asn	Lys	Arg	Asn	Arg	Arg	Ile
			85					90						95	
Gln	Ala	Ser	Arg	Lys	Val	Met	Lys	Gly	Phe	Tyr					
			100					105							

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1481919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

ctgaacgaag	ctctctctct	gattggccgg	atctgccgga	gagaaaaatg	acgacgagta	60
ttcacatcac	agctctcgac	ggaatcgta	acgtgaactc	actcttcaca	ctcgccgtat	120
tcacgggatt	agcttggaac	cctaccgata	cagacaacag	cctcgtaacc	gaccctaatt	180
gcgtccccac	agctcgatg	gctgagaatc	tcgtcgctt	ccatgtgtac	tctttcgcat	240
cattcctatt	ctcaagtctc	atcgctctag	gtctcaaaca	agcaatgagg	ctcaacatag	300
cttcttcggt	tcacatctct	actcgaatcg	atcctgtggt	ttactatgtg	aacaagacgg	360
ctcttagatt	tgggatgggt	acatccgggt	tgggatcggt	ttgtggatgt	gggtttctca	420
tgttggtttt	gattaatggt	gttcagatca	agcttgggac	tttgggctgt	ggtgctagt	480
gtcatactta	tgcagctgtt	gtgccgcttt	gtgattctgg	ttccttctgc	acttttcac	540
tatgtttctc	ttatgttata	tgcttttact	cgttagagac	atggtttttg	attccatggt	600
tgatgcaatt	aggggttatgt	ttgtatgatg	atgatatgat	ggaaatgaga	atgattctat	660
gytttgatat	gggt					

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1481920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Glu	Arg	Ser	Ser	Leu	Ser	Asp	Trp	Pro	Asp	Leu	Pro	Glu	Arg	Lys	Met
1				5				10						15	
Thr	Thr	Ser	Ile	His	Ile	Thr	Ala	Leu	Asp	Gly	Ile	Val	Asn	Val	Asn
				20				25					30		
Ser	Leu	Phe	Thr	Leu	Ala	Val	Phe	Ile	Gly	Leu	Ala	Trp	Asn	Pro	Thr
				35				40					45		
Asp	Pro	Asp	Asn	Ser	Leu	Val	Thr	Asp	Pro	Asn	Cys	Val	Pro	Thr	Ala
				50				55					60		
Arg	Met	Ala	Glu	Asn	Leu	Val	Ala	Phe	His	Val	Tyr	Ser	Phe	Ala	Ser
65				70				75						80	
Phe	Leu	Phe	Ser	Ser	Leu	Ile	Ala	Leu	Gly	Leu	Lys	Gln	Ala	Met	Arg
				85				90						95	
Leu	Asn	Ile	Ala	Ser	Ser	Phe	His	Ile	Ser	Thr	Arg	Ile	Asp	Pro	Val
				100				105					110		
Val	Tyr	Tyr	Val	Asn	Lys	Thr	Ala	Leu	Arg	Phe	Gly	Met	Val	Thr	Ser
				115				120					125		
Gly	Leu	Gly	Ser	Val	Cys	Gly	Cys	Gly	Phe	Leu	Met	Leu	Ala	Leu	Ile
				130				135					140		
Asn	Val	Val	Gln	Ile	Lys	Leu	Gly	Thr	Leu	Gly	Cys	Gly	Ala	Ser	Gly
145				150				155						160	
His	Thr	Tyr	Ala	Ala	Val	Val	Pro	Leu	Cys	Asp	Ser	Gly	Ser	Phe	Cys
				165				170						175	
Thr	Phe	His	Leu	Cys	Phe	Ser	Tyr	Val	Ile	Cys	Phe	Tyr	Ser	Leu	Glu
				180				185						190	
Thr	Trp	Phe	Leu	Ile	Pro	Trp	Leu	Met	Gln	Leu	Gly	Leu	Cys	Leu	Tyr

195	200	205
Asp Asp Asp Met Met Glu Met Arg Met Ile Leu Xaa Phe Asp Met Val		
210	215	220

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1481921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Met	Thr	Thr	Ser	Ile	His	Ile	Thr	Ala	Leu	Asp	Gly	Ile	Val	Asn	Val
1			5						10					15	
Asn	Ser	Leu	Phe	Thr	Leu	Ala	Val	Phe	Ile	Gly	Leu	Ala	Trp	Asn	Pro
		20						25					30		
Thr	Asp	Pro	Asp	Asn	Ser	Leu	Val	Thr	Asp	Pro	Asn	Cys	Val	Pro	Thr
		35					40					45			
Ala	Arg	Met	Ala	Glu	Asn	Leu	Val	Ala	Phe	His	Val	Tyr	Ser	Phe	Ala
		50				55					60				
Ser	Phe	Leu	Phe	Ser	Ser	Leu	Ile	Ala	Leu	Gly	Leu	Lys	Gln	Ala	Met
65					70					75					80
Arg	Leu	Asn	Ile	Ala	Ser	Ser	Phe	His	Ile	Ser	Thr	Arg	Ile	Asp	Pro
			85						90					95	
Val	Val	Tyr	Tyr	Val	Asn	Lys	Thr	Ala	Leu	Arg	Phe	Gly	Met	Val	Thr
			100					105					110		
Ser	Gly	Leu	Gly	Ser	Val	Cys	Gly	Cys	Gly	Phe	Leu	Met	Leu	Ala	Leu
		115					120					125			
Ile	Asn	Val	Val	Gln	Ile	Lys	Leu	Gly	Thr	Leu	Gly	Cys	Gly	Ala	Ser
		130				135					140				
Gly	His	Thr	Tyr	Ala	Ala	Val	Val	Pro	Leu	Cys	Asp	Ser	Gly	Ser	Phe
145					150					155					160
Cys	Thr	Phe	His	Leu	Cys	Phe	Ser	Tyr	Val	Ile	Cys	Phe	Tyr	Ser	Leu
			165						170					175	
Glu	Thr	Trp	Phe	Leu	Ile	Pro	Trp	Leu	Met	Gln	Leu	Gly	Leu	Cys	Leu
			180					185					190		
Tyr	Asp	Asp	Asp	Met	Met	Glu	Met	Arg	Met	Ile	Leu	Xaa	Phe	Asp	Met
		195					200						205		
Val															

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1481922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met	Ala	Glu	Asn	Leu	Val	Ala	Phe	His	Val	Tyr	Ser	Phe	Ala	Ser	Phe
1				5						10				15	

Leu Phe Ser Ser Leu Ile Ala Leu Gly Leu Lys Gln Ala Met Arg Leu
20 25 30
Asn Ile Ala Ser Ser Phe His Ile Ser Thr Arg Ile Asp Pro Val Val
35 40 45
Tyr Tyr Val Asn Lys Thr Ala Leu Arg Phe Gly Met Val Thr Ser Gly
50 55 60
Leu Gly Ser Val Cys Gly Cys Gly Phe Leu Met Leu Ala Leu Ile Asn
65 70 75 80
Val Val Gln Ile Lys Leu Gly Thr Leu Gly Cys Gly Ala Ser Gly His
85 90 95
Thr Tyr Ala Ala Val Val Pro Leu Cys Asp Ser Gly Ser Phe Cys Thr
100 105 110
Phe His Leu Cys Phe Ser Tyr Val Ile Cys Phe Tyr Ser Leu Glu Thr
115 120 125
Trp Phe Leu Ile Pro Trp Leu Met Gln Leu Gly Leu Cys Leu Tyr Asp
130 135 140
Asp Asp Met Met Glu Met Arg Met Ile Leu Xaa Phe Asp Met Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..724
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

aaaaagaagg atcaagaacc caaaatagag agcccaattt ctcttaaact tgccaaagta	60
gctatcaggt ggttcttgat acggaacttc cagatcccaa gcagcagcag aggcctcatc	120
accgtcgcct ccaccgagga aatctccggc agcgattctt gacttgatga aacggagctt	180
gtgagtggcg agaccgagtg agcttatggc agcgacgctg gtacttgaag cgttgatgc	240
aacggagagt ttgagcgacg gagacgtaga agaagaggtg agagaaggat aggaggcaga	300
tgggtgcccc gcaatggcgg cagtgaagac gacctgaggg ttgagagagg gagaagaaga	360
ttacggcgag gaagatgaag aagagctgaa atagcttggt ggagcttctt cttctgggtg	420
tcaatggctc gtttcttctc taagggtttt tcgaagtggg gctggattat tgagtttagt	480
gcttgtagag cagtttcttt ggggatgaaa ggttggttat tctggtcaat ttcgtcgtcg	540
tagtccgcca ttgaaggact gagaagagag aaaaagtgtt attgggttaga gagatgggtt	600
ggggattgtg tgtagygaac atgtgggtgt ggtytcgtat ctctagacaa gtattatcca	660
tctcaacggt cttgttctga ttttgatgt tttgtccgta ctcaataaat attttactgg	720

gagt

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Lys Lys Lys Asp Gln Glu Pro Lys Ile Glu Ser Pro Ile Ser Leu Lys	
1 5 10 15	
Leu Ala Lys Val Ala Ile Arg Trp Phe Leu Ile Arg Asn Phe Gln Ile	
20 25 30	

Pro Ser Ser Ser Arg Gly Leu Ile Thr Val Ala Ser Thr Glu Glu Ile
35 40 45
Ser Gly Ser Asp Ser
50

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Ala Arg Phe Phe Ser Lys Val Phe Ser Lys Trp Ser Trp Ile Ile
1 5 10 15
Glu Phe Ser Ala Cys Arg Ala Val Ser Leu Gly Met Lys Gly Trp Leu
20 25 30
Phe Trp Ser Ile Ser Ser Ser
35

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..453
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

gcacgcac	gacccccc	tctgcgcacc	cgcaagcyta	ttcgccgcac	ctcctcaggt	60
gaccgggaag	atgatgccgt	tgagccaaac	cgacttctcg	ccgtcgcagt	tcacctcctc	120
ccagaatgcc	gccgccgact	ccaccacgcc	ttccaagatg	cgcgccgcgt	ccagcaccat	180
gcctctcacc	gtgaagcagg	tcgtcgacgc	gcacgagtct	ggcacgggcg	acaagggcgc	240
tccgttcac	gtcaatggcg	tcgagatggc	taacgtaccg	ataatcctct	tgttcgtcct	300
ttggtcctgt	gatatgcaga	tggtctcggc	gttaattcat	ctgccgcggt	tcccttttca	360
gattcgactt	gtggggatgg	tcaatgccaa	ggtggagcgg	acgaccgatg	tgaccttcac	420
gctcgacgat	ggcaccggcc	gcctcgattt	cat			

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

His Arg Ile Asp Pro Pro Ile Cys Ala Pro Ala Ser Xaa Phe Ala Ala
1 5 10 15
Pro Pro Gln Val Thr Gly Lys Met Met Pro Leu Ser Gln Thr Asp Phe
20 25 30
Ser Pro Ser Gln Phe Thr Ser Ser Gln Asn Ala Ala Ala Asp Ser Thr

35	40	45
Thr Pro Ser Lys Met Arg Gly Ala Ser Ser Thr Met Pro Leu Thr Val		
50	55	60
Lys Gln Val Val Asp Ala His Glu Ser Gly Thr Gly Asp Lys Gly Ala		
65	70	75
Pro Phe Ile Val Asn Gly Val Glu Met Ala Asn Val Pro Ile Ile Leu		
85	90	95
Leu Phe Val Leu Trp Ser Val Asp Met Gln Met Phe Ser Ala Leu Ile		
100	105	110
His Leu Pro Arg Phe Pro Phe Gln Ile Arg Leu Val Gly Met Val Asn		
115	120	125
Ala Lys Val Glu Arg Thr Thr Asp Val Thr Phe Thr Leu Asp Asp Gly		
130	135	140
Thr Gly Arg Leu Asp Phe		
145	150	

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Met Met Pro Leu Ser Gln Thr Asp Phe Ser Pro Ser Gln Phe Thr Ser		
1	5	10
Ser Gln Asn Ala Ala Ala Asp Ser Thr Thr Pro Ser Lys Met Arg Gly		
20	25	30
Ala Ser Ser Thr Met Pro Leu Thr Val Lys Gln Val Val Asp Ala His		
35	40	45
Glu Ser Gly Thr Gly Asp Lys Gly Ala Pro Phe Ile Val Asn Gly Val		
50	55	60
Glu Met Ala Asn Val Pro Ile Ile Leu Leu Phe Val Leu Trp Ser Val		
65	70	75
Asp Met Gln Met Phe Ser Ala Leu Ile His Leu Pro Arg Phe Pro Phe		
85	90	95
Gln Ile Arg Leu Val Gly Met Val Asn Ala Lys Val Glu Arg Thr Thr		
100	105	110
Asp Val Thr Phe Thr Leu Asp Asp Gly Thr Gly Arg Leu Asp Phe		
115	120	125

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met Pro Leu Ser Gln Thr Asp Phe Ser Pro Ser Gln Phe Thr Ser Ser		
1	5	10
Gln Asn Ala Ala Ala Asp Ser Thr Thr Pro Ser Lys Met Arg Gly Ala		
20	25	30

Ser Ser Thr Met Pro Leu Thr Val Lys Gln Val Val Asp Ala His Glu
35 40 45
Ser Gly Thr Gly Asp Lys Gly Ala Pro Phe Ile Val Asn Gly Val Glu
50 55 60
Met Ala Asn Val Pro Ile Ile Leu Leu Phe Val Leu Trp Ser Val Asp
65 70 75 80
Met Gln Met Phe Ser Ala Leu Ile His Leu Pro Arg Phe Pro Phe Gln
85 90 95
Ile Arg Leu Val Gly Met Val Asn Ala Lys Val Glu Arg Thr Thr Asp
100 105 110
Val Thr Phe Thr Leu Asp Asp Gly Thr Gly Arg Leu Asp Phe
115 120 125

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..677
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

acattctagt	acaatatagt	ggttggtgctc	ctctattcta	tttccttggt	gctactagtc	60
tgagttgtga	gattagtgtt	gctaacaatt	tggaagacgc	ggastccttt	tcacctctag	120
caaggttctc	caaatcgctc	gctaaatttt	acaggcgctc	ccagagccgc	taattgtcgt	180
ggatcttcag	acgtccgcta	cacgccgatt	cactccctct	cccgcgctag	ggcggaacct	240
tctcccttgc	gtcttcccat	cgcaaggtct	tgtccatgcc	gacagctagt	tcccgcacgga	300
cttcctcgga	ggcggtcagc	accgacgacg	aggaggctgc	gcggggaagc	aagggcgggac	360
gaccctcgcc	gccgcgctgc	tcgtcgtgca	ggtagtcggc	tacttcttac	acggtcgccg	420
ccggtgttgg	gctctccgac	agtgcgtgca	tcgatgggtg	agactctctg	cacagccacg	480
ccgatgagct	ctcctctgtt	gtcgtggaca	tgtttcacgg	ttcctcsctc	gcggccacaa	540
caagcgatgg	tggtggctgg	tcgcgtctag	gtgctcgatg	aaaggtgtgt	ttgtagtctg	600
gcacttttta	ccacaggaaa	gagagagaag	taaacaatat	gcattgcgaag	tcaataaaaag	660
tgaaatcgaa	attctttt					

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Ile Leu Val Gln Tyr Ser Gly Cys Ala Pro Leu Phe Tyr Phe Leu Val
1 5 10 15
Ala Thr Ser Leu Ser Cys Glu Ile Ser Val Ala Asn Asn Leu Glu Asp
20 25 30
Ala Xaa Ser Phe Ser Pro Leu Ala Arg Phe Ser Lys Ser Ser Ala Lys
35 40 45
Phe Tyr Arg Arg Arg Gln Ser Arg
50 55

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1481966
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:
Gln Leu Leu Ala Ile Asp Ser Ala Ala Val Gln Leu Leu Arg Arg
1 5 10 15
Ser Leu Ile Gly Asp Glu Leu Thr Gly Lys Glu Lys Lys Ala Leu Arg
20 25 30
Arg Thr Met Thr Asp Leu Ala Ser Val Ile Pro Ile Gly Ile Leu Met
35 40 45
Leu Leu Pro Val Thr Ala Val Gly His Ala Ala Met Leu Ala Gly Ile
50 55 60
Gln Arg Tyr Val Pro Gly Leu Ile Pro Ser Thr Tyr Gly Ser Glu Arg
65 70 75 80
Leu Asn Leu Leu Arg Gln Leu Glu Lys Ile Lys Glu Leu Gln Thr Asn
85 90 95
Glu Thr Glu Ser Glu Glu Gly Val Glu Glu Ile Ala Leu
100 105

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1481967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Thr Asp Leu Ala Ser Val Ile Pro Ile Gly Ile Leu Met Leu Leu
1 5 10 15
Pro Val Thr Ala Val Gly His Ala Ala Met Leu Ala Gly Ile Gln Arg
20 25 30
Tyr Val Pro Gly Leu Ile Pro Ser Thr Tyr Gly Ser Glu Arg Leu Asn
35 40 45
Leu Leu Arg Gln Leu Glu Lys Ile Lys Glu Leu Gln Thr Asn Glu Thr
50 55 60
Glu Ser Glu Glu Gly Val Glu Glu Ile Ala Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1481968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Ser Arg Arg Lys Gln Tyr Arg Leu Val Pro Leu Phe Thr Leu Phe
1 5 10 15
Gly Asn Ser Leu Pro Lys Ala Ala His Arg Glu Ser Arg Ser Met Cys

20 25 30
Pro Val Leu Arg Val Ser Thr Ser Asp Cys Ser Leu Glu Glu His Leu
35 40 45
Gln Glu Phe Pro Val Leu Asp Thr Ala Lys Asp Glu His Leu Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

accatcacga atcgcgattt ttttttgaga ttacggaagc ttcgcttgat ttgggatttt	60
tagggttttt ttttccgaa gacgactccg agagaccaac agtgatttga caatgacgct	120
acctccaggt ctttactccg gcaccagctc tcttgctctg gtggctcgtg cttcggcttt	180
tgggttgggt ctgctctatg ggaacatgaa gctcaagatc aaatcgatgt cacagaagaa	240
ggttgaagcc accgctcatc attaaaccac tcgttctttc ttacaataa gatgccaaaa	300
gctgggggtg atgtctcccc ggtagtttg atttcttctt tcatgattca tccttttagca	360
taagaaggaa caaatgtgtt ttgaaaagc atattatacg gttttaagac ctttttggag	420
ccataattgc cattggctta aaacccgagt caagaacatc tttccatttg ttgtcatcca	480
ataacaccgt tcacattc	

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

His His Glu Ser Arg Phe Phe Phe Glu Ile Thr Glu Ala Ser Leu Asp	
1 5 10 15	
Leu Gly Phe Leu Gly Phe Ser Phe Ser Glu Asp Asp Ser Glu Arg Pro	
20 25 30	
Thr Val Ile	
35	

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Thr Leu Pro Pro Gly Leu Tyr Ser Gly Thr Ser Ser Leu Ala Leu	
1 5 10 15	
Val Ala Arg Ala Ser Ala Phe Gly Leu Gly Leu Val Tyr Gly Asn Met	

20 25 30
Lys Leu Lys Ile Lys Ser Met Ser Gln Lys Lys Val Glu Ala Thr Ala
35 40 45

His His
50

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..800
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

atctatgcct	acaccaacaa	gcaacgggtca	tgctctctcgc	gtgcagattc	aagaaccaag	60
aataatgtct	cctcttcctc	cttcttcttc	tccaatcgcc	ttcaaggaac	aacaaggtag	120
accacctcca	acaacacaa	aaaccatagc	aggaaaactc	tttagaactc	ttttcaagg	180
tcttctcttc	tcacaactaa	ccttaatctc	acttttggtg	atcgttctca	ccattcgcg	240
tctcatctca	gcaagtacac	accatttcca	cctcaagaaa	tggtaccctc	ctttactagc	300
atctgttgct	gtctcaggaa	ttgcatcttt	agcatggcaa	tgcattctta	tctacaatcc	360
atcaagagca	gtcaaagcaa	cgttctggct	tagtccaata	ctcacctgct	cggtaggaat	420
cttgcttggt	ttgattggct	cagcggtaga	tgcaggtata	ggtgcagtgt	ttgtcccttt	480
cgccattact	cagtcctctc	atggttgctg	gattactccg	aggcttgagt	acaccgataa	540
aatattatca	cttgccacag	catttccacc	tgcaagaacc	agagaagtag	tctgcttata	600
aatcatagtc	agtgtcgttt	actctggttt	cttggtgact	ggaattggag	gagcaacttc	660
cactagaaca	aatcttgata	tcttggttcat	atccgtaatc	ataataagct	tagcatggac	720
gatgcaagtt	atcaagaatg	ttcaacaagt	tgcgatttca	cgggcgagat	atgtaaactt	780
tgcatatgga	gaagatatgg					

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Ser Met Pro Thr Pro Thr Ser Asn Gly His Ala Ser Arg Val Gln Ile	
1 5 10 15	
Gln Glu Pro Arg Ile Met Ser Pro Leu Pro Pro Ser Ser Ser Pro Ile	
20 25 30	
Ala Phe Lys Glu Gln Gln Gly Arg Pro Pro Pro Thr Thr Gln Gln Thr	
35 40 45	
Ile Ala Gly Lys Leu Phe Arg Thr Leu Phe Lys Gly Leu Leu Phe Ser	
50 55 60	
Gln Leu Thr Leu Ile Ser Leu Leu Val Ile Val Leu Thr Ile Arg Gly	
65 70 75 80	
Leu Ile Ser Ala Ser Thr His His Phe His Leu Lys Lys Trp Tyr Pro	
85 90 95	
Pro Leu Leu Ala Ser Val Ala Val Ser Gly Ile Ala Ser Leu Ala Trp	
100 105 110	
Gln Cys Ile Phe Ile Tyr Asn Pro Ser Arg Ala Val Lys Ala Thr Phe	
115 120 125	

Trp Leu Ser Pro Ile Leu Thr Cys Ser Val Gly Ile Leu Leu Val Leu
130 135 140
Ile Gly Ser Ala Val Asp Ala Gly Ile Gly Ala Val Phe Val Leu Phe
145 150 155 160
Ala Ile Thr Gln Ser Leu Tyr Gly Cys Trp Ile Thr Pro Arg Leu Glu
165 170 175
Tyr Thr Asp Lys Ile Leu Ser Leu Ala Thr Ala Phe Pro Pro Ala Arg
180 185 190
Thr Arg Glu Val Val Cys Leu Ser Ile Ile Val Ser Val Val Tyr Ser
195 200 205
Gly Phe Leu Val Thr Gly Ile Gly Gly Ala Thr Ser Thr Arg Thr Asn
210 215 220
Leu Asp Ile Leu Phe Ile Ser Val Ile Ile Ile Ser Leu Ala Trp Thr
225 230 235 240
Met Gln Val Ile Lys Asn Val Gln Gln Val Ala Ile Ser Arg Ala Arg
245 250 255
Tyr Val Asn Phe Ala His Gly Glu Asp Met
260 265

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Pro Thr Pro Thr Ser Asn Gly His Ala Ser Arg Val Gln Ile Gln
1 5 10 15
Glu Pro Arg Ile Met Ser Pro Leu Pro Pro Ser Ser Ser Pro Ile Ala
20 25 30
Phe Lys Glu Gln Gln Gly Arg Pro Pro Thr Thr Gln Gln Thr Ile
35 40 45
Ala Gly Lys Leu Phe Arg Thr Leu Phe Lys Gly Leu Leu Phe Ser Gln
50 55 60
Leu Thr Leu Ile Ser Leu Leu Val Ile Val Leu Thr Ile Arg Gly Leu
65 70 75 80
Ile Ser Ala Ser Thr His His Phe His Leu Lys Lys Trp Tyr Pro Pro
85 90 95
Leu Leu Ala Ser Val Ala Val Ser Gly Ile Ala Ser Leu Ala Trp Gln
100 105 110
Cys Ile Phe Ile Tyr Asn Pro Ser Arg Ala Val Lys Ala Thr Phe Trp
115 120 125
Leu Ser Pro Ile Leu Thr Cys Ser Val Gly Ile Leu Leu Val Leu Ile
130 135 140
Gly Ser Ala Val Asp Ala Gly Ile Gly Ala Val Phe Val Leu Phe Ala
145 150 155 160
Ile Thr Gln Ser Leu Tyr Gly Cys Trp Ile Thr Pro Arg Leu Glu Tyr
165 170 175
Thr Asp Lys Ile Leu Ser Leu Ala Thr Ala Phe Pro Pro Ala Arg Thr
180 185 190
Arg Glu Val Val Cys Leu Ser Ile Ile Val Ser Val Val Tyr Ser Gly
195 200 205
Phe Leu Val Thr Gly Ile Gly Gly Ala Thr Ser Thr Arg Thr Asn Leu
210 215 220
Asp Ile Leu Phe Ile Ser Val Ile Ile Ile Ser Leu Ala Trp Thr Met

(2) INFORMATION FOR SEO ID NO:274:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1481979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

(2) INFORMATION FOR SEQ ID NO:275:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..711

65

70

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..750
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

aacattacac	acagttcaag	aaagagatcg	atgtcgacct	tggaatctcc	attagaggct	60
ctggcggtttg	aatacgctag	cttcgggtgtt	ttcgccgctcg	tcaacaacgt	ctggacatgg	120
atcgccgctcg	tgactgccgc	cgtcagcttc	tggaggatca	gagtcacaac	catcggagtc	180
ggagacggcc	atgcatgtgt	cttgatagaa	gaattaaccg	gttctaaatc	tgaaaacgaa	240
tccggtcgtc	tcgaacccaa	atcaataacc	ggtcgggtca	aagaaacggt	tgacacgagt	300
aagggaacgg	ttacgaaaac	ggagccggtt	atatgcatg	acggagtgac	aaagaggaag	360
ctgacgatgt	actacgaggt	agacgttgac	gttgacggtg	ggaggtgtgt	taacggagat	420
ttaacggcag	ttagctacgg	aggaggtttg	ggtaattgtg	gcggggattg	gstgggagaa	480
atgggatgga	gtggtgagga	tgagaaatgg	tgatgacagt	tggtaccgtt	acgtggattt	540
aacggtgatt	aatggaaatg	tggttaaggt	atgggacgac	aacaaaacac	tagtaacggc	600
ggcatgtgtc	taaattagac	aagtttcata	tttcggaaa	tttttaaata	tagagaaact	660
ttcttgcttt	aaagtttttt	tttttttggt	tgattaagat	ctgtaatttg	taaataattt	720
tcacvrcaag	agaccaagaa	ggaacgcttg				

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Asn	Ile	Thr	His	Ser	Ser	Arg	Lys	Arg	Ser	Met	Ser	Thr	Leu	Glu	Ser	
1				5				10						15		
Pro	Leu	Glu	Ala	Leu	Ala	Phe	Glu	Tyr	Ala	Ser	Phe	Gly	Val	Phe	Ala	
			20					25					30			
Val	Val	Asn	Asn	Val	Trp	Thr	Trp	Ile	Ala	Val	Val	Thr	Ala	Ala	Val	
			35				40					45				
Ser	Phe	Trp	Arg	Ile	Arg	Val	Thr	Thr	Ile	Gly	Val	Gly	Asp	Gly	His	
			50			55				60						
Ala	Cys	Val	Leu	Ile	Glu	Glu	Leu	Thr	Gly	Ser	Lys	Ser	Glu	Asn	Glu	
65					70				75					80		
Ser	Gly	Arg	Leu	Glu	Pro	Lys	Ser	Ile	Thr	Gly	Pro	Val	Lys	Glu	Thr	
				85				90						95		
Val	Ala	Arg	Val	Lys	Glu	Thr	Val	Thr	Lys	Thr	Glu	Pro	Leu	Ile	Cys	
			100					105					110			
Asp	Asp	Gly	Val	Thr	Lys	Arg	Lys	Leu	Thr	Met	Tyr	Tyr	Glu	Val	Asp	
			115				120						125			
Val	Asp	Val	Asp	Gly	Gly	Arg	Cys	Val	Asn	Gly	Asp	Leu	Thr	Ala	Val	
			130				135					140				
Ser	Tyr	Gly	Gly	Gly	Leu	Gly	Asn	Cys	Gly	Gly	Asp	Trp	Xaa	Gly	Glu	
145					150					155					160	
Met	Gly	Trp	Ser	Gly	Glu	Asp	Glu	Lys	Trp							

165170

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1481985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met	Ser	Thr	Leu	Glu	Ser	Pro	Leu	Glu	Ala	Leu	Ala	Phe	Glu	Tyr	Ala
1				5				10					15		
Ser	Phe	Gly	Val	Phe	Ala	Val	Val	Asn	Asn	Val	Trp	Thr	Trp	Ile	Ala
			20					25					30		
Val	Val	Thr	Ala	Ala	Val	Ser	Phe	Trp	Arg	Ile	Arg	Val	Thr	Thr	Ile
			35				40					45			
Gly	Val	Gly	Asp	Gly	His	Ala	Cys	Val	Leu	Ile	Glu	Glu	Leu	Thr	Gly
			50			55					60				
Ser	Lys	Ser	Glu	Asn	Glu	Ser	Gly	Arg	Leu	Glu	Pro	Lys	Ser	Ile	Thr
65				70					75					80	
Gly	Pro	Val	Lys	Glu	Thr	Val	Ala	Arg	Val	Lys	Glu	Thr	Val	Thr	Lys
			85						90					95	
Thr	Glu	Pro	Leu	Ile	Cys	Asp	Asp	Gly	Val	Thr	Lys	Arg	Lys	Leu	Thr
			100					105					110		
Met	Tyr	Tyr	Glu	Val	Asp	Val	Asp	Val	Asp	Gly	Gly	Arg	Cys	Val	Asn
			115				120					125			
Gly	Asp	Leu	Thr	Ala	Val	Ser	Tyr	Gly	Gly	Gly	Leu	Gly	Asn	Cys	Gly
			130				135					140			
Gly	Asp	Trp	Xaa	Gly	Glu	Met	Gly	Trp	Ser	Gly	Glu	Asp	Glu	Lys	Trp
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 598 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..598

(D) OTHER INFORMATION: / Ceres Seq. ID 1481986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

gaaaaggagc	ccttcttcaa	aattgggtca	tgtactcatg	cttcttcttc	ttcttagctt	60
cctattgcac	cataccgaat	ctactttgcc	tcctgatcat	gaacaaactct	caataaatgg	120
gaggagaatt	atggcgtatt	acaagcacga	tggtgccata	gcagcaccac	catcaagaag	180
tggacgaggt	ggtgggtcac	ggaagaggat	gatgccctac	cataagccaa	atgctcctat	240
acaaacacca	ccatcaagaa	gtagacgacg	tgagggtggg	cacaacggga	gtagacagat	300
gggtatatat	aggccaaatg	gagacatata	tacaggacca	tcaaatagtg	gacatgggtg	360
tggtcacatt	catcaaaatt	catctcctta	gttttggggc	aatttacaaa	attggaaact	420
tatctaaaaa	ttcgccaaaa	agattataga	tttgaatgta	atgtgtgttt	catgtgattc	480
caagtatgga	gtggatatgg	tggtgggtcac	attcatcaac	atttcgatct	ccttagtttt	540
ataygatatg	aatgtaattg	tattttatgt	tattccaagt	aaggatatat	aaagtcgc	

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..129
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Lys	Arg	Ser	Pro	Ser	Ser	Lys	Leu	Gly	His	Val	Leu	Met	Leu	Leu	Leu
1				5					10					15	
Leu	Leu	Ser	Phe	Leu	Leu	His	His	Thr	Glu	Ser	Thr	Leu	Pro	Pro	Asp
			20					25					30		
His	Glu	Gln	Leu	Ser	Ile	Asn	Gly	Arg	Arg	Ile	Met	Ala	Tyr	Tyr	Lys
		35					40					45			
His	Asp	Gly	Ala	Ile	Ala	Ala	Pro	Pro	Ser	Arg	Ser	Gly	Arg	Gly	Gly
	50					55					60				
Gly	His	Gly	Lys	Arg	Met	Met	Pro	Tyr	His	Lys	Pro	Asn	Ala	Pro	Ile
65					70				75					80	
Gln	Thr	Pro	Pro	Ser	Arg	Ser	Arg	Arg	Arg	Glu	Gly	Gly	His	Asn	Gly
				85					90					95	
Ser	Arg	Gln	Met	Gly	Ile	Tyr	Arg	Pro	Asn	Gly	Asp	Ile	Tyr	Thr	Gly
			100					105					110		
Pro	Ser	Asn	Ser	Gly	His	Gly	Gly	Gly	His	Ile	His	Gln	Asn	Ser	Ser
		115				120						125			
Pro															

- (2) INFORMATION FOR SEQ ID NO:283:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..117
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481988
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met	Leu	Leu	Leu	Leu	Leu	Ser	Phe	Leu	Leu	His	His	Thr	Glu	Ser	Thr
1					5					10				15	
Leu	Pro	Pro	Asp	His	Glu	Gln	Leu	Ser	Ile	Asn	Gly	Arg	Arg	Ile	Met
			20						25				30		
Ala	Tyr	Tyr	Lys	His	Asp	Gly	Ala	Ile	Ala	Ala	Pro	Pro	Ser	Arg	Ser
			35				40					45			
Gly	Arg	Gly	Gly	Gly	His	Gly	Lys	Arg	Met	Met	Pro	Tyr	His	Lys	Pro
	50					55					60				
Asn	Ala	Pro	Ile	Gln	Thr	Pro	Pro	Ser	Arg	Ser	Arg	Arg	Arg	Glu	Gly
65					70					75				80	
Gly	His	Asn	Gly	Ser	Arg	Gln	Met	Gly	Ile	Tyr	Arg	Pro	Asn	Gly	Asp
			85					90					95		
Ile	Tyr	Thr	Gly	Pro	Ser	Asn	Ser	Gly	His	Gly	Gly	Gly	His	Ile	His
			100					105					110		
Gln	Asn	Ser	Ser	Pro											
			115												

- (2) INFORMATION FOR SEQ ID NO:284:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```
Met Ala Tyr Tyr Lys His Asp Gly Ala Ile Ala Ala Pro Pro Ser Arg
1           5           10           15
Ser Gly Arg Gly Gly Gly His Gly Lys Arg Met Met Pro Tyr His Lys
          20           25           30
Pro Asn Ala Pro Ile Gln Thr Pro Pro Ser Arg Ser Arg Arg Arg Glu
          35           40           45
Gly Gly His Asn Gly Ser Arg Gln Met Gly Ile Tyr Arg Pro Asn Gly
          50           55           60
Asp Ile Tyr Thr Gly Pro Ser Asn Ser Gly His Gly Gly Gly His Ile
65           70           75           80
His Gln Asn Ser Ser Pro
          85
```

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 688 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..688
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```
gtgggtattac cgaacttaaa cctcgtcgtc gagcttcgaa actctttttc tcagttcacc      60
tggaacacga tgcgtcgta caagcagacg ccatgagagc ttgcaggagt ctctggagaa      120
atttgagat ttagatgaac tccaatctat ctgctgatga taatgataag gatttggaat      180
aactataagg gtaaatacag attcttcctc tcaaattgcc gctctttctc gtcaatcaaa      240
cgaccccaaa tcccagaaag cgaagagact agcctctcga tcacacaacg aagattcgac      300
ccagatttag ctctatcaa gactagagtt tacgtctctc tcttccatac tctctttcgg      360
ctctatttaa gctgtgagag actctacgga gcagcaagga cgctctctgc gatgtgcaat      420
ttcgggggtt ttccggattc gcgctctatg aacagtctga ttcatcaatt caatgtcaat      480
ggtttggtac acgatcaggt atcgctgatt tacagcaaga tgatagcttg tggagtttct      540
cccgatgttt ttgctctcaa tgtattgatt cattcttttt gcaaagtggg tcggttgagt      600
tttgcaatta gtttacttag aaatagagta atcagcatcg atactgttac ttataacact      660
gtgatttcgg gtttatgtga acatggct
```

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..177
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1481991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
Met Ile Met Ile Arg Ile Trp Asn Asn Tyr Lys Gly Lys Tyr Arg Phe
1           5           10           15
```

Phe Leu Ser Asn Cys Arg Ser Phe Ser Ser Ile Lys Arg Pro Gln Ile
20 25 30
Pro Glu Ser Glu Glu Thr Ser Leu Ser Ile Thr Gln Arg Arg Phe Asp
35 40 45
Pro Asp Leu Ala Pro Ile Lys Thr Arg Val Tyr Val Ser Leu Phe His
50 55 60
Thr Leu Phe Arg Leu Tyr Leu Ser Cys Glu Arg Leu Tyr Gly Ala Ala
65 70 75 80
Arg Thr Leu Ser Ala Met Cys Thr Phe Gly Val Val Pro Asp Ser Arg
85 90 95
Leu Trp Asn Ser Leu Ile His Gln Phe Asn Val Asn Gly Leu Val His
100 105 110
Asp Gln Val Ser Leu Ile Tyr Ser Lys Met Ile Ala Cys Gly Val Ser
115 120 125
Pro Asp Val Phe Ala Leu Asn Val Leu Ile His Ser Phe Cys Lys Val
130 135 140
Gly Arg Leu Ser Phe Ala Ile Ser Leu Leu Arg Asn Arg Val Ile Ser
145 150 155 160
Ile Asp Thr Val Thr Tyr Asn Thr Val Ile Ser Gly Leu Cys Glu His
165 170 175
Gly

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met Ile Arg Ile Trp Asn Asn Tyr Lys Gly Lys Tyr Arg Phe Phe Leu
1 5 10 15
Ser Asn Cys Arg Ser Phe Ser Ser Ile Lys Arg Pro Gln Ile Pro Glu
20 25 30
Ser Glu Glu Thr Ser Leu Ser Ile Thr Gln Arg Arg Phe Asp Pro Asp
35 40 45
Leu Ala Pro Ile Lys Thr Arg Val Tyr Val Ser Leu Phe His Thr Leu
50 55 60
Phe Arg Leu Tyr Leu Ser Cys Glu Arg Leu Tyr Gly Ala Ala Arg Thr
65 70 75 80
Leu Ser Ala Met Cys Thr Phe Gly Val Val Pro Asp Ser Arg Leu Trp
85 90 95
Asn Ser Leu Ile His Gln Phe Asn Val Asn Gly Leu Val His Asp Gln
100 105 110
Val Ser Leu Ile Tyr Ser Lys Met Ile Ala Cys Gly Val Ser Pro Asp
115 120 125
Val Phe Ala Leu Asn Val Leu Ile His Ser Phe Cys Lys Val Gly Arg
130 135 140
Leu Ser Phe Ala Ile Ser Leu Leu Arg Asn Arg Val Ile Ser Ile Asp
145 150 155 160
Thr Val Thr Tyr Asn Thr Val Ile Ser Gly Leu Cys Glu His Gly
165 170 175

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1481993
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:
Met Cys Thr Phe Gly Val Val Pro Asp Ser Arg Leu Trp Asn Ser Leu
1 5 10 15
Ile His Gln Phe Asn Val Asn Gly Leu Val His Asp Gln Val Ser Leu
20 25 30
Ile Tyr Ser Lys Met Ile Ala Cys Gly Val Ser Pro Asp Val Phe Ala
35 40 45
Leu Asn Val Leu Ile His Ser Phe Cys Lys Val Gly Arg Leu Ser Phe
50 55 60
Ala Ile Ser Leu Leu Arg Asn Arg Val Ile Ser Ile Asp Thr Val Thr
65 70 75 80
Tyr Asn Thr Val Ile Ser Gly Leu Cys Glu His Gly
85 90

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..499
(D) OTHER INFORMATION: / Ceres Seq. ID 1481994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

attgtaactt gtaaccagtg tcggctaatt tcgacttttg tagatctttt tctgctcttt 60
ctctctctct ctgctctctc tctctctctc tctctcttgt attatttcta tctccccgcg 120
cgctcgaaaga gaaacgctcg tcggagaacc tttgaaatgt cgactggatt agatatgtct 180
ctcgacgaca tgatcgccaa gaaccgtaag tctcgtggtg gagccggccc cgctcgtgga 240
accgcatccg gatccggacc gggtccgact cgccgcaaca accctaatacg gaaatcaacc 300
cgatctgctc cataccaatc agccaaggcg ccggagtcca cctgggggtca cgacatgttc 360
tccgatagat ctgaagatca ccgatcggga cgttcctccg ccggaatcga aactggaacc 420
aagctctaca tttccaattt ggayttacgg tgatcatgaac gaagacatca aggaactgtt 480
tgctgaagtt ggagaactt

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1481995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Ile Val Thr Cys Asn Gln Cys Arg Leu Ile Ser Thr Phe Val Asp Leu
1 5 10 15
Phe Leu Leu Phe Leu Ser Leu Ser Ala Leu Ser Leu Ser Leu Ser Leu
20 25 30
Leu Tyr Tyr Phe Tyr Leu Pro Arg Arg Arg Lys Arg Asn Val Asp Arg

35	40	45
Arg Thr Phe Glu Met Ser	Thr Gly Leu Asp Met Ser	Leu Asp Asp Met
50	55	60
Ile Ala Lys Asn Arg Lys	Ser Arg Gly Gly Ala Gly	Pro Ala Arg Gly
65	70	75
Thr Gly Ser Gly Ser Gly	Pro Gly Pro Thr Arg Arg	Asn Asn Pro Asn
85	90	95
Arg Lys Ser Thr Arg Ser	Ala Pro Tyr Gln Ser Ala	Lys Ala Pro Glu
100	105	110
Ser Thr Trp Gly His Asp	Met Phe Ser Asp Arg Ser	Glu Asp His Arg
115	120	125
Ser Gly Arg Ser Ser Ala	Gly Ile Glu Thr Gly Thr	Lys Leu Tyr Ile
130	135	140
Ser Asn Leu Xaa Leu Arg	Cys His Glu Arg Arg His	Gln Gly Thr Val
145	150	155
Cys		160

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Ser Thr Gly Leu Asp Met Ser Leu Asp Asp Met Ile Ala Lys Asn	
1	5 10 15
Arg Lys Ser Arg Gly Gly Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly	
20	25 30
Ser Gly Pro Gly Pro Thr Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr	
35	40 45
Arg Ser Ala Pro Tyr Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly	
50	55 60
His Asp Met Phe Ser Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser	
65	70 75 80
Ser Ala Gly Ile Glu Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Xaa	
85	90 95
Leu Arg Cys His Glu Arg Arg His Gln Gly Thr Val Cys	
100	105

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly Gly	
1	5 10 15
Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro Thr	
20	25 30

Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr Gln
35 40 45
Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser Asp
50 55 60
Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu Thr
65 70 75 80
Gly Thr Lys Leu Tyr Ile Ser Asn Leu Xaa Leu Arg Cys His Glu Arg
85 90 95
Arg His Gln Gly Thr Val Cys
100

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..851
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

agagagaatc	gcattaacaa	aaaaacaaac	gaatcttttg	agtttaaaac	cctttttcac	60
ttaccggaga	aatggagaga	tcgacgcccg	aacatgtctc	ctccgcacac	aagcgcataa	120
gcgtgagctt	cctcgtgtct	ctcatggtag	tttgtgctag	acacgcaagc	agagtttcca	180
agaagcttaa	acccaagaag	actcggaaag	aaactcatct	tgaagactat	ctcgaaagcc	240
ctaagtctaa	cggaaacggt	agcgaagacg	gtagaggagg	aggaagggtt	ggatggagtc	300
cggcaaggac	tttttctcct	atgagggtgc	gtcctaagga	gctctacacg	accttgagca	360
acaaggcgat	gactatgggt	ggccggaaaa	acaaagctta	cgacgggtggt	ccgacgaaga	420
agacggcggt	ggagatgggt	atggaggagg	atgaggaaga	gtacggcggt	tggcagaggg	480
agattttgat	gggaggaaaa	tgtgagccgt	tggattactc	aggcgtgatc	tactacgatt	540
gtagtgga	tcagctaaaa	caagtgcctc	caaggctctc	acgtgccagt	ttggttcccg	600
agcgcccgac	tcgttcttat	gtcgggtcat	tgttaaacc	gacgggaaag	gaaattttaa	660
ttttagtttg	agaatttgaa	attttagtag	gagtatttga	ttgttggttg	aggtgtcatc	720
acgtaagtgg	taaattctct	aggagctttg	ttggtccttt	gtcattagta	gatgcatgac	780
atgtttttat	gcattatggt	gtgtagttta	tgtatttaag	acgtttggca	attttaaaac	840
tttagtagtt	t					

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met	Glu	Arg	Ser	Thr	Pro	Glu	His	Val	Ser	Ser	Ala	His	Lys	Arg	Ile
1			5						10				15		
Ser	Val	Ser	Phe	Leu	Val	Ser	Leu	Met	Val	Leu	Cys	Ala	Arg	His	Ala
			20					25					30		
Ser	Arg	Val	Ser	Lys	Lys	Leu	Lys	Pro	Lys	Lys	Thr	Arg	Lys	Gln	Thr
			35				40				45				
His	Leu	Glu	Asp	Tyr	Leu	Glu	Ser	Pro	Lys	Ser	Asn	Gly	Asn	Gly	Ser
			50				55				60				
Glu	Asp	Gly	Arg	Gly	Gly	Gly	Arg	Phe	Gly	Trp	Ser	Pro	Ala	Arg	Thr
65					70				75					80	

[illegible]

(2) INFORMATION FOR SEO ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1482011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met	Val	Leu	Cys	Ala	Arg	His	Ala	Ser	Arg	Val	Ser	Lys	Lys	Leu	Lys
1				5					10					15	
Pro	Lys	Lys	Thr	Arg	Lys	Gln	Thr	His	Leu	Glu	Asp	Tyr	Leu	Glu	Ser
			20					25					30		
Pro	Lys	Ser	Asn	Gly	Asn	Gly	Ser	Glu	Asp	Gly	Arg	Gly	Gly	Gly	Arg
		35					40					45			
Phe	Gly	Trp	Ser	Pro	Ala	Arg	Thr	Phe	Ser	Pro	Met	Arg	Val	Arg	Pro
	50					55				60					
Lys	Glu	Leu	Tyr	Thr	Thr	Leu	Ser	Asn	Lys	Ala	Met	Thr	Met	Val	Gly
65				70						75					80
Arg	Lys	Asn	Lys	Ala	Tyr	Asp	Gly	Gly	Pro	Thr	Lys	Lys	Thr	Ala	Val
				85					90					95	
Glu	Met	Val	Met	Glu	Glu	Asp	Glu	Glu	Glu	Tyr	Gly	Val	Trp	Gln	Arg
			100					105					110		
Glu	Ile	Leu	Met	Gly	Gly	Lys	Cys	Glu	Pro	Leu	Asp	Tyr	Ser	Gly	Val
		115					120					125			
Ile	Tyr	Tyr	Asp	Cys	Ser	Gly	His	Gln	Leu	Lys	Gln	Val	Pro	Pro	Arg
	130					135					140				
Ser	Pro	Arg	Ala	Ser	Leu	Val	Pro	Glu	Arg	Pro	Thr	Arg	Ser	Tyr	Val
145				150						155					160
Gly	Ser	Leu	Leu	Asn	Pro	Thr	Gly	Lys	Glu	Ile					
				165					170						

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1482012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met	Arg	Val	Arg	Pro	Lys	Glu	Leu	Tyr	Thr	Thr	Leu	Ser	Asn	Lys	Ala
1				5					10					15	
Met	Thr	Met	Val	Gly	Arg	Lys	Asn	Lys	Ala	Tyr	Asp	Gly	Gly	Pro	Thr
			20					25					30		
Lys	Lys	Thr	Ala	Val	Glu	Met	Val	Met	Glu	Glu	Asp	Glu	Glu	Glu	Tyr
		35					40					45			
Gly	Val	Trp	Gln	Arg	Glu	Ile	Leu	Met	Gly	Gly	Lys	Cys	Glu	Pro	Leu
	50					55					60				
Asp	Tyr	Ser	Gly	Val	Ile	Tyr	Tyr	Asp	Cys	Ser	Gly	His	Gln	Leu	Lys
65					70					75				80	
Gln	Val	Pro	Pro	Arg	Ser	Pro	Arg	Ala	Ser	Leu	Val	Pro	Glu	Arg	Pro
				85					90					95	
Thr	Arg	Ser	Tyr	Val	Gly	Ser	Leu	Leu	Asn	Pro	Thr	Gly	Lys	Glu	Ile
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1482013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

agatttgc	at	tcgcaggg	ga	taaggatc	aa	aatggagg	ag	caaaaggg	aa	cctgtgaag	60
acgtattg	ct	tgctagt	ttc	aaagatgg	gg	ttagtcct	ga	gaaaatcg	aa	gagctcat	120
aaggttac	gc	caatctcg	tc	aatctcat	cg	aacctatg	aa	agctttcc	ac	tggggaaa	180
atgtgagc	at	tgagaat	ctg	catcaagg	gt	acacacac	at	ctttgaat	cc	acatttg	240
gtaaaga	aag	c	tggtgcag	ag	tacattg	ctc	atcctg	ctca	cg	ttaaatt	300
tccttgg	cag	cttggata	aaa	gttttg	gtta	ttgactac	aa	gcctac	ctct	gtctct	360
aattatc	ttg	tagcagca	tt	ttcatcat	tg	atcttttt	ct	cgggtat	gca	tcttgat	420
tgaataa	agt	atattc	cttt	tgagttt	tcc	tgcattg	ttc	tcatgtt	ttc	ctgtga	480
ctctctt	ttt	tgttgt	ttg	ttgttt	ctc	tctgtt	gtat	tatactt	gat	ctgtaaa	540
atcatg	agtt	tattaag	agt	gtttgat	ttc	agactc					

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1482014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met	Glu	Glu	Ala	Lys	Gly	Pro	Val	Lys	His	Val	Leu	Leu	Ala	Ser	Phe
1				5					10					15	
Lys	Asp	Gly	Val	Ser	Pro	Glu	Lys	Ile	Glu	Glu	Leu	Ile	Lys	Gly	Tyr
			20					25					30		
Ala	Asn	Leu	Val	Asn	Leu	Ile	Glu	Pro	Met	Lys	Ala	Phe	His	Trp	Gly
	35					40					45				

Lys Asp Val Ser Ile Glu Asn Leu His Gln Gly Tyr Thr His Ile Phe
50 55 60
Glu Ser Thr Phe Glu Ser Lys Glu Ala Val Ala Glu Tyr Ile Ala His
65 70 75 80
Pro Ala His Val Lys Phe Ala Thr Ile Phe Leu Gly Ser Leu Asp Lys
85 90 95
Val Leu Val Ile Asp Tyr Lys Pro Thr Ser Val Ser Leu
100 105

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Met Lys Ala Phe His Trp Gly Lys Asp Val Ser Ile Glu Asn Leu His
1 5 10 15
Gln Gly Tyr Thr His Ile Phe Glu Ser Thr Phe Glu Ser Lys Glu Ala
20 25 30
Val Ala Glu Tyr Ile Ala His Pro Ala His Val Lys Phe Ala Thr Ile
35 40 45
Phe Leu Gly Ser Leu Asp Lys Val Leu Val Ile Asp Tyr Lys Pro Thr
50 55 60
Ser Val Ser Leu
65

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..664
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

gattaatttt tgagagagct gtctctcttg acagagattt tggaaggtaa gagagacgat 60
gacgtatcac gtttttagac gagactatgg cgatggagag tgaattttgc ctttttggaa 120
ttcccacgac tctctgtatc tttcttttagg cgagactatg gcgataaaga ttgaattttg 180
cttcgacaat tgaggggtgaa attaacggca aattcaaaat tgcggtttct gacaagtcgt 240
tccgctggat tcgtcagctt tctcaccatc ggcgaagcga ggttcaccta atcggagatt 300
tgcgactccc agttggagag taatcgttga ggagaggcaa cgagtgcac gagcatatca 360
cttctctcgc cattcttcgt acccatcgca agctaggtct cgtcactaag ctcagtgtg 420
ccgctcaggc tgctatggaa cagcttaaag gtatgataaa cgacatggat cgtgtccaac 480
tggaatgagg actcttgtgt gttacaccta tcgtcaatgc ccaactgata tgttgtgtct 540
tataaccata aattttacttt gatccaaaca cttttgagaa gctgtcttca agtgggtcaa 600
aggtagcaac tcttttttct tgtgttaattg taatcatctg tgttatgaag tattgccatt 660
ttcg

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..958
(D) OTHER INFORMATION: / Ceres Seq. ID 1482021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

aaagccctaa	aaatcagaga	ttccattttc	tcttatctct	ctctctctct	ctttctcttt	60
ttccgattct	gattctatct	tttcttcacc	aaccacacaa	aacaattcta	cgtttgatct	120
cttcttcttt	ctccgtccaa	attaatctct	acgtttaatt	tctcttggtc	aatcatggga	180
cacgaaacaa	tgacgcgggc	aacaacaacg	ctcgtgttca	cgtagcgaac	tctaaagaga	240
ggattctcaa	atcatgtcct	gatgcaagat	ctgatccgat	ctggtgacgc	ttctttcaaa	300
ggtgtttacc	aaactctaga	caaatatcct	ctcgtctgtg	gaccttaccg	agtccctttc	360
ctcctcaaca	aacctggatc	gggctatcac	gtcaccggcg	agctttacgc	ggtttctcct	420
cgcggtctct	ctcgtctcga	tgagcttgaa	ggaatcagtc	gcggtcatta	catccggcaa	480
ccgatacggt	ctcgcggcgg	cggaggaaga	agaagaagaa	ggagatctgg	aaacagaggc	540
gccgtcgtcg	tgctgtgttg	aggcgtatta	cgctcataag	agttatgagg	aagagctgtg	600
gaagaggaat	agaggaagat	cattcggcgc	gtacacggaa	aacgaagcgc	gtggatatgt	660
gaaacgcaat	gataggcctc	agcatcttag	cttcttggat	catatccgta	ttttcgtatc	720
ttctccatgt	gattgatttt	tatttctttc	gtggctcttc	ccgctcgtcg	cttttctatg	780
tttgtttggt	tttttctcgg	gacaaaagaa	acaaaaaaaa	aacacaaaca	caaactagtt	840
ttacaacttg	taagggtccc	accagtcctg	ccgtccgtcg	tctccgtatc	gatttgatta	900
gagagattgt	tgggtgtaaa	acttatgatt	cccattctaa	ataagtttta	ggttgttt	

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1482022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met	Gly	His	Glu	Thr	Met	Thr	Pro	Ala	Thr	Thr	Leu	Val	Phe	Thr
1				5					10				15	
Tyr	Gly	Thr	Leu	Lys	Arg	Gly	Phe	Ser	Asn	His	Val	Leu	Met	Gln
			20					25				30		Asp
Leu	Ile	Arg	Ser	Gly	Asp	Ala	Ser	Phe	Lys	Gly	Val	Tyr	Gln	Thr
			35				40				45			Leu
Asp	Lys	Tyr	Pro	Leu	Val	Cys	Gly	Pro	Tyr	Arg	Val	Pro	Phe	Leu
	50					55				60				Leu
Asn	Lys	Pro	Gly	Ser	Gly	Tyr	His	Val	Thr	Gly	Glu	Leu	Tyr	Ala
	65				70					75				80
Ser	Pro	Arg	Gly	Leu	Ser	Arg	Leu	Asp	Glu	Leu	Glu	Gly	Ile	Ser
			85					90					95	Arg
Gly	His	Tyr	Ile	Arg	Gln	Pro	Ile	Arg	Ser	Arg	Gly	Gly	Gly	Arg
			100					105					110	
Arg	Arg	Arg	Arg	Ser	Gly	Asn	Arg	Gly	Ala	Val	Val	Val	Arg	Gly
			115			120						125		
Gly	Gly	Val	Leu	Arg	Ser									

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1482023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```
Met Thr Pro Ala Thr Thr Thr Leu Val Phe Thr Tyr Gly Thr Leu Lys
1      5      10      15
Arg Gly Phe Ser Asn His Val Leu Met Gln Asp Leu Ile Arg Ser Gly
      20      25      30
Asp Ala Ser Phe Lys Gly Val Tyr Gln Thr Leu Asp Lys Tyr Pro Leu
      35      40      45
Val Cys Gly Pro Tyr Arg Val Pro Phe Leu Leu Asn Lys Pro Gly Ser
      50      55      60
Gly Tyr His Val Thr Gly Glu Leu Tyr Ala Val Ser Pro Arg Gly Leu
      65      70      75      80
Ser Arg Leu Asp Glu Leu Glu Gly Ile Ser Arg Gly His Tyr Ile Arg
      85      90      95
Gln Pro Ile Arg Ser Arg Gly Gly Gly Arg Arg Arg Arg Arg Arg
      100     105     110
Ser Gly Asn Arg Gly Ala Val Val Val Arg Gly Gly Gly Val Leu Arg
      115     120     125
Ser
```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1482024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```
Met Gln Asp Leu Ile Arg Ser Gly Asp Ala Ser Phe Lys Gly Val Tyr
1      5      10      15
Gln Thr Leu Asp Lys Tyr Pro Leu Val Cys Gly Pro Tyr Arg Val Pro
      20      25      30
Phe Leu Leu Asn Lys Pro Gly Ser Gly Tyr His Val Thr Gly Glu Leu
      35      40      45
Tyr Ala Val Ser Pro Arg Gly Leu Ser Arg Leu Asp Glu Leu Glu Gly
      50      55      60
Ile Ser Arg Gly His Tyr Ile Arg Gln Pro Ile Arg Ser Arg Gly Gly
      65      70      75      80
Gly Gly Arg Arg Arg Arg Arg Arg Ser Gly Asn Arg Gly Ala Val Val
      85      90      95
Val Arg Gly Gly Gly Val Leu Arg Ser
      100     105
```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 535 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..535

(D) OTHER INFORMATION: / Ceres Seq. ID 1482029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

atcataactct	ctcaacttca	tctctctctc	tctctcaatc	tcttaagatc	ccacaagtca	60
cttttcttct	tcttaatcac	ctttaatggc	gaatttgatc	cttaagcaat	ctctaatacat	120
actcctaatac	atatattcaa	caccaatctt	gagttctcaa	gctcgaatcc	tccgtacata	180
tgcgccacaca	accatgggcg	atatggatag	tcaggttctc	ctacgtgaac	tcgggattga	240
tctctctaag	ttcaaaggtc	aagacgagag	acgggtttta	gtggattccg	aaagggtttc	300
tccgggggggt	cctgatccac	aacaccattg	actgatcttt	accgatatat	atatacttta	360
ccgaagatcg	aagcacacat	ataactgtga	ctgatccatg	caagtcaatt	taaatatcgt	420
catttacatg	cttttcttdt	ctttttcata	aatcttccct	acacttttgt	tgtatcaaga	480
ttttggtatt	ctttwgtacc	ttccttatct	ttaaacaatca	aggttttact	cchtt	

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1482030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met	Ala	Asn	Leu	Ile	Leu	Lys	Gln	Ser	Leu	Ile	Ile	Leu	Leu	Ile	Ile
1			5						10					15	
Tyr	Ser	Thr	Pro	Ile	Leu	Ser	Ser	Gln	Ala	Arg	Ile	Leu	Arg	Thr	Tyr
			20					25					30		
Arg	Pro	Thr	Thr	Met	Gly	Asp	Met	Asp	Ser	Gln	Val	Leu	Leu	Arg	Glu
			35				40					45			
Leu	Gly	Ile	Asp	Leu	Ser	Lys	Phe	Lys	Gly	Gln	Asp	Glu	Arg	Arg	Phe
	50					55				60					
Leu	Val	Asp	Ser	Glu	Arg	Val	Ser	Pro	Gly	Gly	Pro	Asp	Pro	Gln	His
65					70					75					80
His															

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1482031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met	Gly	Asp	Met	Asp	Ser	Gln	Val	Leu	Leu	Arg	Glu	Leu	Gly	Ile	Asp
1			5						10					15	
Leu	Ser	Lys	Phe	Lys	Gly	Gln	Asp	Glu	Arg	Arg	Phe	Leu	Val	Asp	Ser
			20					25					30		
Glu	Arg	Val	Ser	Pro	Gly	Gly	Pro	Asp	Pro	Gln	His	His			
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..42
(D) OTHER INFORMATION: / Ceres Seq. ID 1482032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Asp Ser Gln Val Leu Leu Arg Glu Leu Gly Ile Asp Leu Ser Lys
1 5 10 15
Phe Lys Gly Gln Asp Glu Arg Arg Phe Leu Val Asp Ser Glu Arg Val
20 25 30
Ser Pro Gly Gly Pro Asp Pro Gln His His
35 40

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..903
(D) OTHER INFORMATION: / Ceres Seq. ID 1482033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

aatgtcgcgt gcgccacta gatttttccct gacgcggtgt ctgctccac tccccctcct 60
ctccccagc tggcgccagc ggcggcgagg tagcatttgt gctacgagg cttttgcaat 120
ggcggttcg gggttcggcg gcggcgaggc gttccggctc tcggccgcac caggggcccg 180
cttactgaag ctgcacaagg gcgacatcac cctctggtcc gtcgactgcg ccaccgacgc 240
catcgtaaag gctgctaag agcgaatgtt aggtggcgga ggtgttgatg gagctataca 300
tcaagctgct ggaccagagc tagtgcaagc atgccgaaa gttccagagg tcaaaccagg 360
agttcggtgt cctactggag aagctaggat tactcctgct tttgagcttc ctgcctctcg 420
ggtgattcac actggtggcc ctatatatga tttggacaag catcctgagg tgtcattaaa 480
gaaggcctat gaaaatagct tgaagcttgc taaagataat ggcattcagt acatcgcat 540
ccctgctata tcttgtggtg tttatcgta tctcccaag gaagcatcaa aaatagctgt 600
ttctaccgca cagaaatttt cagagggtat caaagaggc cattttgttc tgttctcgga 660
tgacctttac aatatatggc gcgagactgc ccagcagttg ctatcacagt ttgagaaatg 720
aatggtccat aggagttttg cttagcactag cagttgccca gcagtcgttg tctagtgttg 780
agatgtgagc gccataggca gtttgccctg tgtaataaaa atgggtgtat cagacaacgt 840
ttaaattctg atgaaaccgt gtattgcacc tgtggtataa tgctgaatga gtaaagttg 900
gcc

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..239
(D) OTHER INFORMATION: / Ceres Seq. ID 1482034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ser Arg Ala Thr Arg Phe Phe Leu Thr Arg Cys Leu Leu Pro
1 5 10 15
Leu Pro Leu Leu Ser Pro Arg Trp Arg Gln Arg Arg Arg Gly Ser Ile
20 25 30
Cys Ala Thr Arg Ala Phe Ala Met Ala Ala Ser Gly Phe Gly Gly Gly
35 40 45

Glu Ala Phe Arg Leu Ser Ala Ala Pro Gly Ala Gly Leu Leu Lys Leu
50 55 60
His Lys Gly Asp Ile Thr Leu Trp Ser Val Asp Cys Ala Thr Asp Ala
65 70 75 80
Ile Val Asn Ala Ala Asn Glu Arg Met Leu Gly Gly Gly Gly Val Asp
85 90 95
Gly Ala Ile His Gln Ala Ala Gly Pro Glu Leu Val Gln Ala Cys Arg
100 105 110
Lys Val Pro Glu Val Lys Pro Gly Val Arg Cys Pro Thr Gly Glu Ala
115 120 125
Arg Ile Thr Pro Ala Phe Glu Leu Pro Ala Ser Arg Val Ile His Thr
130 135 140
Val Gly Pro Ile Tyr Asp Leu Asp Lys His Pro Glu Val Ser Leu Lys
145 150 155 160
Lys Ala Tyr Glu Asn Ser Leu Lys Leu Ala Lys Asp Asn Gly Ile Gln
165 170 175
Tyr Ile Ala Phe Pro Ala Ile Ser Cys Gly Val Tyr Arg Tyr Pro Pro
180 185 190
Lys Glu Ala Ser Lys Ile Ala Val Ser Thr Ala Gln Lys Phe Ser Glu
195 200 205
Gly Ile Lys Glu Val His Phe Val Leu Phe Ser Asp Asp Leu Tyr Asn
210 215 220
Ile Trp Arg Glu Thr Ala Gln Gln Leu Leu Ser Gln Phe Glu Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1482035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ser Arg Ala Ala Thr Arg Phe Phe Leu Thr Arg Cys Leu Leu Pro
1 5 10 15
Leu Pro Leu Leu Ser Pro Arg Trp Arg Gln Arg Arg Arg Gly Ser Ile
20 25 30
Cys Ala Thr Arg Ala Phe Ala Met Ala Ala Ser Gly Phe Gly Gly Gly
35 40 45
Glu Ala Phe Arg Leu Ser Ala Ala Pro Gly Ala Gly Leu Leu Lys Leu
50 55 60
His Lys Gly Asp Ile Thr Leu Trp Ser Val Asp Cys Ala Thr Asp Ala
65 70 75 80
Ile Val Asn Ala Ala Asn Glu Arg Met Leu Gly Gly Gly Gly Val Asp
85 90 95
Gly Ala Ile His Gln Ala Ala Gly Pro Glu Leu Val Gln Ala Cys Arg
100 105 110
Lys Val Pro Glu Val Lys Pro Gly Val Arg Cys Pro Thr Gly Glu Ala
115 120 125
Arg Ile Thr Pro Ala Phe Glu Leu Pro Ala Ser Arg Val Ile His Thr
130 135 140
Val Gly Pro Ile Tyr Asp Leu Asp Lys His Pro Glu Val Ser Leu Lys
145 150 155 160
Lys Ala Tyr Glu Asn Ser Leu Lys Leu Ala Lys Asp Asn Gly Ile Gln
165 170 175
Tyr Ile Ala Phe Pro Ala Ile Ser Cys Gly Val Tyr Arg Tyr Pro Pro

	180		185		190										
Lys	Glu	Ala	Ser	Lys	Ile	Ala	Val	Ser	Thr	Ala	Gln	Lys	Phe	Ser	Glu
	195						200					205			
Gly	Ile	Lys	Glu	Val	His	Phe	Val	Leu	Phe	Ser	Asp	Asp	Leu	Tyr	Asn
	210					215					220				
Ile	Trp	Arg	Glu	Thr	Ala	Gln	Gln	Leu	Leu	Ser	Gln	Phe	Glu	Lys	
225			230							235					

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met	Ala	Ala	Ser	Gly	Phe	Gly	Gly	Gly	Glu	Ala	Phe	Arg	Leu	Ser	Ala
1			5					10					15		
Ala	Pro	Gly	Ala	Gly	Leu	Leu	Lys	Leu	His	Lys	Gly	Asp	Ile	Thr	Leu
	20						25					30			
Trp	Ser	Val	Asp	Cys	Ala	Thr	Asp	Ala	Ile	Val	Asn	Ala	Ala	Asn	Glu
	35						40				45				
Arg	Met	Leu	Gly	Gly	Gly	Gly	Val	Asp	Gly	Ala	Ile	His	Gln	Ala	Ala
	50				55					60					
Gly	Pro	Glu	Leu	Val	Gln	Ala	Cys	Arg	Lys	Val	Pro	Glu	Val	Lys	Pro
65					70				75					80	
Gly	Val	Arg	Cys	Pro	Thr	Gly	Glu	Ala	Arg	Ile	Thr	Pro	Ala	Phe	Glu
			85					90						95	
Leu	Pro	Ala	Ser	Arg	Val	Ile	His	Thr	Val	Gly	Pro	Ile	Tyr	Asp	Leu
	100						105					110			
Asp	Lys	His	Pro	Glu	Val	Ser	Leu	Lys	Lys	Ala	Tyr	Glu	Asn	Ser	Leu
	115						120					125			
Lys	Leu	Ala	Lys	Asp	Asn	Gly	Ile	Gln	Tyr	Ile	Ala	Phe	Pro	Ala	Ile
	130					135					140				
Ser	Cys	Gly	Val	Tyr	Arg	Tyr	Pro	Pro	Lys	Glu	Ala	Ser	Lys	Ile	Ala
145					150					155				160	
Val	Ser	Thr	Ala	Gln	Lys	Phe	Ser	Glu	Gly	Ile	Lys	Glu	Val	His	Phe
			165					170						175	
Val	Leu	Phe	Ser	Asp	Asp	Leu	Tyr	Asn	Ile	Trp	Arg	Glu	Thr	Ala	Gln
	180						185						190		
Gln	Leu	Leu	Ser	Gln	Phe	Glu	Lys								
	195					200									

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..806
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

aatttgcagc	ttgttcccca	cgagcttcct	ctgttcatca	tcgtcctcga	gcttcctctg	60
ttcatcaagc	tcctctgttc	ttgaacatcg	acgaaatcag	aggctgtggc	agatgcgaac	120

```
aaagcaattg agttggatca ttcattaatc aaagcttacc taagaaaagg gttacaactc 180
aagtgttttg agaaagaaga tggctaaaga tgtaagtgtt ttggttttta ttttagagtt 240
ttggtcaatc agtttgctaa tgagtggcta ggttgagcat aaacgtgctt aacctttgat 300
ataacctcag tcaagcatga agaggagcta gctgaggtaa atatgaatgt ctttggtgta 360
ggctaaatat agccattgga tgtattcatt ttgtgtttgt aatatttagg ttgggtaacc 420
aaattggtgg cttctaacat gggtatattg aatatgcagc ctcaagaaat tgtggcagtg 480
aaagattgac atgttttggt tgtcttatgt gctatttatg cagctcggag atagatttat 540
ctatgaagtt gtggatgaag tgaataactt ccttcacttc tatggtccta tcaaaacctt 600
cgttcctctt cctttggatt atgttgtaaa agttgagaag ttaacattca tcaattgcaa 660
tttcacctgc agcttttttg acttgatgat tcagtggttt atgtgtaatt gcaatgtcac 720
tcttttaata atgtaattaa gagagatttg ttttctattc acaaaacagt gtatttatac 780
tattattaca atgcaagatt aagatc
```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```
Ile Cys Ser Leu Phe Pro Thr Ser Phe Leu Cys Ser Ser Ser Ser Ser
1      5      10      15
Ser Phe Leu Cys Ser Ser Ser Ser Ser Val Leu Glu His Arg Arg Asn
      20      25      30
Gln Arg Leu Trp Gln Met Arg Thr Lys Gln Leu Ser Trp Ile Ile His
      35      40      45
```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```
Met Phe Cys Leu Ser Tyr Val Leu Phe Met Gln Leu Gly Asp Arg Phe
1      5      10      15
Ile Tyr Glu Val Val Asp Glu Val Asn Asn Phe Pro His Phe Tyr Gly
      20      25      30
Pro Ile Lys Thr Phe Val Pro Leu Pro Leu Asp Tyr Val Val Lys Val
      35      40      45
Glu Lys Leu Thr Phe Ile Asn Cys Asn Phe Thr Cys Ser Phe Phe Asp
      50      55      60
Leu Met Ile Gln Trp Phe Met Cys Asn Cys Asn Val Thr Leu Leu Ile
      65      70      75      80
Met
```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1482044
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:
Met Gln Leu Gly Asp Arg Phe Ile Tyr Glu Val Val Asp Glu Val Asn
1 5 10 15
Asn Phe Pro His Phe Tyr Gly Pro Ile Lys Thr Phe Val Pro Leu Pro
20 25 30
Leu Asp Tyr Val Val Lys Val Glu Lys Leu Thr Phe Ile Asn Cys Asn
35 40 45
Phe Thr Cys Ser Phe Phe Asp Leu Met Ile Gln Trp Phe Met Cys Asn
50 55 60
Cys Asn Val Thr Leu Leu Ile Met
65 70

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1482045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

gtcggactca	gtggagaaga	aggaagatcc	aaatcgatcc	gttgaaaagg	aatttcgaat	60
ttgctgtgcg	atgtcgagtg	cgggtggacgc	tacgggaaac	ccgatcccta	cttcggcggt	120
tttaacggcg	tcagcgaagc	atataggtat	gaggtgtatg	ccggagaatg	ttgcgttcct	180
caaatgcaag	aagaatgatc	caaaccacaga	gaagtgtctc	gacaaaaggtc	gtgacgtcac	240
tcgctgcgtg	cttggcttga	aaaggagatg	ggattatgtt	gggtgtatgt	attactacac	300
aaacgagttt	gatctgtgta	ggaaagagca	agaagccttc	gagaaagtgt	gtcccttgaa	360
atgagaatca	caagttcttg	tcatgttttg	atttgtatct	cataataaag	caaaatgttc	420
atTTTTgaat	gagctttact	ctctccatct	cttgtttgtt	gtcatcccat	ttatttcctc	480
tcagatgctt	tcgtagttag	ttccaaagac	aactaaatga	ctcagtttta	ttgttcgatg	540
gttcactaat	cagcacagaa	tggaacaatt	gttttt			

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1482046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Ser Asp Ser Val Glu Lys Lys Glu Asp Pro Asn Arg Ser Val Glu Lys	
1 5 10 15	
Glu Phe Arg Ile Cys Cys Ala Met Ser Ser Ala Val Asp Ala Thr Gly	
20 25 30	
Asn Pro Ile Pro Thr Ser Ala Val Leu Thr Ala Ser Ala Lys His Ile	
35 40 45	

Gly Met Arg Cys Met Pro Glu Asn Val Ala Phe Leu Lys Cys Lys Lys
50 55 60
Asn Asp Pro Asn Pro Glu Lys Cys Leu Asp Lys Gly Arg Asp Val Thr
65 70 75 80
Arg Cys Val Leu Gly Leu Lys Arg Arg Trp Asp Tyr Val Gly Cys Met
85 90 95
Tyr Tyr Tyr Thr Asn Glu Phe Asp Leu Cys Arg Lys Glu Gln Glu Ala
100 105 110
Phe Glu Lys Val Cys Pro Leu Lys
115 120

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Ser Ser Ala Val Asp Ala Thr Gly Asn Pro Ile Pro Thr Ser Ala
1 5 10 15
Val Leu Thr Ala Ser Ala Lys His Ile Gly Met Arg Cys Met Pro Glu
20 25 30
Asn Val Ala Phe Leu Lys Cys Lys Lys Asn Asp Pro Asn Pro Glu Lys
35 40 45
Cys Leu Asp Lys Gly Arg Asp Val Thr Arg Cys Val Leu Gly Leu Lys
50 55 60
Arg Arg Trp Asp Tyr Val Gly Cys Met Tyr Tyr Tyr Thr Asn Glu Phe
65 70 75 80
Asp Leu Cys Arg Lys Glu Gln Glu Ala Phe Glu Lys Val Cys Pro Leu
85 90 95
Lys

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Arg Cys Met Pro Glu Asn Val Ala Phe Leu Lys Cys Lys Lys Asn
1 5 10 15
Asp Pro Asn Pro Glu Lys Cys Leu Asp Lys Gly Arg Asp Val Thr Arg
20 25 30
Cys Val Leu Gly Leu Lys Arg Arg Trp Asp Tyr Val Gly Cys Met Tyr
35 40 45
Tyr Tyr Thr Asn Glu Phe Asp Leu Cys Arg Lys Glu Gln Glu Ala Phe
50 55 60
Glu Lys Val Cys Pro Leu Lys
65 70

(2) INFORMATION FOR SEQ ID NO:321:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

(2) INFORMATION FOR SEO ID NO:322:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:322:

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..150
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Thr Thr Ala Ile Ser Met Asn Pro Ser Leu Phe Arg Val Ile Cys
1 5 10 15
Ile Leu His Ser Ile Ile Ala Leu Thr Ser Gly Thr Leu Met Met Phe
 20 25 30
Tyr Thr Glu Lys Ala Ser Ile Phe Gly Pro Gly Ser Glu Ile Ala Ser
 35 40 45
Lys Leu Lys Gly Ser Thr Pro His Asp Glu Leu Leu Ile Gln Ile Ser
 50 55 60
Gln Ser Phe Ser Gly Leu Leu Phe Ala Ile Gly Leu Val Leu Phe
65 70 75 80
Met Val Ser Phe Val Lys Asp Lys Glu Phe His Ser Phe Phe Ala Ser
 85 90 95
Gly Ser Val Ile Leu Tyr Val Leu Met Ala Met Trp Arg Val Leu Phe
 100 105 110
Glu Trp Lys Ile Glu Asp Leu Ala Tyr Glu Trp Pro Lys Gln Ala Leu
 115 120 125
Gly Asp Ile Ala Leu Ala Ile Ser Trp Val Phe Phe Leu Val Tyr Ser
130 135 140
Trp Arg Glu Lys Tyr Asp
145 150

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..144
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Asn Pro Ser Leu Phe Arg Val Ile Cys Ile Leu His Ser Ile Ile
1 5 10 15
Ala Leu Thr Ser Gly Thr Leu Met Met Phe Tyr Thr Glu Lys Ala Ser
 20 25 30
Ile Phe Gly Pro Gly Ser Glu Ile Ala Ser Lys Leu Lys Gly Ser Thr
 35 40 45
Pro His Asp Glu Leu Leu Ile Gln Ile Ser Gln Ser Phe Ser Gly Leu
 50 55 60
Leu Leu Phe Ala Ile Gly Leu Val Leu Phe Met Val Ser Phe Val Lys
65 70 75 80
Asp Lys Glu Phe His Ser Phe Phe Ala Ser Gly Ser Val Ile Leu Tyr
 85 90 95
Val Leu Met Ala Met Trp Arg Val Leu Phe Glu Trp Lys Ile Glu Asp
 100 105 110
Leu Ala Tyr Glu Trp Pro Lys Gln Ala Leu Gly Asp Ile Ala Leu Ala
 115 120 125
Ile Ser Trp Val Phe Phe Leu Val Tyr Ser Trp Arg Glu Lys Tyr Asp
130 135 140

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..623
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

aagaagagat	gggggaaatg	ggaaaggcga	taggattgct	gataagcggg	accttggtga	60
tcaccattgc	gctaatacgca	acgcgactct	tctctcgctc	atctccgacg	ttctcatcgt	120
tctcttatct	tcaactcgcca	ttctcggcct	tctttttcgt	cacctcaatg	tctcggtacc	180
tgtggatcca	ttagagtggc	aaatatcaca	agacacagcc	tgtaacattg	tggcgcgctt	240
agctaatact	gttggagcag	ctgaatccgt	tctgcgggtt	gcagcaacag	gacatgacaa	300
gaggctcttt	gttaagggtg	tgatctgtct	ttacttcttg	gcagctctag	gacgaatcat	360
atcggtgac	cattgcctat	gcaggactat	gtttgttctg	tctctccatg	ctttttcgga	420
gttcaattag	aaactccgta	ttgaaccgaa	gaaacggaga	gattttggat	tgcgaaacac	480
cttcagagtt	gtaatacaca	atttgcctaa	acgtgttata	ttctttgtcc	tctttccacc	540
tttacatgtt	catagctttg	gatagtgtga	ataatgcttt	cagttcctaa	atgtagaaat	600
attaatcata	gttaatcttt	tct				

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Arg	Arg	Asp	Gly	Gly	Asn	Gly	Lys	Gly	Asp	Arg	Ile	Ala	Asp	Lys	Arg	
1				5				10						15		
Asp	Leu	Val	Tyr	His	His	Cys	Ala	Asn	Arg	Asn	Ala	Thr	Leu	Leu	Ser	
				20				25						30		
Leu	Ile	Ser	Asp	Val	Leu	Ile	Val	Leu	Leu	Ser	Ser	Leu	Ala	Ile	Leu	
				35				40						45		
Gly	Leu	Leu	Phe	Arg	His	Leu	Asn	Val	Ser	Val	Pro	Val	Asp	Pro	Leu	
				50				55						60		
Glu	Trp	Gln	Ile	Ser	Gln	Asp	Thr	Ala	Cys	Asn	Ile	Val	Ala	Arg	Leu	
				65				70						75		
Ala	Asn	Thr	Val	Gly	Ala	Ala	Glu	Ser	Val	Leu	Arg	Val	Ala	Ala	Thr	
				85				90						95		
Gly	His	Asp	Lys	Arg	Leu	Phe	Val	Lys	Val	Val	Ile	Cys	Leu	Tyr	Phe	
				100				105						110		
Leu	Ala	Ala	Leu	Gly	Arg	Ile	Ile	Ser	Gly	Asp	His	Cys	Leu	Cys	Arg	
				115				120						125		
Thr	Met	Phe	Val	Leu	Ser	Leu	His	Ala	Phe	Ser	Glu	Phe	Asn			
				130				135						140		

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1482066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

gttccttagc	gcagaagcgt	ttcctggcat	ctccctatct	ccttcacggc	atcagaaacc	60
agcacattct	tcctcctcct	ctttgattcc	gcgcaggagc	aagggagctc	ccatggccac	120
cttcgtggcg	ccctctcgcc	cctgctctct	cctaggccgt	cggctctgcc	ttcccagtg	180
cctgctcggtg	gtctcccca	ccgacgccc	agctccctca	actgcccattg	gcgccacaaa	240
tctccagccg	gcttccccctg	cgtcttctc	cctgcgctcc	tgcaggcctc	cctggcgccac	300
ctcgccagca	gcagggatct	ttccctctcc	ccatggcggtg	caagcmctga	gctccccccac	360
acgtgttccc	ttccccaggc	gcgtgastcc	ctccggcgctc	ggccaatagg	caagtttgag	420
caccgagctc	atccatggmg	cmtccmctmc	mctcggtctc	agcmccctcg	agctccattt	480
ctgcgtmcga	gctcgagcag	cttgc				

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1482067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Phe	Leu	Ser	Ala	Glu	Ala	Phe	Pro	Gly	Ile	Ser	Leu	Ser	Pro	Ser	Arg	
1			5					10					15			
His	Gln	Lys	Pro	Ala	His	Ser	Ser	Ser	Ser	Ser	Leu	Ile	Pro	Arg	Arg	
			20					25					30			
Ser	Lys	Gly	Ala	Pro	Met	Ala	Thr	Phe	Val	Ala	Pro	Ser	Arg	Pro	Cys	
			35				40					45				
Ser	Leu	Leu	Gly	Arg	Arg	Leu	Cys	Leu	Pro	Ser	Ala	Leu	Leu	Val	Val	
			50				55				60					
Ser	Pro	Thr	Asp	Ala	Arg	Ala	Pro	Ser	Thr	Ala	His	Gly	Ala	Thr	Asn	
			65				70				75			80		
Leu	Gln	Pro	Ala	Ser	Pro	Ala	Ser	Ser	Ser	Leu	Arg	Ser	Cys	Arg	Pro	
			85					90					95			
Pro	Trp	Arg	Thr	Ser	Pro	Ala	Ala	Gly	Ile	Phe	Pro	Ser	Pro	His	Gly	
			100					105					110			
Val	Gln	Xaa	Leu	Ser	Ser	Pro	Thr	Arg	Val	Pro	Phe	Pro	Arg	Arg	Val	
			115				120						125			
Xaa	Pro	Ser	Gly	Val	Gly	Gln										
			130			135										

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1482068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met	Ala	Thr	Phe	Val	Ala	Pro	Ser	Arg	Pro	Cys	Ser	Leu	Leu	Gly	Arg	
1				5					10					15		

Arg Leu Cys Leu Pro Ser Ala Leu Leu Val Val Ser Pro Thr Asp Ala
20 25 30
Arg Ala Pro Ser Thr Ala His Gly Ala Thr Asn Leu Gln Pro Ala Ser
35 40 45
Pro Ala Ser Ser Ser Leu Arg Ser Cys Arg Pro Pro Trp Arg Thr Ser
50 55 60
Pro Ala Ala Gly Ile Phe Pro Ser Pro His Gly Val Gln Xaa Leu Ser
65 70 75 80
Ser Pro Thr Arg Val Pro Phe Pro Arg Arg Val Xaa Pro Ser Gly Val
85 90 95
Gly Gln

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

aaaaaagaaa aggtctaatt actcgctct cttgctcgcc aacgccagtg nccagaggcc	60
agagcttcgt caaagacacg ccgaaaagag ggggaggcga ctcggccgag gtccgggttcc	120
gaactccggt cctccgattt gcgcgtccgg atctaccagc catggcatca tcttcggacc	180
cgtggatgaa ggagtacaat gaagcatcca gacttgctga tgacatcagt tccatgattg	240
ctgatagagg gtcccttcca caatcaggcc cagaaattat gcggcatact tcagccatcc	300
ggagaaaaat aactattctt gggactagac tggatagctt ggagtcgttg cttggcagaa	360
ttcctccaaa gtcaatcact gacaaggaga tgcataagcg ccaagacatg ttttccagtt	420
tgaagtctaa agcaaagcag atggcgacaa gtttcaacat gtcaaacttt gctaacaggg	480
aggatctgct tggtcagagt aaaaaggcag atgacatgag cagagttgct ggggttagata	540
ac	

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Lys Arg Lys Gly Leu Ile Thr Arg Leu Ser Cys Ser Pro Thr Pro Val
1 5 10 15
Xaa Arg Gly Gln Ser Phe Val Lys Asp Thr Pro Lys Arg Gly Gly Gly
20 25 30
Asp Ser Ala Glu Val Arg Phe Arg Thr Pro Val Leu Arg Phe Ala Arg
35 40 45
Pro Asp Leu Pro Ala Met Ala Ser Ser Ser Asp Pro Trp Met Lys Glu
50 55 60
Tyr Asn Glu Ala Ser Arg Leu Ala Asp Asp Ile Ser Ser Met Ile Ala
65 70 75 80
Asp Arg Gly Ser Leu Pro Gln Ser Gly Pro Glu Ile Met Arg His Thr
85 90 95
Ser Ala Ile Arg Arg Lys Ile Thr Ile Leu Gly Thr Arg Leu Asp Ser

100 105 110
Leu Glu Ser Leu Leu Gly Arg Ile Pro Pro Lys Ser Ile Thr Asp Lys
115 120 125
Glu Met His Lys Arg Gln Asp Met Phe Ser Ser Leu Lys Ser Lys Ala
130 135 140
Lys Gln Met Ala Thr Ser Phe Asn Met Ser Asn Phe Ala Asn Arg Glu
145 150 155 160
Asp Leu Leu Gly Gln Ser Lys Lys Ala Asp Asp Met Ser Arg Val Ala
165 170 175
Gly Leu Asp Asn
180

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Ala Ser Ser Ser Asp Pro Trp Met Lys Glu Tyr Asn Glu Ala Ser
1 5 10 15
Arg Leu Ala Asp Asp Ile Ser Ser Met Ile Ala Asp Arg Gly Ser Leu
20 25 30
Pro Gln Ser Gly Pro Glu Ile Met Arg His Thr Ser Ala Ile Arg Arg
35 40 45
Lys Ile Thr Ile Leu Gly Thr Arg Leu Asp Ser Leu Glu Ser Leu Leu
50 55 60
Gly Arg Ile Pro Pro Lys Ser Ile Thr Asp Lys Glu Met His Lys Arg
65 70 75 80
Gln Asp Met Phe Ser Ser Leu Lys Ser Lys Ala Lys Gln Met Ala Thr
85 90 95
Ser Phe Asn Met Ser Asn Phe Ala Asn Arg Glu Asp Leu Leu Gly Gln
100 105 110
Ser Lys Lys Ala Asp Asp Met Ser Arg Val Ala Gly Leu Asp Asn
115 120 125

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Lys Glu Tyr Asn Glu Ala Ser Arg Leu Ala Asp Asp Ile Ser Ser
1 5 10 15
Met Ile Ala Asp Arg Gly Ser Leu Pro Gln Ser Gly Pro Glu Ile Met
20 25 30
Arg His Thr Ser Ala Ile Arg Arg Lys Ile Thr Ile Leu Gly Thr Arg
35 40 45
Leu Asp Ser Leu Glu Ser Leu Leu Gly Arg Ile Pro Pro Lys Ser Ile
50 55 60

Thr Asp Lys Glu Met His Lys Arg Gln Asp Met Phe Ser Ser Leu Lys
65 70 75 80
Ser Lys Ala Lys Gln Met Ala Thr Ser Phe Asn Met Ser Asn Phe Ala
85 90 95
Asn Arg Glu Asp Leu Leu Gly Gln Ser Lys Lys Ala Asp Asp Met Ser
100 105 110
Arg Val Ala Gly Leu Asp Asn
115

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..652
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

gaaaaacgca accaagtcaa ccaacgtcgg cttgaaattc ggccatcacc gttcggatct 60
ttccccacc cggttgtata aaagcgggcg cctgggattc ccctctcacc cctccttcac 120
catcagcaaa tcggtctgcc ctggtttccc ccgtcgtgaa gcagaaacct ctctgctgcc 180
attaccgtgc tgcgcgccgt cgcggtgagg cttggccaca accgtggaac ctgtctccat 240
atggcgtagg cggcgtagcg agcttcgcct gatggatttg cagtccagtg ggcccataat 300
ttctcgccgg accgcgagca gcaacaacct ctctcgccg gccatgacct ctacgcactc 360
caagctctcc tccgaggacc gtcattctcg tgcattgagt cgagtaaggc cagcaggatc 420
tgaagaatca ccctgggtatc tggaatctca agtgctagga gaagagcagg tggttcagga 480
ggagccgcct aacactgagg agttcgatct gatctagggt gcgtttccca gtcgacattg 540
gcgcccagca tccttagttc gttttatgtt tattctttta ttttgaata agtcttccgc 600
tatgtaataa gtactctgat gttttatgac atttatctct atacactctg tg

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Lys Asn Ala Thr Lys Ser Thr Asn Val Gly Leu Lys Phe Gly His His
1 5 10 15
Arg Ser Asp Leu Ser Pro Thr Arg Leu Tyr Lys Ser Gly Arg Leu Gly
20 25 30
Phe Pro Ser His Pro Ser Phe Thr Ile Ser Lys Ser Val Cys Pro Gly
35 40 45
Phe Pro Arg Arg Glu Ala Glu Thr Ser Leu Leu Pro Leu Pro Cys Cys
50 55 60
Ala Pro Ser Arg
65

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```
Met Asp Leu Gln Ser Ser Gly Pro Ile Ser Arg Arg Thr Ala Ser
1          5          10          15
Ser Asn Asn Leu Ser Ser Pro Ala Met Thr Ser Thr His Ser Lys Leu
20          25          30
Ser Ser Glu Asp Arg His Leu Arg Ala Cys Ser Arg Val Arg Ser Arg
35          40          45
Gly Ser Glu Glu Ser Pro Trp Tyr Leu Glu Ser Gln Val Leu Gly Glu
50          55          60
Glu Gln Val Val Gln Glu Glu Pro Pro Asn Thr Glu Glu Phe Asp Leu
65          70          75          80
Ile
```

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..57
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```
Met Thr Ser Thr His Ser Lys Leu Ser Ser Glu Asp Arg His Leu Arg
1          5          10          15
Ala Cys Ser Arg Val Arg Ser Arg Gly Ser Glu Glu Ser Pro Trp Tyr
20          25          30
Leu Glu Ser Gln Val Leu Gly Glu Gln Val Val Gln Glu Glu Pro
35          40          45
Pro Asn Thr Glu Glu Phe Asp Leu Ile
50          55
```

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..814
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```
attctacatg cgcacacttc gtcgaggaca tgagccagct acttactcgg cttcgcgga 60
gtacagatcc ggccgacact tcactcgtcaa gctctcgcca ttacaactc cttgctccgc 120
cgacctcgac gcaaactgca acttctcgct cgcgcctgtc caggatctgc tctcgccatg 180
gacaggaag ccaagaaaga agcggttcagg aagtatcttg aatccagtgg cgtgctcgat 240
accctcacga aagctcttgt ggcgctgtac gaggagaacg ataagccttc atctgcagtc 300
gaatttggtc agcagaagtt ggggtggccg tcaatctctg actatgaaaa gctcaaggca 360
gagaagctgg acttgcaatt gaagtatgat aagcttttag aaaccacaa ggaaacatgc 420
agacagctgg aggaacttaa gaatatgaag tacgggtgcac cctggaactg aaataacgtg 480
tgttgacact gtaaattgtat catgaagcat gtacttttta cacctctctg aagcattgct 540
```

aagctcttttg tacaatggaa acatctcatg tatctgattt tagccatctg gatccctttt 600
ggattatgaa gacacccaac tcactgtagg tcccaggtat cagatatcac caatgcagga 660
taaaggatgt gacaactatc atagttgaac catgagcaat tgtttaacca gtaatccagt 720
atcgacaaaag agtgtggtct attgacttga gacttctctt ggcattggctt gtaagcagat 780
tttagtagat ttcagtggaa gagatatggc gtgc

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1482082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Phe Tyr Met Pro Thr Leu Arg Arg Gly His Glu Pro Ala Thr Tyr Ser
1 5 10 15
Ala Ser Arg Gln Tyr Arg Ser Gly Arg His Phe Ile Val Lys Leu Ser
20 25 30
Pro Phe Thr Thr Pro Cys Ser Ala Asp Leu Asp Ala Asn Cys Asn Phe
35 40 45
Ser Leu Ala Pro Val Gln Asp Leu Leu Ser Pro Trp Thr Gly Lys Pro
50 55 60
Arg Lys Lys Arg Ser Gly Ser Ile Leu Asn Pro Val Ala Cys Ser Ile
65 70 75 80
Pro Ser Arg Lys Leu Leu Trp Arg Cys Thr Arg Arg Thr Ile Ser Leu
85 90 95
His Leu Gln Ser Asn Leu Phe Ser Arg Ser Trp Val Ala Arg Gln Ser
100 105 110
Leu Thr Met Lys Ser Ser Arg Gln Arg Ser Trp Thr Cys Asn
115 120 125

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1482083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met Pro Thr Leu Arg Arg Gly His Glu Pro Ala Thr Tyr Ser Ala Ser
1 5 10 15
Arg Gln Tyr Arg Ser Gly Arg His Phe Ile Val Lys Leu Ser Pro Phe
20 25 30
Thr Thr Pro Cys Ser Ala Asp Leu Asp Ala Asn Cys Asn Phe Ser Leu
35 40 45
Ala Pro Val Gln Asp Leu Leu Ser Pro Trp Thr Gly Lys Pro Arg Lys
50 55 60
Lys Arg Ser Gly Ser Ile Leu Asn Pro Val Ala Cys Ser Ile Pro Ser
65 70 75 80
Arg Lys Leu Leu Trp Arg Cys Thr Arg Arg Thr Ile Ser Leu His Leu
85 90 95
Gln Ser Asn Leu Phe Ser Arg Ser Trp Val Ala Arg Gln Ser Leu Thr
100 105 110

Met Lys Ser Ser Arg Gln Arg Ser Trp Thr Cys Asn
115 120

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Asp Arg Glu Ala Lys Lys Glu Ala Phe Arg Lys Tyr Leu Glu Ser
1 5 10 15
Ser Gly Val Leu Asp Thr Leu Thr Lys Ala Leu Val Ala Leu Tyr Glu
20 25 30
Glu Asn Asp Lys Pro Ser Ser Ala Val Glu Phe Val Gln Gln Lys Leu
35 40 45
Gly Gly Pro Ser Ile Ser Asp Tyr Glu Lys Leu Lys Ala Glu Lys Leu
50 55 60
Asp Leu Gln Leu Lys Tyr Asp Lys Leu Leu Glu Thr His Lys Glu Thr
65 70 75 80
Cys Arg Gln Leu Glu Leu Lys Asn Met Lys Tyr Gly Ala Pro Trp
85 90 95
Asn

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

gaagaatagc cttgtctagc aagaagaaga tagagggatg atgtgattat acgcaaaata 60
ctaaaacctt ggggtgtagt acaagcagta gttatgagca ggcctcttct ctttctttcc 120
tggtccggtt tttttctttt tccctgcgga attccccttc ttccctagtg cctcgattcg 180
atatttcgat tggattggat taccaaggga cagagggagg gaatcccaca cacacctctg 240
gccctgcgga ggccaaggga agggaagcac tcagcaccca gcagcagaag gaccgccgta 300
aatggcgctg ccggtggcga actggggacc ctggcgctgc ggacgctgtc caagcccatc 360
gccagccgcc tcaagagcca ggccgctgtc caccccaagt tccgcaactt catcatcgcc 420
atcgcccagg caaaccacca gatcaccaca aagatacaga ggcgcattta tgagcatgcc 480
acagatgtgg cgatcaggcc tttggatgag cagaaagctg ttcaagctgc tacagatctc 540
atcggggaag cctttatctt ctcggtcgct gtttgctgct ctaatttttg ag

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1482086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```
Met Ala Leu Pro Val Ala Asn Trp Gly Pro Trp Arg Cys Gly Arg Cys
1           5           10           15
Pro Ser Pro Ser Pro Ala Ala Ser Arg Ala Arg Pro Leu Ser Thr Pro
20           25           30
Ser Ser Ala Thr Ser Ser Ser Pro Ser Pro Arg Gln Thr Thr Arg Ser
35           40           45
Pro Gln Arg Tyr Arg Gly Ala Phe Met Ser Met Pro Gln Met Trp Arg
50           55           60
Ser Gly Leu Trp Met Ser Arg Lys Leu Phe Lys Leu Leu Gln Ile Ser
65           70           75           80
Ser Gly Lys Pro Leu Ser Ser Arg Ser Leu Phe Ala Ala Leu Ile Phe
85           90           95
Glu
```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..624

(D) OTHER INFORMATION: / Ceres Seq. ID 1482091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```
gattaaactc acagcccaac tcctcttctc gccctcgtct gacttcgttt cggacctccc      60
cagtttttcc cctccggccg ccgcacggag aagcagaagc catgcaggcc gccgccgcgc      120
gcgcccgcgc cctcctcgcc ttaccggcgg cctcggggat ccccggaata ctctccggac      180
cgatcccagg gcgcgcacatc tacgccgagg gcgttctcct ttaccgtctc aatggcgctc      240
ccgcttcgcc gtcttctccg cagcatacca ggggcttctc ctctcctgc ttcgcctccc      300
gatcacactg taacctccca tcgcctacca tagcttctca atggttgaat gagaaatcag      360
tacactatca catgacgaca gcacacttct caacggaagc aagtdacatg gaccacccta      420
cagaagctgt agaggagatg taccagaaaa tgttgaaatc tgttgaagct gagaccatgc      480
ctccaaatgc ctgggtgtgg tcaatgattg atagctgctc caataaggag gacatcaaac      540
ttctttttca aattttgcag aaactcagag tatttagact atcaaattct cgcacatcagtg      600
caacttcaat gagcatctct gcag
```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1482092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```
Ile Lys Leu Thr Ala Gln Leu Leu Phe Ser Pro Ser Ser Asp Phe Val
1           5           10           15
Ser Asp Leu Pro Ser Phe Ser Pro Pro Ala Ala Ala Arg Arg Ser Arg
20           25           30
Ser His Ala Gly Arg Arg Arg Ala Arg Pro Pro Pro Pro Arg Leu Thr
35           40           45
Gly Gly Leu Gly Asp Pro Arg Asn Thr Leu Arg Thr Asp Pro Arg Ala
```

50 55 60
Arg Ile Ile Arg Arg Gly Arg Ser Pro Leu Pro Ser Gln Trp Arg Ser
65 70 75 80
Arg Phe Ala Val Phe Ser Ala Ala Tyr Gln Gly Leu Leu Leu Leu Leu
85 90 95
Leu Arg Leu Pro Ile Thr Leu
100

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..207
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Leu Asn Ser Gln Pro Asn Ser Ser Ser Arg Pro Arg Leu Thr Ser Phe
1 5 10 15
Arg Thr Ser Pro Val Phe Pro Leu Arg Pro Pro His Gly Glu Ala Glu
20 25 30
Ala Met Gln Ala Ala Ala Ala Arg Ala Arg Arg Leu Leu Ala Leu Pro
35 40 45
Ala Ala Ser Gly Ile Pro Gly Ile Leu Ser Gly Pro Ile Pro Gly Arg
50 55 60
Ala Ser Tyr Ala Glu Gly Val Leu Leu Tyr Arg Leu Asn Gly Ala Pro
65 70 75 80
Ala Ser Pro Ser Ser Pro Gln His Thr Arg Gly Phe Ser Ser Ser Cys
85 90 95
Phe Ala Ser Arg Ser His Cys Asn Leu Pro Ser Pro Thr Ile Ala Ser
100 105 110
Gln Trp Leu Asn Glu Lys Ser Val His Tyr His Met Thr Thr Ala His
115 120 125
Phe Ser Thr Glu Ala Ser Xaa Met Asp His Pro Thr Glu Ala Val Glu
130 135 140
Glu Met Tyr Gln Lys Met Leu Lys Ser Val Glu Ala Glu Thr Met Pro
145 150 155 160
Pro Asn Ala Trp Leu Trp Ser Met Ile Asp Ser Cys Ser Asn Lys Glu
165 170 175
Asp Ile Lys Leu Leu Phe Gln Ile Leu Gln Lys Leu Arg Val Phe Arg
180 185 190
Leu Ser Asn Leu Arg Ile Ser Ala Thr Ser Met Ser Ile Ser Ala
195 200 205

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Gln Ala Ala Ala Ala Arg Ala Arg Arg Leu Leu Ala Leu Pro Ala
1 5 10 15

Ala Ser Gly Ile Pro Gly Ile Leu Ser Gly Pro Ile Pro Gly Arg Ala
20 25 30
Ser Tyr Ala Glu Gly Val Leu Leu Tyr Arg Leu Asn Gly Ala Pro Ala
35 40 45
Ser Pro Ser Ser Pro Gln His Thr Arg Gly Phe Ser Ser Ser Cys Phe
50 55 60
Ala Ser Arg Ser His Cys Asn Leu Pro Ser Pro Thr Ile Ala Ser Gln
65 70 75 80
Trp Leu Asn Glu Lys Ser Val His Tyr His Met Thr Thr Ala His Phe
85 90 95
Ser Thr Glu Ala Ser Xaa Met Asp His Pro Thr Glu Ala Val Glu Glu
100 105 110
Met Tyr Gln Lys Met Leu Lys Ser Val Glu Ala Glu Thr Met Pro Pro
115 120 125
Asn Ala Trp Leu Trp Ser Met Ile Asp Ser Cys Ser Asn Lys Glu Asp
130 135 140
Ile Lys Leu Leu Phe Gln Ile Leu Gln Lys Leu Arg Val Phe Arg Leu
145 150 155 160
Ser Asn Leu Arg Ile Ser Ala Thr Ser Met Ser Ile Ser Ala
165 170

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..558
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

atgtataacg cgacccccct cccagtcgcc cccagcggca aggcgggaac cgttctcccg	60
cgccccgcac tccccccct tttccttttg ctccttcctt cctcggaag cctagggctt	120
aggctttaag cgccgcgant gtacggcggc ggcgcgcg cggggacta cgacggaggc	180
agcgggtggc cggggaacgc taacgcgcgc ttcggcgggc ggggcttcat gccctcacag	240
tccacgggtg tccccggaga cagcggcctc tctaagggtc ggagcgcgca gacgctgctc	300
ccgctcaccg tgaacacagc catggacgcg gcgcaaacca gcggtgacag gtctaatttc	360
gccatcaacg gcgttgaggt gtctacgatt aggcttggtg gacgcatgct aggtaagggt	420
gagcgtgtca cagatgttgt attcactctt gatgatggtg ctggcaagat agatgtgaat	480
cgctgggaaa atgaggcttc cgatgctaag gagatggctg atgctaataa cgagaactat	540
gtcatagtca ttggcggg	

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Met Pro Ser Gln Ser Thr Val Val Pro Glu Asn Ser Gly Leu Ser Lys
1 5 10 15
Gly Arg Ser Ala Gln Thr Leu Leu Pro Leu Thr Val Lys Gln Thr Met
20 25 30
Asp Ala Ala Gln Thr Ser Gly Asp Arg Ser Asn Phe Ala Ile Asn Gly

```

      35              40              45
Val Glu Val Ser Thr Ile Arg Leu Val Gly Arg Met Leu Gly Lys Val
      50              55              60
Glu Arg Val Thr Asp Val Val Phe Thr Leu Asp Asp Gly Thr Gly Lys
65              70              75              80
Ile Asp Val Asn Arg Trp Glu Asn Glu Ala Ser Asp Ala Lys Glu Met
      85              90              95
Ala Asp Ala Asn Asn Glu Asn Tyr Val Ile Val Ile Gly Gly
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Asp Ala Ala Gln Thr Ser Gly Asp Arg Ser Asn Phe Ala Ile Asn
1              5              10              15
Gly Val Glu Val Ser Thr Ile Arg Leu Val Gly Arg Met Leu Gly Lys
      20              25              30
Val Glu Arg Val Thr Asp Val Val Phe Thr Leu Asp Asp Gly Thr Gly
      35              40              45
Lys Ile Asp Val Asn Arg Trp Glu Asn Glu Ala Ser Asp Ala Lys Glu
      50              55              60
Met Ala Asp Ala Asn Asn Glu Asn Tyr Val Ile Val Ile Gly Gly
65              70              75

```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..581
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

aaagatatatt gtgtagataa cagtagatta aagtctaaaa taagagagga gatggtggat      60
gaaatagggg agttttgaca gcctaattgt aattggaagc ctttcttggc ctgccctcgg      120
cgcggaaccg tcccgcactc acgcatcagc gtcgcacact cgcacgtgcc tccgtcttcg      180
ctccctcggg ccctccgcag cgtcagatcg accgtcgctc gcggasccta gcgacgccgt      240
tctcaagtcc gagccggagt agcacgagag ccttgcggna tatgagtcgc gccgcggcag      300
caagaacgat ggatgaggaa gccgagtaac tggagacggc tcggggccgac cgctccgtgt      360
ggctcatgaa gtgccccccg gtcgtttccc gcgcctggca ggccgcctcc gcctcttcc      420
ccgatgctgc caacgccaac ccgctcgttg ccaaggtcgt cctttccctt gacctgttgc      480
gccaagaaga acgcccggaa gagcctacgc tccagttcaa gatggaattg gctcaacta      540
acaccgggaa tacacctaag agctactctt tgaatatgtt c

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1482103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Ser Arg Ala Ala Ala Arg Thr Met Asp Glu Glu Ala Glu Tyr
1 5 10 15
Leu Glu Thr Ala Arg Ala Asp Arg Ser Val Trp Leu Met Lys Cys Pro
20 25 30
Pro Val Val Ser Arg Ala Trp Gln Ala Ala Ser Ala Ser Ser Ser Asp
35 40 45
Ala Ala Asn Ala Asn Pro Val Val Ala Lys Val Val Leu Ser Leu Asp
50 55 60
Leu Leu Arg Gln Glu Glu Arg Pro Glu Glu Pro Thr Leu Gln Phe Lys
65 70 75 80
Met Glu Leu Ala Gln Thr Asn Thr Gly Asn Thr Pro Lys Ser Tyr Ser
85 90 95
Leu Asn Met Phe
100

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1482104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met Asp Glu Glu Ala Glu Tyr Leu Glu Thr Ala Arg Ala Asp Arg Ser
1 5 10 15
Val Trp Leu Met Lys Cys Pro Pro Val Val Ser Arg Ala Trp Gln Ala
20 25 30
Ala Ser Ala Ser Ser Ser Asp Ala Ala Asn Ala Asn Pro Val Val Ala
35 40 45
Lys Val Val Leu Ser Leu Asp Leu Leu Arg Gln Glu Glu Arg Pro Glu
50 55 60
Glu Pro Thr Leu Gln Phe Lys Met Glu Leu Ala Gln Thr Asn Thr Gly
65 70 75 80
Asn Thr Pro Lys Ser Tyr Ser Leu Asn Met Phe
85 90

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1482105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Lys Cys Pro Pro Val Val Ser Arg Ala Trp Gln Ala Ala Ser Ala
1 5 10 15
Ser Ser Ser Asp Ala Ala Asn Ala Asn Pro Val Val Ala Lys Val Val

20 25 30
Leu Ser Leu Asp Leu Leu Arg Gln Glu Glu Arg Pro Glu Glu Pro Thr
35 40 45
Leu Gln Phe Lys Met Glu Leu Ala Gln Thr Asn Thr Gly Asn Thr Pro
50 55 60
Lys Ser Tyr Ser Leu Asn Met Phe
65 70

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..812
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

gatcgagttg gctcattaac aattcagttt cgtaaacaag cctggaggga aaaaggacac 60
atcacccaaa ggcacaggga atcgaccat cgtgggaccc gtacagcgca ccgcccagcc 120
gccggatctg cgccggcgac ggcggcgac gtcggatcta cgccgcccga ggarggggga 180
ggcgggcgctg tggccgttct ctgcccgtga ggcggcgat cgtcccgc gcaaggatta 240
tgatccgaa agagaagcca aatgtatcga gcagtccacc aacaccacgg ctggactgca 300
taaaatgctt tgatattgctc tggttctggt actcaccatt ccaccagatg cagaattatt 360
accggtatgg ggagttcgac acctgcttcg gcaagtgggg cgatcttatg ggctgcctcg 420
ctctcaagac aaagcggaag gcagaggtgg aggagatcct catcgcgcg ggagaaggcca 480
aaccacatat ctggacctac cggacggctg atgaggcatc ggagaattgg tggcggtatg 540
acaagcatgc tgtgatgatg tcaccactgc cagggttctgc tcagcttcct cccaggtccg 600
atgaatcttg atagtcgagg ggatttgtgc aagtgttttg tttgcgctta tgtcacatta 660
tggcattagc gatcatttct gttcaaaatc ttactgtaaa ctacaatacc aagagatgga 720
accattgagg taggcagaac atgtactgct gaagattgag aatttgaaat cgccttgat 780
tcagaagcaa ataaatgaac gaggtttcct tt

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Ser Ser Trp Leu Ile Asn Asn Ser Val Ser Leu Thr Ser Leu Glu Gly
1 5 10 15
Lys Arg Thr His His Pro Lys Ala Gln Gly Ile Ala Pro Ser Trp Asp
20 25 30
Pro Tyr Ser Ala Pro Pro Ser Arg Arg Ile Cys Ala Gly Asp Ala Pro
35 40 45
Gly Arg Arg Ile Tyr Ala Ala Ala Gly Xaa Gly Arg Arg Arg Cys Gly
50 55 60
Arg Ser Leu Pro Val Ser Ala Arg Ile Arg Pro Ala Ala Arg Ile Met
65 70 75 80
Asp Pro Lys Glu Lys Pro Asn Val Ser Ser Ser Pro Pro Thr Pro Arg
85 90 95
Leu Asp Cys Ile Lys Cys Phe Asp Met Leu Trp Phe Cys Tyr Ser Pro
100 105 110

Phe His Gln Met Gln Asn Tyr Tyr Arg Tyr Gly Glu Phe Asp Thr Cys
115 120 125
Phe Gly Lys Trp Gly Asp Leu Met Gly Cys Leu Ala Leu Lys Thr Lys
130 135 140
Arg Lys Ala Glu Val Glu Ile Leu Ile Ala Arg Glu Lys Ala Lys
145 150 155 160
Pro His Ile Trp Thr Tyr Arg Thr Val Asp Glu Ala Ser Glu Asn Trp
165 170 175
Trp Arg Met Tyr Lys His Ala Val Met Met Ser Pro Leu Pro Gly Ser
180 185 190
Ala Gln Leu Pro Pro Arg Ser Asp Glu Ser
195 200

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1482108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Met Asp Pro Lys Glu Lys Pro Asn Val Ser Ser Pro Pro Thr Pro
1 5 10 15
Arg Leu Asp Cys Ile Lys Cys Phe Asp Met Leu Trp Phe Cys Tyr Ser
20 25 30
Pro Phe His Gln Met Gln Asn Tyr Tyr Arg Tyr Gly Glu Phe Asp Thr
35 40 45
Cys Phe Gly Lys Trp Gly Asp Leu Met Gly Cys Leu Ala Leu Lys Thr
50 55 60
Lys Arg Lys Ala Glu Val Glu Glu Ile Leu Ile Ala Arg Glu Lys Ala
65 70 75 80
Lys Pro His Ile Trp Thr Tyr Arg Thr Val Asp Glu Ala Ser Glu Asn
85 90 95
Trp Trp Arg Met Tyr Lys His Ala Val Met Met Ser Pro Leu Pro Gly
100 105 110
Ser Ala Gln Leu Pro Pro Arg Ser Asp Glu Ser
115 120

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1482113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

ataaatcccg	agaccaaacc	ctcgccctcca	ttcgcccccc	gccgcgcgcg	ctcccagttct	60
ctacgcggaa	gcagcgcctc	gcaccgctcc	tacccaatgg	cgccgacgtc	gaagctgtcg	120
atgagcatca	agcgtgcgtc	gcgctcgcac	gcgtaccacc	gccgtgggct	ctggggccatc	180
aaggccaaga	acggcggcgt	cttcccgaag	gccgagaaac	mngcmgcccgc	cgcggaaccc	240
aagttctacc	ccgcgcacga	cgtcaagcct	cgcgttccca	gcacccgcaa	gcctaataccc	300
accaagctca	ggtcgagcat	cacgcctggg	acggtgctga	tcctcctcgc	ggggcagaac	360
ttgggtttccg	cggcggcggc	kcgcgccggg	tccgacggcg	cggccgcggc	gcaggcggcg	420

gccttcgga aggccaacga gggcaaggcg tagctgcctg tgctgtgcat atgcatgtgt 480
ggttaattag ctggagtgt cccgtcgctt aatctgttgg atttgatggt ttgttggttg 540
tgtgcgcgtg tgtttcagtg atttgctcct ttttttttct ttctcgtgga tctatcgatg 600
gatgaacatg aatgaatgaa ccgaactgca cagctccgtt gtgagctgat gcatgcatgc 660
actagctagt agctg

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1482114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Ile Asn Pro Glu Thr Lys Pro Ser Pro Pro Phe Val Pro Arg Arg Arg
1 5 10 15
Arg Ser Gln Ser Leu Arg Gly Ser Ser Ala Ser His Arg Ser Tyr Pro
20 25 30
Met Ala Pro Thr Ser Lys Leu Ser Met Ser Ile Lys Arg Ala Ser Arg
35 40 45
Ser His Ala Tyr His Arg Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn
50 55 60
Gly Gly Val Phe Pro Lys Ala Glu Lys Xaa Xaa Ala Ala Ala Glu Pro
65 70 75 80
Lys Phe Tyr Pro Ala Asp Asp Val Lys Pro Arg Val Pro Ser Thr Arg
85 90 95
Lys Pro Asn Pro Thr Lys Leu Arg Ser Ser Ile Thr Pro Gly Thr Val
100 105 110
Leu Ile Leu Leu Ala Gly Gln Asn Leu Gly Ser Ala Ala Ala Xaa Ala
115 120 125
Ala Gly Ser Asp Gly Ala Ala Ala Ala Gln Ala Ala Ala Phe Arg Lys
130 135 140
Ala Asn Glu Gly Lys Ala
145 150

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1482115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Met Ala Pro Thr Ser Lys Leu Ser Met Ser Ile Lys Arg Ala Ser Arg
1 5 10 15
Ser His Ala Tyr His Arg Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn
20 25 30
Gly Gly Val Phe Pro Lys Ala Glu Lys Xaa Xaa Ala Ala Ala Glu Pro
35 40 45
Lys Phe Tyr Pro Ala Asp Asp Val Lys Pro Arg Val Pro Ser Thr Arg
50 55 60
Lys Pro Asn Pro Thr Lys Leu Arg Ser Ser Ile Thr Pro Gly Thr Val
65 70 75 80

Leu Ile Leu Leu Ala Gly Gln Asn Leu Gly Ser Ala Ala Ala Xaa Ala
85 90 95
Ala Gly Ser Asp Gly Ala Ala Ala Ala Gln Ala Ala Ala Phe Arg Lys
100 105 110
Ala Asn Glu Gly Lys Ala
115

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Met Ser Ile Lys Arg Ala Ser Arg Ser His Ala Tyr His Arg Arg Gly
1 5 10 15
Leu Trp Ala Ile Lys Ala Lys Asn Gly Gly Val Phe Pro Lys Ala Glu
20 25 30
Lys Xaa Xaa Ala Ala Ala Glu Pro Lys Phe Tyr Pro Ala Asp Asp Val
35 40 45
Lys Pro Arg Val Pro Ser Thr Arg Lys Pro Asn Pro Thr Lys Leu Arg
50 55 60
Ser Ser Ile Thr Pro Gly Thr Val Leu Ile Leu Leu Ala Gly Gln Asn
65 70 75 80
Leu Gly Ser Ala Ala Ala Xaa Ala Ala Gly Ser Asp Gly Ala Ala Ala
85 90 95
Ala Gln Ala Ala Ala Phe Arg Lys Ala Asn Glu Gly Lys Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..871
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

gagccaaaca	tgcccgtccg	cccagtctcg	ctccaaacca	aagccatcgg	aggagcaact	60
ggacgaccat	ggcctcgccg	ctgctcaagt	cacactctca	gctcgccgcc	gccgccgccc	120
tgcactccgt	gaggagagcc	gaccgctgcc	ctgcgacact	acacctgggc	aagttccatg	180
accacgggct	caggtccggc	cgttctaaga	gatccggttc	agcgaggggtg	ggcgccttcc	240
cgtcgctgga	cgtaggtgccg	ctgatggtga	cgatggtgga	gcacgtggac	atgtcgcggg	300
actacgtcgt	gaccaagtcc	atctggcatc	tcagcgacgt	agccctcaag	agcgtctata	360
ccttctacgc	catgttcacc	gtctggggag	tctgcttctt	cgcgcccatg	aaggatccct	420
tctacgacag	cgagacgtac	aggagccagg	gtggcgacgg	gaccgtgcac	tggtactacg	480
acaggcaaga	ggacctggag	gcgtctgcga	gggaggagct	gctgcgggag	gagctgctcg	540
aggagattga	gcagagggtt	gggggcctca	gggagctgga	ggaagcgagc	aaggaggagc	600
agctcacaaa	gtgatcacgc	gcgggcgaat	accgaatggg	atggatacgg	gctactcatc	660
agctctctat	ctgagcttcg	ttagcaaata	agttcagact	tctttactgc	cctgctcaag	720
tctgtatatg	gccaaaaccc	aaaacgattg	atcaactgcg	ctactgcagt	gcaatagcag	780
gatacgtata	gttttttttt	caagggaaac	aggaggggag	tgcagtgcac	ccctgcccac	840
actgcatgtt	attaataaaa	gaaagttatt	t			

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1482118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Ala Lys His Ala Arg Pro Pro Ser Leu Ala Pro Asn Gln Ser His Arg
1 5 10 15
Arg Ser Asn Trp Thr Thr Met Ala Ser Pro Leu Leu Lys Ser His Ser
20 25 30
Gln Leu Ala Ala Ala Ala Leu His Ser Val Arg Arg Ala Asp Arg
35 40 45
Cys Pro Ala Thr Leu His Leu Gly Lys Phe His Asp His Gly Leu Arg
50 55 60
Ser Gly Arg Ser Lys Arg Ser Gly Ser Ala Arg Val Gly Ala Phe Pro
65 70 75 80
Ser Leu Asp Val Val Pro Leu Met Val Thr Met Val Glu His Val Asp
85 90 95
Met Ser Arg Asp Tyr Val Val Thr Lys Ser Ile Trp His Leu Ser Asp
100 105 110
Val Ala Leu Lys Ser Val Tyr Thr Phe Tyr Ala Met Phe Thr Val Trp
115 120 125
Gly Val Cys Phe Phe Ala Ser Met Lys Asp Pro Phe Tyr Asp Ser Glu
130 135 140
Thr Tyr Arg Ser Gln Gly Gly Asp Gly Thr Val His Trp Tyr Tyr Asp
145 150 155 160
Arg Gln Glu Asp Leu Glu Ala Ser Ala Arg Glu Glu Leu Leu Arg Glu
165 170 175
Glu Leu Leu Glu Glu Ile Glu Gln Arg Val Gly Gly Leu Arg Glu Leu
180 185 190
Glu Glu Ala Ser Lys Glu Glu Gln Leu Thr Lys
195 200

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1482119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met Ala Ser Pro Leu Leu Lys Ser His Ser Gln Leu Ala Ala Ala Ala
1 5 10 15
Ala Leu His Ser Val Arg Arg Ala Asp Arg Cys Pro Ala Thr Leu His
20 25 30
Leu Gly Lys Phe His Asp His Gly Leu Arg Ser Gly Arg Ser Lys Arg
35 40 45
Ser Gly Ser Ala Arg Val Gly Ala Phe Pro Ser Leu Asp Val Val Pro
50 55 60
Leu Met Val Thr Met Val Glu His Val Asp Met Ser Arg Asp Tyr Val

65				70					75					80	
Val	Thr	Lys	Ser	Ile	Trp	His	Leu	Ser	Asp	Val	Ala	Leu	Lys	Ser	Val
				85					90					95	
Tyr	Thr	Phe	Tyr	Ala	Met	Phe	Thr	Val	Trp	Gly	Val	Cys	Phe	Phe	Ala
				100					105					110	
Ser	Met	Lys	Asp	Pro	Phe	Tyr	Asp	Ser	Glu	Thr	Tyr	Arg	Ser	Gln	Gly
				115					120					125	
Gly	Asp	Gly	Thr	Val	His	Trp	Tyr	Tyr	Asp	Arg	Gln	Glu	Asp	Leu	Glu
				130					135					140	
Ala	Ser	Ala	Arg	Glu	Glu	Leu	Leu	Arg	Glu	Glu	Leu	Leu	Glu	Glu	Ile
				145					150					155	
Glu	Gln	Arg	Val	Gly	Gly	Leu	Arg	Glu	Leu	Glu	Glu	Ala	Ser	Lys	Glu
				165					170					175	
Glu	Gln	Leu	Thr	Lys											
				180											

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1482120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met	Val	Thr	Met	Val	Glu	His	Val	Asp	Met	Ser	Arg	Asp	Tyr	Val	Val
1				5					10					15	
Thr	Lys	Ser	Ile	Trp	His	Leu	Ser	Asp	Val	Ala	Leu	Lys	Ser	Val	Tyr
				20					25					30	
Thr	Phe	Tyr	Ala	Met	Phe	Thr	Val	Trp	Gly	Val	Cys	Phe	Phe	Ala	Ser
				35					40					45	
Met	Lys	Asp	Pro	Phe	Tyr	Asp	Ser	Glu	Thr	Tyr	Arg	Ser	Gln	Gly	Gly
				50					55					60	
Asp	Gly	Thr	Val	His	Trp	Tyr	Tyr	Asp	Arg	Gln	Glu	Asp	Leu	Glu	Ala
				65					70					75	
Ser	Ala	Arg	Glu	Glu	Leu	Leu	Arg	Glu	Glu	Leu	Leu	Glu	Glu	Ile	Glu
				85					90					95	
Gln	Arg	Val	Gly	Gly	Leu	Arg	Glu	Leu	Glu	Glu	Ala	Ser	Lys	Glu	Glu
				100					105					110	
Gln	Leu	Thr	Lys												
				115											

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1482121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

tatggacttc	attaccgcca	cttaataacg	gatctacaga	gcatccgaaa	cctttaatat	60
tggctattgc	gtctcaagac	tctgcatcgt	tttttcggga	ccgtagtctt	ggttcagatt	120
ctcccatatc	tggattgatt	gctttgctca	ctgctgttga	tgctctttct	cacattcatg	180
gtctaagcaa	gcttaagaaa	cagcttggtg	tcgctgtttt	taatggtgag	gcctgggggt	240

```

atcttggttag tcggaaattc ttacaggaat tagatgaagg cgctgcttct gtgaatggaa 300
ttagtagctt aaagattgac caggtagtgg agattggttc tgttggaag gctatacttg 360
aggaatatcc atcattttat gtgcatgctg aagggaaatcc atcagcttca aaggaaatat 420
tagatgcaact gcaaagtsca gcaagtctct tggttctgat aatgttaaag taaaacaagc 480
agcttcatca aatcctggtg ttccaccatc ttcattaatg tcattcataa g

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1482122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Trp Thr Ser Leu Pro Leu Asn Asn Gly Ser Thr Glu His Pro Lys
1      5      10      15
Pro Leu Ile Leu Ala Ile Ala Ser Gln Asp Ser Ala Ser Phe Phe Arg
20     25     30
Asp Arg Ser Leu Gly Ser Asp Ser Pro Ile Ser Gly Leu Ile Ala Leu
35     40     45
Leu Thr Ala Val Asp Ala Leu Ser His Ile His Gly Leu Ser Lys Leu
50     55     60
Lys Lys Gln Leu Val Phe Ala Val Phe Asn Gly Glu Ala Trp Gly Tyr
65     70     75     80
Leu Gly Ser Arg Lys Phe Leu Gln Glu Leu Asp Glu Gly Ala Ala Ser
85     90     95
Val Asn Gly Ile Ser Ser Leu Lys Ile Asp Gln Val Leu Glu Ile Gly
100    105    110
Ser Val Gly Lys Ala Ile Leu Glu Tyr Pro Ser Phe Tyr Val His
115    120    125
Ala Glu Gly Asn Pro Ser Ala Ser Lys Glu Ile Leu Asp Ala Leu Gln
130    135    140
Ser Xaa Ala Ser Leu Leu Val Leu Ile Met Leu Lys
145    150    155

```

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 985 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..985

(D) OTHER INFORMATION: / Ceres Seq. ID 1482127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```

aaatttctcg atcaaacatg ctctattgcc ctgtatctat cctctatcga agccggagac 60
cccagaaaaga gtccgtaaac aactcccggc catggcgacc gcagaccggg tcgccgccac 120
cttcctctcc tctttcccca ctcaccatcc cgcccccttt tccctccgtt cctcgtgac 180
aaacctgtgc ctaccgtct ccttcggg ccgtgtcaca ggtggccac ggctcgctc 240
ccgtctccgg gtccaccgcg tcggcgccgc cgctcgccag ctccccacca cgaatccgga 300
ggtagcttct ggggagaaga agatcagatg gtcatcaagg gctgtgcggt cttttgcgat 360
ggcagagctg gagggccgga agatgaggta ccctaccaca ggcaccgagg ggctcctcat 420
gggcattctt gttgaaggaa ctagtggcgc asaaaacttt tgcgtgctaa tggaaccaca 480
cttctcaaag tgcgtgagga ggcagcgaat gttcttgagg aatcagaaat gttttacttt 540
agtcccatgc atccaccatt gacagaagct gcacaacgag cccttgattg ggctgtcaat 600

```

gaaaaattga aatcaggtga ggatggagaa gtaaccgcca atcatttgct actygggata 660
tggtcagata aagagtcggc tggtcataaa atcctgtatt cgcctggatt tgacgatgag 720
aaagccagtt tactggccaa aacggctggt gaagaggctg caatgagtct tagagagcaa 780
ggagagcacc taatttattc gtcaacttaa gttgggtatt tgcactagct tttatgcact 840
tcttggtgcc tcgagacgtt gacctggaga ggctgcctct acaaacttta gaacttatta 900
tgagatatg ttaggtcaga tacgatattt gtactctcac gattgccgat gcctgtgaaa 960
acgttgcgct ttgtttgtca cgggg

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1482128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Asn	Phe	Ser	Ile	Lys	His	Ala	Leu	Leu	Pro	Cys	Ile	Tyr	Pro	Leu	Ser
1				5					10					15	
Lys	Pro	Glu	Thr	Pro	Glu	Arg	Val	Arg	Lys	Gln	Leu	Pro	Ala	Met	Ala
			20					25					30		
Thr	Ala	Asp	Arg	Val	Ala	Ala	Thr	Phe	Leu	Ser	Ser	Phe	Pro	Thr	His
		35					40					45			
His	Pro	Arg	Pro	Phe	Ser	Ser	Val	Ser	Leu	Val	Thr	Asn	Pro	Val	Leu
		50					55				60				
Pro	Val	Ser	Leu	Arg	Ala	Ala	Val	Thr	Gly	Gly	Pro	Arg	Leu	Ala	Ser
65					70					75				80	
Arg	Leu	Arg	Val	His	Arg	Val	Gly	Ala	Ala	Val	Ala	Gln	Leu	Pro	Thr
				85				90					95		
Thr	Asn	Pro	Glu	Val	Ala	Ser	Gly	Glu	Lys	Lys	Ile	Arg	Trp	Ser	Ser
			100					105					110		
Arg	Ala	Val	Arg	Ser	Phe	Ala	Met	Ala	Glu	Leu	Glu	Ala	Arg	Lys	Met
		115					120					125			
Arg	Tyr	Pro	Thr	Thr	Gly	Thr	Glu	Gly	Leu	Leu	Met	Gly	Ile	Leu	Val
		130				135					140				
Glu	Gly	Thr	Ser	Gly	Ala	Xaa	Asn	Phe	Cys	Val	Leu	Met	Glu	Pro	His
145					150					155				160	
Phe	Ser	Lys	Cys	Val	Arg	Arg	Gln	Arg	Met	Phe	Leu	Gly	Asn	Gln	Lys
			165					170					175		
Cys	Phe	Thr	Leu	Val	Pro	Cys	Ile	His	His						
			180				185								

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1482129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met	Ala	Thr	Ala	Asp	Arg	Val	Ala	Ala	Thr	Phe	Leu	Ser	Ser	Phe	Pro
1						5			10					15	
Thr	His	His	Pro	Arg	Pro	Phe	Ser	Ser	Val	Ser	Leu	Val	Thr	Asn	Pro
			20					25					30		

Val Leu Pro Val Ser Leu Arg Ala Ala Val Thr Gly Gly Pro Arg Leu
35 40 45
Ala Ser Arg Leu Arg Val His Arg Val Gly Ala Ala Val Ala Gln Leu
50 55 60
Pro Thr Thr Asn Pro Glu Val Ala Ser Gly Glu Lys Lys Ile Arg Trp
65 70 75 80
Ser Ser Arg Ala Val Arg Ser Phe Ala Met Ala Glu Leu Glu Ala Arg
85 90 95
Lys Met Arg Tyr Pro Thr Thr Gly Thr Glu Gly Leu Leu Met Gly Ile
100 105 110
Leu Val Glu Gly Thr Ser Gly Ala Xaa Asn Phe Cys Val Leu Met Glu
115 120 125
Pro His Phe Ser Lys Cys Val Arg Arg Gln Arg Met Phe Leu Gly Asn
130 135 140
Gln Lys Cys Phe Thr Leu Val Pro Cys Ile His His
145 150 155

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Met Phe Tyr Phe Ser Pro Met His Pro Pro Leu Thr Glu Ala Ala Gln
1 5 10 15
Arg Ala Leu Asp Trp Ala Val Asn Glu Lys Leu Lys Ser Gly Glu Asp
20 25 30
Gly Glu Val Thr Ala Asn His Leu Leu Leu Gly Ile Trp Ser Asp Lys
35 40 45
Glu Ser Ala Gly His Lys Ile Leu Tyr Ser Leu Gly Phe Asp Asp Glu
50 55 60
Lys Ala Ser Leu Leu Ala Lys Thr Ala Gly Glu Glu Ala Ala Met Ser
65 70 75 80
Leu Arg Glu Gln Gly Glu His Leu Ile Tyr Ser Ser Thr
85 90

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..852
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

ataggtgggt	cgaacttcga	aggggttcga	ggacttcagc	tatggcatct	gtgggacgtg	60
caggacgagg	agggaaagga	gatggaggga	agggagaagg	gtcgctggct	cgcagggcgt	120
ggaggcagta	cctgctccag	ctccagcaac	atcctctccg	cacaaagatg	atcacggcgg	180
ggtgcctcgc	cggcgtcagt	gactccgtgg	cgcagaagct	ctctgggttc	cagaagattg	240
agaaacgcag	actcctgctc	aagatgctct	ttggttttgc	atatggtggc	ccatttggac	300
atttcttgca	caaaattttg	gattacatct	tccaagggaa	gaaggatacc	aaaaccatag	360
caaagaaggt	gttattggag	caagtgacat	cttctccctg	gaataacata	ttgttcttgt	420

tctattatgg	atatgttggt	gagaggaggc	ctttgaagga	ggtgacgacc	agggtgaaga	480
aacaataccc	ttctgtgcaa	ctcagcgctt	ggatgttttg	gccgatagtt	ggttggataa	540
accaccagta	catgccttta	caattccgag	tgatcttcca	cagctttgtc	gcatgttggt	600
gggggatttt	cctgaacctt	cgtgcaaggg	ctatgtctct	gaagcaggcc	tagatggttt	660
agaaggaacg	tatagcagca	aagctcctgc	ccggtgctaa	ctaaagcagc	cgaagaagga	720
ggatgctgga	agctgtatcc	tgcacgggta	caaaaaccgt	tgttttatttc	ctggtagtag	780
tcggttttatt	tgaatgtcaa	cgcattgcgaa	gacagattat	gctttttgta	aaaaaaaaatt	840
gtgatgggag	cg					

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1482132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Arg	Trp	Val	Glu	Leu	Arg	Arg	Gly	Ser	Arg	Thr	Ser	Ala	Met	Ala	Ser
1				5				10					15		
Val	Gly	Arg	Ala	Gly	Arg	Gly	Gly	Lys	Gly	Asp	Gly	Gly	Lys	Gly	Glu
			20					25					30		
Gly	Ser	Leu	Ala	Arg	Arg	Ala	Trp	Arg	Gln	Tyr	Leu	Leu	Gln	Leu	Gln
		35					40					45			
Gln	His	Pro	Leu	Arg	Thr	Lys	Met	Ile	Thr	Ala	Gly	Cys	Leu	Ala	Gly
	50					55					60				
Val	Ser	Asp	Ser	Val	Ala	Gln	Lys	Leu	Ser	Gly	Phe	Gln	Lys	Ile	Glu
65					70					75				80	
Lys	Arg	Arg	Leu	Leu	Leu	Lys	Met	Leu	Phe	Gly	Phe	Ala	Tyr	Gly	Gly
			85					90					95		
Pro	Phe	Gly	His	Phe	Leu	His	Lys	Ile	Leu	Asp	Tyr	Ile	Phe	Gln	Gly
		100					105						110		
Lys	Lys	Asp	Thr	Lys	Thr	Ile	Ala	Lys	Lys	Val	Leu	Leu	Glu	Gln	Val
		115					120						125		
Thr	Ser	Ser	Pro	Trp	Asn	Asn	Ile	Leu	Phe	Leu	Phe	Tyr	Tyr	Gly	Tyr
	130					135						140			
Val	Val	Glu	Arg	Arg	Pro	Leu	Lys	Glu	Val	Thr	Thr	Arg	Val	Lys	Lys
145					150					155				160	
Gln	Tyr	Pro	Ser	Val	Gln	Leu	Ser	Ala	Trp	Met	Phe	Trp	Pro	Ile	Val
			165						170					175	
Gly	Trp	Ile	Asn	His	Gln	Tyr	Met	Pro	Leu	Gln	Phe	Arg	Val	Ile	Phe
		180					185						190		
His	Ser	Phe	Val	Ala	Cys	Cys	Trp	Gly	Ile	Phe	Leu	Asn	Leu	Arg	Ala
	195						200					205			
Arg	Ala	Met	Ser	Leu	Lys	Gln	Ala								
	210					215									

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1482133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met	Ala	Ser	Val	Gly	Arg	Ala	Gly	Arg	Gly	Gly	Lys	Gly	Asp	Gly	Gly		
1				5				10						15			
Lys	Gly	Glu	Gly	Ser	Leu	Ala	Arg	Arg	Ala	Trp	Arg	Gln	Tyr	Leu	Leu		
		20					25					30					
Gln	Leu	Gln	Gln	His	Pro	Leu	Arg	Thr	Lys	Met	Ile	Thr	Ala	Gly	Cys		
		35					40					45					
Leu	Ala	Gly	Val	Ser	Asp	Ser	Val	Ala	Gln	Lys	Leu	Ser	Gly	Phe	Gln		
	50					55					60						
Lys	Ile	Glu	Lys	Arg	Arg	Leu	Leu	Leu	Lys	Met	Leu	Phe	Gly	Phe	Ala		
65					70					75					80		
Tyr	Gly	Gly	Pro	Phe	Gly	His	Phe	Leu	His	Lys	Ile	Leu	Asp	Tyr	Ile		
				85					90					95			
Phe	Gln	Gly	Lys	Lys	Asp	Thr	Lys	Thr	Ile	Ala	Lys	Lys	Val	Leu	Leu		
			100				105						110				
Glu	Gln	Val	Thr	Ser	Ser	Pro	Trp	Asn	Asn	Ile	Leu	Phe	Leu	Phe	Tyr		
		115					120					125					
Tyr	Gly	Tyr	Val	Val	Glu	Arg	Pro	Leu	Lys	Glu	Val	Thr	Thr	Arg			
		130				135					140						
Val	Lys	Lys	Gln	Tyr	Pro	Ser	Val	Gln	Leu	Ser	Ala	Trp	Met	Phe	Trp		
145						150				155					160		
Pro	Ile	Val	Gly	Trp	Ile	Asn	His	Gln	Tyr	Met	Pro	Leu	Gln	Phe	Arg		
				165					170					175			
Val	Ile	Phe	His	Ser	Phe	Val	Ala	Cys	Cys	Trp	Gly	Ile	Phe	Leu	Asn		
			180					185					190				
Leu	Arg	Ala	Arg	Ala	Met	Ser	Leu	Lys	Gln	Ala							
		195					200										

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met	Ile	Thr	Ala	Gly	Cys	Leu	Ala	Gly	Val	Ser	Asp	Ser	Val	Ala	Gln		
1				5				10						15			
Lys	Leu	Ser	Gly	Phe	Gln	Lys	Ile	Glu	Lys	Arg	Arg	Leu	Leu	Lys			
		20						25					30				
Met	Leu	Phe	Gly	Phe	Ala	Tyr	Gly	Gly	Pro	Phe	Gly	His	Phe	Leu	His		
		35					40					45					
Lys	Ile	Leu	Asp	Tyr	Ile	Phe	Gln	Gly	Lys	Lys	Asp	Thr	Lys	Thr	Ile		
	50					55					60						
Ala	Lys	Lys	Val	Leu	Leu	Glu	Gln	Val	Thr	Ser	Ser	Pro	Trp	Asn	Asn		
65					70					75				80			
Ile	Leu	Phe	Leu	Phe	Tyr	Tyr	Gly	Tyr	Val	Val	Glu	Arg	Arg	Pro	Leu		
				85					90					95			
Lys	Glu	Val	Thr	Arg	Val	Lys	Lys	Gln	Tyr	Pro	Ser	Val	Gln	Leu			
		100					105						110				
Ser	Ala	Trp	Met	Phe	Trp	Pro	Ile	Val	Gly	Trp	Ile	Asn	His	Gln	Tyr		
		115					120					125					
Met	Pro	Leu	Gln	Phe	Arg	Val	Ile	Phe	His	Ser	Phe	Val	Ala	Cys	Cys		
	130					135					140						
Trp	Gly	Ile	Phe	Leu	Asn	Leu	Arg	Ala	Arg	Ala	Met	Ser	Leu	Lys	Gln		
145					150					155					160		

Ala

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

cgaaaaatgg attcattcag acgtgatcct tggcccttga attgggagac cttctgcaga	60
gacgcacaag cccaggggga aaaaagtttc agtcagtaag ggagaataag cattgcaaac	120
cgaaacagag gtaatcaata aaggatggga aacatggata aggatcaatt agagcatcta	180
accccgcat tccaaccaat gactcggtga atcgctgac taggaatact ctgatattac	240
atctgctctg ccatcataa tctgttcacg ttctacaacg aakcctataa gttgaagcaa	300
ccgcagatgc aattgtagga gtattttgtt tcttttctgt gatttggctt cagcacaac	360
agcacaaggg catctccaaa gacagtcagc taccgtgacc gtgaggcatg acatcgttta	420
ttcagtgaag gaaaaaaaaa tgcaacgagc agctaagggtc gcaagtaccc aagctagtca	480
tcgctaagct gtaastgaga gtatgtatca gtttctacag acgactgtgg aag	

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Arg Lys Met Asp Ser Phe Arg Arg Asp Pro Trp Pro Leu Asn Trp Glu	
1 5 10 15	
Thr Phe Cys Arg Asp Ala Gln Ala Gln Gly Glu Lys Ser Phe Ser Gln	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Met Asp Ser Phe Arg Arg Asp Pro Trp Pro Leu Asn Trp Glu Thr Phe	
1 5 10 15	
Cys Arg Asp Ala Gln Ala Gln Gly Glu Lys Ser Phe Ser Gln	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1482142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

attcgaattt cgaacgccgc cggtcgctcc ctgttcccta gctctctcct ccgcgggtcc	60
gcctccggcc tccacgggtt cgcaggcaga gatgaagaag gcgtccgcgg cgtcgcgcta	120
cgcgccctac gactccccgt ccccttcgcc gcgcgcgcgc gscncttccg cggccgccgc	180
gaccccgga gcagcgcacg gcagcagccg cgccttggtg gtcgcgggga gatccggccg	240
cgatctactg ggcgccaagc cgcaagccca cggcaacctt ggctccgtgc tacggcggtc	300
catctccatg gacaagaagc cgccttcctc caagaaccag ctcccggttc cccctgcmgc	360
mgcmgccgca gcagcagcag cagcgaagaa caacggtggc gggaagctgc mggggctgtm	420
gcggaagtgt ttccagaaa cctcgtccac	

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1482143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Ile Arg Ile Ser Asn Ala Ala Gly Arg Ser Leu Phe Pro Ser Ser Leu	
1 5 10 15	
Leu Arg Gly Ser Ala Ser Gly Leu His Gly Phe Ala Gly Arg Asp Glu	
20 25 30	
Glu Gly Val Arg Gly Val Ala Leu Arg Gly Leu Arg Leu Pro Val Pro	
35 40 45	
Phe Ala Ala Pro Arg Xaa Xaa Phe Arg Gly Arg Arg Asp Pro Gly Ser	
50 55 60	
Ser Ala Arg Gln Gln Pro Arg Pro Gly Gly Arg Gly Glu Ile Arg Pro	
65 70 75 80	
Arg Ser Thr Gly Arg Gln Ala Ala Ser Pro Arg Gln Pro Arg Leu Arg	
85 90 95	
Ala Thr Ala Ala His Leu His Gly Gln Glu Ala Ala Phe Leu Gln Glu	
100 105 110	
Pro Ala Pro Gly Ser Pro Cys Xaa Xaa Xaa Arg Ser Ser Ser Ser Ser	
115 120 125	
Glu Glu Gln Arg Trp Arg Glu Ala Xaa Gly Ala Xaa Ala Glu Val Val	
130 135 140	
Pro Glu Ser Leu Val His	
145 150	

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1482144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Phe Glu Phe Arg Thr Pro Pro Val Ala Pro Cys Ser Leu Ala Leu Ser
1 5 10 15
Ser Ala Ala Pro Pro Ala Ser Thr Val Ser Gln Ala Glu Met Lys
20 25 30
Lys Ala Ser Ala Ala Ser Arg Tyr Ala Ala Tyr Asp Ser Pro Ser Pro
35 40 45
Ser Pro Arg Arg Ala Xaa Xaa Ser Ala Ala Ala Ala Thr Pro Gly Ala
50 55 60
Ala His Gly Ser Ser Arg Ala Leu Val Val Ala Gly Arg Ser Gly Arg
65 70 75 80
Asp Leu Leu Gly Ala Lys Pro Gln Ala His Gly Asn Leu Gly Ser Val
85 90 95
Leu Arg Arg Leu Ile Ser Met Asp Lys Lys Pro Pro Ser Ser Lys Asn
100 105 110
Gln Leu Pro Val Pro Pro Xaa Xaa Xaa Ala Ala Ala Ala Ala Ala Ala
115 120 125
Lys Asn Asn Gly Gly Gly Lys Leu Xaa Gly Leu Xaa Arg Lys Leu Phe
130 135 140
Gln Lys Ala Ser Ser
145

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1482145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Lys Lys Ala Ser Ala Ala Ser Arg Tyr Ala Ala Tyr Asp Ser Pro
1 5 10 15
Ser Pro Ser Pro Arg Arg Ala Xaa Xaa Ser Ala Ala Ala Ala Thr Pro
20 25 30
Gly Ala Ala His Gly Ser Ser Arg Ala Leu Val Val Ala Gly Arg Ser
35 40 45
Gly Arg Asp Leu Leu Gly Ala Lys Pro Gln Ala His Gly Asn Leu Gly
50 55 60
Ser Val Leu Arg Arg Leu Ile Ser Met Asp Lys Lys Pro Pro Ser Ser
65 70 75 80
Lys Asn Gln Leu Pro Val Pro Pro Xaa Xaa Xaa Ala Ala Ala Ala Ala
85 90 95
Ala Ala Lys Asn Asn Gly Gly Gly Lys Leu Xaa Gly Leu Xaa Arg Lys
100 105 110
Leu Phe Gln Lys Ala Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..434

(D) OTHER INFORMATION: / Ceres Seq. ID 1482153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

gaaggggga	gcgctgcaga	tagtctcaag	tccgcttcct	gtgctgggcc	gccgtcgctc	60
tctgttcgcc	gtccgccgtg	cgcgccatcc	gccccgctcc	acgcagcttg	ggaataacgg	120
atcgccgctc	gtatccctc	gacctcggtg	gaaagttcca	aacgaccacg	acgtcctctt	180
gggtctccgc	tgatcatcag	ccgcaattcc	gcatttctat	tgctcttttt	ccgtcgcatc	240
cgtttcgtct	ctttgctcgc	atctggcctc	aagcccccca	ggcctcagct	caccaccacg	300
aaccaaccga	cagaaagagg	gacgaatggc	gagctctcag	tgctgcgata	acccgccggc	360
cctgaaccgc	gcctgcgggg	agggcaaggt	cgctgcacag	ttcggcgggc	tcaaggccta	420
cgtygccggc	ccc					

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1482154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Glu	Gly	Gly	Ser	Ala	Ala	Asp	Ser	Leu	Lys	Ser	Ala	Ser	Cys	Ala	Gly
1			5					10					15		
Pro	Pro	Ser	Leu	Ser	Val	Arg	Arg	Pro	Pro	Cys	Arg	Pro	Ser	Ala	Pro
			20					25					30		
Leu	His	Ala	Ala	Trp	Glu										
			35												

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1482155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Lys	Gly	Gly	Ala	Leu	Gln	Ile	Val	Ser	Ser	Pro	Leu	Pro	Val	Leu	Val
1			5					10					15		
Arg	Arg	Arg	Ser	Leu	Phe	Ala	Val	Arg	Arg	Ala	Val	His	Pro	Pro	Arg
			20					25				30			
Ser	Thr	Gln	Leu	Gly	Asn	Asn	Gly	Ser	Pro	Leu	Ala	Ile	Pro	Arg	Pro
			35				40					45			
Arg															

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1482156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Ala Ser Ser Gln Cys Cys Asp Asn Pro Pro Ala Leu Asn Pro Ala
1 5 10 15
Cys Gly Glu Gly Lys Val Val Asp Ser Phe Gly Gly Leu Lys Ala Tyr
20 25 30
Xaa Ala Gly Pro
35

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 633 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..633

(D) OTHER INFORMATION: / Ceres Seq. ID 1482157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

agagttcagg ggggagccag cgaagacaag acaagccagg ccagcggcgg aggagagggg 60
gagagagaga gagagagcac gcgacagtag gcaggagggc gaggaggagc ttgtagaggg 120
ttaaggaagg cgaccgccat gggggactcc agcggctccg tgctcggtcga cgtcgagcgg 180
atcttcttcg gcggcaagga gcatcgagta agaacgaggc atggctctct ttcggtttct 240
gtgtatggag acgaggacaa gccgcgcgtc gtaacttatc cggatgtagc cttaaatcac 300
atgtcttgct tccaaggatt gttcttctgt ccggaggctg cgtccctggt gcttcacagt 360
ttctgcgtgt accacatcac acctcaagga cagcagtttg gagcagctcc gatttcagct 420
gatgtgcctg tgccatctgt cgacgacctt gcagatcagg ttgctgatgt cctcgatttt 480
ttcagtttag ggtctgtcat gtgcttgggt gtcactgctg gtgcctatgt tctcaccctc 540
tttgcaacta agtatcgga gaggggtcct ggccatcatg tggtttcacc tgtatgcaaa 600
gccccctcct ggagcgagtg gctgtataat aag

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1482158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Gly Asp Ser Ser Gly Ser Val Ser Val Asp Val Glu Arg Ile Phe
1 5 10 15
Phe Gly Gly Lys Glu His Arg Val Arg Thr Arg His Gly Ser Leu Ser
20 25 30
Val Ser Val Tyr Gly Asp Glu Asp Lys Pro Ala Leu Val Thr Tyr Pro
35 40 45
Asp Val Ala Leu Asn His Met Ser Cys Phe Gln Gly Leu Phe Phe Cys
50 55 60
Pro Glu Ala Ala Ser Leu Leu Leu His Ser Phe Cys Val Tyr His Ile
65 70 75 80
Thr Pro Gln Gly His Glu Leu Gly Ala Ala Pro Ile Ser Ala Asp Val
85 90 95
Pro Val Pro Ser Val Asp Asp Leu Ala Asp Gln Val Ala Asp Val Leu
100 105 110
Asp Phe Phe Ser Leu Gly Ser Val Met Cys Leu Gly Val Thr Ala Gly

115 120 125
Ala Tyr Val Leu Thr Leu Phe Ala Thr Lys Tyr Arg Glu Arg Val Leu
130 135 140
Gly Leu Met Leu Val Ser Pro Val Cys Lys Ala Pro Ser Trp Ser Glu
145 150 155 160
Trp Leu Tyr Asn Lys
165

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Ser Cys Phe Gln Gly Leu Phe Phe Cys Pro Glu Ala Ala Ser Leu
1 5 10 15
Leu Leu His Ser Phe Cys Val Tyr His Ile Thr Pro Gln Gly His Glu
20 25 30
Leu Gly Ala Ala Pro Ile Ser Ala Asp Val Pro Val Pro Ser Val Asp
35 40 45
Asp Leu Ala Asp Gln Val Ala Asp Val Leu Asp Phe Phe Ser Leu Gly
50 55 60
Ser Val Met Cys Leu Gly Val Thr Ala Gly Ala Tyr Val Leu Thr Leu
65 70 75 80
Phe Ala Thr Lys Tyr Arg Glu Arg Val Leu Gly Leu Met Leu Val Ser
85 90 95
Pro Val Cys Lys Ala Pro Ser Trp Ser Glu Trp Leu Tyr Asn Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

ctcgagtcca gccaaccgaa gccgaacata cccacccatc gtctcgtcgt ctcgtcgcgc 60
gtgggctgtg ctctctctcc cccacactcc tcttttaaga cgacgccatc gccagccggc 120
cctccctcgc cgtccggcgc cgtcctcctt cgtccttccc tctcatcaca gtttccacct 180
cgcgaggggc tcgcgcgcgc gcccatcccg gccgatcgac tcacgaattc gcgcgcgatc 240
atattcgtgc aagggcaccc ccgcacggcc ggaagcacgg aatcacttcc ccgcccccca 300
attcccgggc tctcggcgc mgatccctcg ccggtgttcg ctttccggcg gtttccgcgg 360
cgtgtcgcgc gcaggcgcag gcggctcggc tcggttgttt cctcctcgtg ccatcatcca 420
tggaggcgaa sagcgcmcgc ggcacggcgg ggagaggagg c

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Leu Glu Ser Ser Glu Pro Lys Pro Asn Ile Pro Thr His Arg Leu Val
1 5 10 15
Val Ser Ser Arg Val Gly Val Ala Leu Ser Pro Pro Thr Ser Ser Phe
20 25 30
Lys Thr Thr Pro Ser Pro Ala Gly Pro Pro Ser Pro Ser Gly Ala Val
35 40 45
Leu Leu Arg Pro Ser Leu Ser Ser Gln Phe Pro Pro Arg Glu Gly Leu
50 55 60
Ala Arg Ala Pro Ile Pro Ala Asp Arg Leu Thr Asn Ser Arg Ala Ile
65 70 75 80
Ile Phe Val Gln Gly His Pro Arg Thr Ala Gly Ser Thr Glu Ser Leu
85 90 95
Pro Arg Pro Pro Ile Pro Gly Leu Leu Gly Xaa Asp Pro Ser Pro Val
100 105 110
Phe Ala Phe Arg Arg Phe Pro Arg Arg Val Ala Gly Arg Arg Arg Arg
115 120 125
Leu Gly Ser Val Val Ser Ser Ser Cys His His Pro Trp Arg Arg Xaa
130 135 140
Ala Xaa Ala Ala Arg Arg Gly Glu Glu
145 150

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Ser Ser Arg Ala Asn Arg Ser Arg Thr Tyr Pro Pro Ile Val Ser Ser
1 5 10 15
Ser Arg Arg Ala Trp Ala Trp Leu Ser Leu Pro Pro Pro Pro Leu Leu
20 25 30
Arg Arg Arg His Arg Gln Pro Ala Leu Pro Arg Arg Pro Ala Pro Ser
35 40 45
Ser Phe Val Leu Pro Ser His His Ser Phe His Leu Ala Arg Gly Ser
50 55 60
Arg Ala Arg Pro Ser Arg Pro Ile Asp Ser Arg Ile Arg Ala Arg Ser
65 70 75 80
Tyr Ser Cys Lys Gly Ile Pro Ala Arg Pro Glu Ala Arg Asn His Phe
85 90 95
Pro Ala Pro Gln Phe Pro Gly Ser Ser Ala Xaa Ile Pro Arg Arg Cys
100 105 110
Ser Leu Ser Gly Gly Phe Arg Gly Val Ser Arg Ala Gly Ala Gly Gly
115 120 125
Ser Ala Arg Leu Phe Pro Pro Arg Ala Ile Ile His Gly Gly Glu Xaa
130 135 140
Arg Xaa Arg His Gly Gly Glu Arg Arg
145 150

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..615
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482167
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

aaaacccaaaa	agaagggttg	ctcccaacgc	aacgaactgc	ctttcccgtc	agcagcagca	60
gcagctgcys	cntgctgctg	tccatctcca	tctcccccat	cgcccgactg	gattttctccc	120
tcgaattcgc	acctccggcc	tccccctca	cttcgctgtg	tctcatcaac	gccggcatca	180
ccgcgaggac	tgggccagcg	ctccctccct	ttctcctccc	tccgccttta	ttgctgacgg	240
cgacgactgg	gcgagctctg	ccgcgcgtct	gcgctaggtg	cccaggtcct	cctcgggcac	300
ttcacccggc	acgagcacc	atcaggagcg	aaatggacga	ggctgttcct	gctttggcta	360
ctggccaagc	ttcaaccgac	ggcgtgacag	agcagcctgt	gaatgtgtac	atatgggaca	420
tggatgagac	actcattttg	ctcaagtcac	ttctggatgg	ctcatatgct	ggggcttttg	480
atggcctcaa	ggatcatgag	aaaagtactg	aaataggaaa	gcgatgggag	aacctcattc	540
ttgaactctg	tgatgagcac	ttcttttatg	aggagattga	gaactacaat	gaaccctatc	600
tcaatgcctt	gaatg					

- (2) INFORMATION FOR SEQ ID NO:394:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..204
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482168
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Asn	Gln	Lys	Glu	Gly	Leu	Leu	Pro	Thr	Gln	Arg	Thr	Ala	Phe	Pro	Val
1				5					10					15	
Ser	Ser	Ser	Ser	Ser	Cys	Xaa	Xaa	Leu	Leu	Ser	Ile	Ser	Ile	Leu	Pro
				20					25					30	
Ile	Ala	Arg	Leu	Asp	Phe	Ser	Leu	Glu	Phe	Ala	Pro	Pro	Ala	Ser	Pro
				35					40					45	
Leu	Thr	Ser	Leu	Cys	Leu	Ile	Asn	Ala	Gly	Ile	Thr	Ala	Arg	Thr	Gly
				50					55					60	
Pro	Ala	Leu	Pro	Pro	Phe	Leu	Leu	Pro	Pro	Pro	Leu	Leu	Leu	Thr	Ala
				65					70					75	
Thr	Thr	Gly	Arg	Ala	Leu	Pro	Pro	Leu	Cys	Ala	Arg	Cys	Pro	Gly	Leu
				85					90					95	
Pro	Arg	Ala	Leu	His	Arg	Arg	Arg	Ala	Pro	Ile	Arg	Ser	Glu	Met	Asp
				100					105					110	
Glu	Ala	Val	Pro	Ala	Leu	Ala	Thr	Gly	Gln	Ala	Ser	Thr	Asp	Gly	Val
				115					120					125	
Thr	Glu	Gln	Pro	Val	Asn	Val	Tyr	Ile	Trp	Asp	Met	Asp	Glu	Thr	Leu
				130					135					140	
Ile	Leu	Leu	Lys	Ser	Leu	Leu	Asp	Gly	Ser	Tyr	Ala	Gly	Ala	Phe	Asp
				145					150					155	
Gly	Leu	Lys	Asp	His	Glu	Lys	Ser	Thr	Glu	Ile	Gly	Lys	Arg	Trp	Glu
				165					170					175	
Asn	Leu	Ile	Leu	Glu	Leu	Cys	Asp	Glu	His	Phe	Phe	Tyr	Glu	Glu	Ile
				180					185					190	
Glu	Asn	Tyr	Asn	Glu	Pro	Tyr	Leu	Asn	Ala	Leu	Asn				

195 200

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1482169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

attcgataac	caagaacaaa	ccattgtttg	acgcgttccc	ctcctgcacg	caacctcatc	60
tcgtcctcca	gatccaggat	ggccgtcctc	cttgagacct	tgccctcccc	agtgctctcg	120
gtgagctact	ttgtttcgat	ttatcaggaa	atccgtttgc	ttcatgtttg	gcaggctcat	180
atctgattgc	tggaattcgg	aaaccgcgt	tggaacctgt	atcggttagt	ccttgccctgc	240
aaggttcttg	ttgtwttgtt	ttggtggtcg	agcatcgcat	gttctgcttc	tggatccaga	300
tctggagaaa	tcgcgaagtc	gtcgtcgttc	ggttcggagc	ggatctgagg	cgacgataga	360
tggaggcggc	gggatctctc	ggtctgcagt	cctgctccac	ctcgatggat	gatgtctctg	420
cgctgataat	tattggatca	atttcgataa	ttatwagtag	atctatgaga	tatgccgcgt	480
ggaagaggcg	aggtaagctg	cagcatgt				

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1482170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Phe	Asp	Asn	Gln	Glu	Gln	Thr	Ile	Val	Gly	Arg	Val	Pro	Leu	Leu	His
1			5					10					15		
Ala	Thr	Ser	Ser	Arg	Pro	Pro	Asp	Pro	Gly	Trp	Pro	Ser	Ser	Leu	Arg
			20				25					30			
Pro	Cys	Leu	Pro	Glu	Cys	Ser	Arg								
		35				40									

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1482171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met	Ala	Val	Leu	Glu	Thr	Leu	Pro	Pro	Arg	Val	Leu	Ser	Val	Ser	
1			5				10					15			
Tyr	Phe	Val	Ser	Ile	Tyr	Gln	Glu	Ile	Arg	Leu	Leu	His	Val	Val	Gln
			20				25					30			
Ala	His	Ile													
		35													

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..49
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482172
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:
Met Glu Ala Ala Gly Ser Leu Gly Leu Gln Ser Cys Ser Thr Ser Met
1 5 10 15
Asp Asp Val Ser Ala Leu Ile Ile Ile Gly Ser Ile Ser Ile Ile Xaa
 20 25 30
Ser Arg Ser Met Arg Tyr Ala Ala Trp Lys Arg Arg Gly Lys Leu Gln
 35 40 45
His

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 597 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..597
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482177
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:
aatcctaccc cgcgggggga attctctctc agttctctcg gcgacgactg ggagaccgcc 60
gccgccgcca tctactcca ggtgccctga gaactcgatc ggagtcttcg ctggcgacga 120
acaccacca gctatcaggt gtacaacctat gtacttcacc gtgtccgccc ctgcaatgct 180
tctatgatcc tccagctacg gtagacgccc cgttcgctag ctgaggacct cctgggttcct 240
gtgagcaggc ggcgtgggta gctgctgcct tcaagcatgc agagacccaa cgcgccgctc 300
gcttgcgcta ccatcacctt cgcggaggct ctaaggaggg agatggagta ccgcaagtgg 360
gtggagagga cccaccaca tctgctcgtc ggaatctgcg gasccctgaa atgcagagag 420
atttcagtgc aggaccagta cctgatgcga tcaagagaaa actagctgcc gagaccagtg 480
tgccctccaca acaatcaagt ttcagctgtg taactggaca gaagcagccc caaaactggt 540
acccacaaaa gaaaaagggtg aaagttccac atcttccgtc gcagattctg cagtgtc

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..61
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482178
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:
Ile Leu Pro Arg Gly Gly Asn Ser Leu Ser Val Leu Ser Ala Thr Thr
1 5 10 15
Gly Arg Pro Pro Pro Pro Pro Ser Tyr Ser Arg Cys Pro Glu Asn Ser
 20 25 30
Ile Gly Val Phe Ala Gly Asp Glu His Pro Pro Ala Ile Arg Cys Thr
 35 40 45

Thr Met Tyr Phe Thr Val Ser Ala Pro Ala Met Ser Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Ser Tyr Pro Ala Gly Gly Ile Leu Ser Gln Phe Ser Arg Arg Arg Leu
1 5 10 15
Gly Asp Arg Arg Arg His Pro Thr Pro Gly Ala Leu Arg Thr Arg
20 25 30
Ser Glu Ser Ser Leu Ala Thr Asn Thr His Gln Leu Ser Gly Val Gln
35 40 45
Pro Cys Thr Ser Pro Cys Pro Pro Leu Gln Cys Leu Tyr Asp Pro Pro
50 55 60
Ala Thr Val Asp Ala Pro Phe Ala Ser
65 70

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Gln Arg Pro Asn Ala Pro Ser Ala Cys Ala Thr Ile Thr Phe Ala
1 5 10 15
Glu Ala Leu Arg Arg Glu Met Glu Tyr Arg Lys Trp Val Glu Arg Thr
20 25 30
His Pro His Leu Leu Val Gly Ile Cys Gly Xaa Leu Lys Cys Arg Glu
35 40 45
Ile Ser Val Gln Asp Gln Tyr Leu Met Arg Ser Arg Glu Asn
50 55 60

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

aggattcaca agtgctcgta gcaaattctac aaaatcccca accgcctctc aacaaagtct 60
ccccacggag gtacacagct acgcgcaaac cgcgtctcgc gcgaagaatc cgcatttccc 120
cttccccgca ccgcaccgca cccaaccccc gtcggagaga gagatggcat cgggtggcgga 180

```
gatgcagccc ctgcgcgcgg cgggggtaccg cscgcgcggg agatgaagga gaaggtggag      240
gcgtcgggtg tggacctgga ggccgggacc ggggagacgc tgtaccgggg gatctcgcgc      300
ggggagagcg ccttccgatg gggcttcgtc cgcaaggctt acggcatcct cgctgcgcas      360
tgctcctcac caccgccgtc tccgcmctca ccgttctcca cccaccctc aacgccacgc      420
tctccgactc cccgggmctm gcgctmgtrc tccgcmgtmt gcccttmatc ctgatgatcc      480
cattgtatca ttatcagcac aagcaccac acaattccgt tttcctgggt ctgttcacgt      540
tggtgcttga gcttcagcat cggcgtgggt tgtgct
```

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```
Asp Ser Gln Val Leu Val Ala Asn Leu Gln Asn Pro Gln Pro Pro Leu
1          5          10          15
Asn Lys Val Ser Pro Arg Arg Tyr Thr Ala Thr Arg Lys Pro Arg Leu
20          25          30
Ala Arg Arg Ile Arg Ile Ser Pro His Arg Thr Ala Pro Asn
35          40          45
Pro Arg Arg Arg Glu Arg Trp His Arg Trp Arg Arg Cys Ser Pro Ser
50          55          60
Arg Arg Arg Gly Thr Xaa Arg Ala Gly Asp Glu Gly Glu Gly Gly Gly
65          70          75          80
Val Gly Gly Gly Pro Gly Gly Arg Asp Arg Gly Asp Ala Val Pro Gly
85          90          95
Asp Leu Ala Arg Gly Glu Arg Pro Pro Met Gly Leu Arg Pro Gln Gly
100         105         110
Leu Arg His Pro Arg Cys Ala Xaa Leu Leu Thr Thr Ala Val Ser Xaa
115         120         125
Leu Thr Val Leu His Pro Thr Leu Asn Ala Thr Leu Ser Asp Ser Pro
130         135         140
Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa Pro Xaa Ile Leu Met Ile Pro
145         150         155         160
Leu Tyr His Tyr Gln His Lys His Pro His Asn Ser Val Phe Leu Gly
165         170         175
Leu Phe Thr Leu Val Leu Glu Leu Gln His Arg Arg Gly Leu Cys
180         185         190
```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```
actccactct actccacccg cgcacaacag atcgacgccc tcggttcctt ccaactcgacg      60
cttctcccg ccttaacccc tagtaccttc gctcgctctg ccgcctccgc cgacgacgcg      120
ccagatccgc gcrsagtggg gtctctccgc gcggatcgag ctcccgatcc gcgcagtggg      180
agtggcgggc agcgcaggag cgctcggccg ggggttccgc gaggctggag acggaggagg      240
```

aaggagcg tagttccg gtagtagatc cgccggctc gtcgcccggag atggactcat 300
ctgtcgagaa gcaggggagc gtggcgctgg atccggacga gcgcrcgcgc gcgtccggcg 360
aaaccaaggc ctgcaccgag tgccacacca ccaagacccc gctctggcgc gg

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Thr	Pro	Leu	Tyr	Ser	Thr	Arg	Ala	Gln	Gln	Ile	Ala	Arg	Leu	Gly	Ser
1				5				10					15		
Leu	His	Ser	Thr	Leu	Leu	Pro	Leu	Leu	Thr	Pro	Ser	Thr	Phe	Ala	Arg
			20				25						30		
Ser	Ala	Ala	Ser	Ala	Asp	Asp	Ala	Pro	Asp	Pro	Arg	Xaa	Val	Val	Ser
		35					40					45			
Ser	Ala	Ala	Asp	Arg	Ala	Pro	Asp	Pro	Arg	Ser	Gly	Ser	Gly	Gly	Glu
	50				55						60				
Arg	Arg	Ser	Ala	Arg	Pro	Gly	Val	Pro	Arg	Gly	Trp	Arg	Arg	Arg	Arg
65				70				75						80	
Lys	Gly	Ala	Val	Val	Pro	Arg	Trp								
				85											

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

attcattacc	ggaagagaaa	aaagtaactc	ggaaaagaag	gagacgccga	aaattcgaaa	60
ggggagggga	aagcaaagct	gatggcggag	gcccagggga	aagcaaagca	aatggcggag	120
gccccgagca	agatcgaatc	catgaggaag	tgggtcgctc	agcacaagct	ccgagccgta	180
gttgccctctg	gctaggtggg	atcagcagtt	cgatcgccct	caactggctc	cggcccaata	240
tgaagcctag	cgtaagatc	atccacgcaa	ggttgcatgc	tcaagctcta	accctggctg	300
cattagttgg	ttctgcatgc	gtggagtact	atgaccagaa	gtatggttct	tctgggccaa	360
aggtggacaa	atacacaagc	caatacctgg	cccattcgca	taaagattaa	aggtcgccat	420
gttggttcct	gcatgccgga	ttaattttgg	gctcatctcg	ggttgctcat	gagtcatgac	480
ccgccc						

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Ser Leu Pro Glu Glu Lys Lys Val Thr Arg Lys Arg Arg Arg Arg Arg
1 5 10 15
Lys Phe Glu Arg Gly Gly Glu Ser Lys Ala Asp Gly Gly Gly Pro Gly
20 25 30
Glu Ser Lys Ala Asn Gly Gly Gly Pro Glu Gln Asp Arg Ile His Glu
35 40 45
Glu Val Gly Arg Arg Ala Gln Ala Pro Ser Arg Ser Cys Leu Trp Leu
50 55 60
Gly Gly Ile Ser Ser Ser Ile Ala Tyr Asn Trp Ser Arg Pro Asn Met
65 70 75 80
Lys Pro Ser Val Lys Ile Ile His Ala Arg Leu His Ala Gln Ala Leu
85 90 95
Thr Leu Ala Ala Leu Val Gly Ser Ala Cys Val Glu Tyr Tyr Asp Gln
100 105 110
Lys Tyr Gly Ser Ser Gly Pro Lys Val Asp Lys Tyr Thr Ser Gln Tyr
115 120 125
Leu Ala His Ser His Lys Asp
130 135

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..778
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

ggcagaggca	cggagcctca	actccactgc	cctgctgcaa	ttttttctct	gttagtcgat	60
cagccagcga	gtgaaaccaa	gaaattcatg	gcgggttgaa	ggagacacgg	gagggaggta	120
tgcattgtcc	tggcgaggtg	ctcccagcgg	cgtagtccacc	agtctgttga	ctcatgggga	180
catggtcata	gtcggcgctcg	gcttgctcga	gtgccagcag	caaccatggc	cctattcgca	240
gccatagggg	gtcagccttc	ttgcgctctc	atggcatcgg	tggagctgat	agaggggtctt	300
gggggggctcc	ccgtcgacgg	gtctccagcg	gccactgcag	caccacgaag	cacaatgttg	360
ttgcccgggt	ctgccagggg	ggcgctgtcg	aagggtcgac	ccaagaagcg	gatctcgatg	420
ttgagtggcg	cagcgtgctc	cactttgcat	ctcccagatg	tggctctcca	ccggcggcga	480
gccccgggtg	aggtggagct	cttgtggctg	gaaggcggag	gggaggaatg	gatcggtaga	540
tgggagggag	aggaaggtct	tscggtgggg	aggaatacac	ggatggcga	tgcggagggg	600
acgacggcga	tctactaggg	tttagtttgg	gcgtgagggg	atgagggcgg	atggcgatct	660
ggagacaatg	acggcggttc	agattagggt	tgcgagcggc	tcgatgggcg	cgtacgtggg	720
gtggatccga	gcggtccgcc	gcgtcacaac	tcaactat	tttttatgta	aaacggat	

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met Phe Leu Ala Arg Cys Ser Gln Arg Arg Ser His Gln Ser Val Asp
1 5 10 15
Ser Trp Gly His Gly His Ser Arg Arg Arg Leu Ala Arg Val Pro Ala

	20		25		30
Ala Thr Met	Ala Leu Phe	Ala Ala Ile	Gly Gly Gln	Pro Ser Cys	Ala
35		40		45	
Leu Met Ala	Ser Val Glu	Leu Ile Glu	Gly Leu Gly	Gly Leu Pro	Val
50		55		60	
Asp Gly Ser	Pro Ala Ala	Thr Ala Ala	Pro Arg Ser	Thr Met Leu	Leu
65		70		75	80
Pro Gly Ser	Ala Arg Gly	Ala Leu Ser	Lys Gly Arg	Pro Lys Lys	Arg
	85		90		95
Ile Ser Met	Leu Ser Gly	Ala Ala Cys	Ser Thr Leu	His Leu Pro	Asp
100		105		110	
Val Val Leu	His Arg Arg	Arg Ala Arg	Val Glu Val	Glu Leu Leu	Trp
115		120		125	
Leu Glu Gly	Gly Gly Glu	Glu Trp Ile	Gly Arg Trp	Glu Gly Glu	Glu
130		135		140	
Gly Leu Xaa	Val Gly Arg	Asn Thr Arg	Met Ala Ile	Arg Glu Gly	Thr
145		150		155	160
Thr Ala Ile	Tyr				

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1482209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Ala Leu	Phe Ala Ala	Ile Gly Gly	Gln Pro Ser	Cys Ala Leu	Met
1	5	10		15	
Ala Ser Val	Glu Leu Ile	Glu Gly Leu	Gly Gly Leu	Pro Val Asp	Gly
20		25		30	
Ser Pro Ala	Ala Thr Ala	Ala Pro Arg	Ser Thr Met	Leu Leu Pro	Gly
35		40		45	
Ser Ala Arg	Gly Ala Leu	Ser Lys Gly	Arg Pro Lys	Lys Arg Ile	Ser
50		55		60	
Met Leu Ser	Gly Ala Ala	Cys Ser Thr	Leu His Leu	Pro Asp Val	Val
65		70		75	80
Leu His Arg	Arg Arg Arg	Ala Arg Val	Glu Val Glu	Leu Leu Trp	Leu
85		90		95	
Gly Gly Gly	Glu Glu Trp	Ile Gly Arg	Trp Glu Gly	Glu Glu Gly	Leu
100		105		110	
Xaa Val Gly	Arg Asn Thr	Arg Met Ala	Ile Arg Glu	Gly Thr Thr	Ala
115		120		125	
Ile Tyr					
130					

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1482210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ala Ser Val Glu Leu Ile Glu Gly Leu Gly Gly Leu Pro Val Asp
1 5 10 15
Gly Ser Pro Ala Ala Thr Ala Ala Pro Arg Ser Thr Met Leu Leu Pro
20 25 30
Gly Ser Ala Arg Gly Ala Leu Ser Lys Gly Arg Pro Lys Lys Arg Ile
35 40 45
Ser Met Leu Ser Gly Ala Ala Cys Ser Thr Leu His Leu Pro Asp Val
50 55 60
Val Leu His Arg Arg Arg Ala Arg Val Glu Val Glu Leu Leu Trp Leu
65 70 75 80
Glu Gly Gly Gly Glu Glu Trp Ile Gly Arg Trp Glu Gly Glu Glu Gly
85 90 95
Leu Xaa Val Gly Arg Asn Thr Arg Met Ala Ile Arg Glu Gly Thr Thr
100 105 110
Ala Ile Tyr
115

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..721
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

atcggtgggc cggcgcaaac cctagtcgcc acatcactgc ctccctcacac catctgcctg 60
tggttcccat gtcacccccc ccggtttgag gtcttcctgc tccttcagat ccgtctatgt 120
gtgtgtttgt cgtgcctgat actggctcgg aaggtattcc gatctgtttc ttcggtgccg 180
tatatttcgt tgcgattttg gttcggttct ttcttgctct tcgtgggtcg ttgctggata 240
acacggatcg ttgatgctgt tcaagaagta ctgcgttatc ttctctgatgc aagtgttagg 300
ccctcgttac gaaggcttcc tgacgacaca aatatcttgc tgagatccaa gtgcgcaact 360
tctctctttt ttctctttct tttccgtatt tctcgccgtc tgctttttct cctctggatt 420
gaattttgcg tacagttagg tttttaccaa atgcaatcgt aacttacggg caggatgggt 480
tcagcaacga agtaaaggag gagattattc cgtcaaccgt aaggtgccgc taagagcttt 540
agaatatgaa aggcattagt ggtaacaaga tttgatttgg ttaggtgtta gtacaaaaaa 600
atgagattcg attccaatgc tgttgggggg actgctagtg aatatggccg ggcattctatc 660
acggtgttgt atgtgtacga aataatgtct gctttcgata cggtaagttt tgctttaagt 720
t

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Ile Val Gly Pro Ala Gln Thr Leu Val Ala Thr Ser Leu Pro Pro His
1 5 10 15
Thr Ile Cys Leu Trp Phe Pro Cys His Pro Pro Pro Phe Glu Val Phe
20 25 30

Leu Leu Leu Gln Ile Arg Leu Cys Val Cys Leu Ser Cys Leu Ile Leu
35 40 45
Ala Arg Lys Val Phe Arg Ser Val Ser Ser Val Pro Tyr Ile Ser Leu
50 55 60
Arg Phe Trp Phe Gly Ser Phe Leu Leu Phe Val Gly Arg Cys Trp Ile
65 70 75 80
Thr Arg Ile Val Asp Ala Val Gln Glu Val Leu Arg Tyr Leu Pro Asp
85 90 95
Ala Ser Val Arg Pro Ser Leu Arg Arg Leu Pro Asp Asp Thr Asn Ile
100 105 110
Leu Leu Arg Ser Lys Cys Ala Thr Ser Leu Phe Phe Leu Phe Leu Phe
115 120 125
Arg Ile Ser Arg Arg Leu Leu Phe Leu Leu Trp Ile Glu Phe Cys Val
130 135 140
Gln Phe Ser Phe Tyr Gln Met Gln Ser
145 150

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

acgtctgttg	ctctctaccg	gagacggatc	agcgtgtcaa	ctgacagccc	tatgtccttc	60
gccgctttct	catggccgtt	tcgccgccgg	ggcggggctg	gcagcagtgg	cgcaasaagt	120
ccgccgccac	ggcagaggag	gacgaggagc	tgggcgtgac	cccgcagctc	ctcgacttcc	180
tccggacgct	ctcgcccgcac	gccttcaagg	ccgccgcact	ccagctccaa	ggagggtcca	240
cggaggcggc	cgccggncga	cctcaccagc	tggcaggagc	ggcacgccgt	gctcgtgcta	300
tccaaagcta	aggaactcgc	caagattcgg	tatgatctgt	gccctcggca	cctgaaggat	360
aagcagttct	ggaggatata	cttcctgctc	gccaagagtt	acatctcacc	gtatgaacta	420
cgtgccatac	agaaggaaaa	actcagacgg	atggagacag	aaaactgcaa	gccccaaaca	480
gtgatctctg	ttgaggtgga	gatgcaagaa	tcgaagcgca	ctagtctctc	acaagcatca	540
gaagtagatc	tagaatctca	ggtttagttt	tgcagttata	gcttctaaca	gatctagctt	600
aggtaacgca	atcagtagcc	cttttatgat	tcctccacac	accaaatagc	tccacgagtt	660
cttcagatct	tggatcgact	ctcgctagac	taccagtccg	ctgtgtgctt	ttgtgtactg	720
aaaccaagta	ggtccttttc	tgcattacgc	agcatatgtg	cttgttggct	gtgctccgat	780
ccactgacat	gtaaatctag	ggtatcttgc	gcgtgaacaa	aaacgactgc	gtttcatgta	840
gctatagatt	atgtcaactt	cgattctgct	gtgcatgtgt	tgg		

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Arg Leu Leu Leu Ser Thr Gly Asp Gly Ser Ala Cys Gln Leu Thr Ala
1 5 10 15
Leu Cys Pro Ser Pro Leu Ser His Gly Arg Phe Ala Ala Gly Ala Gly
20 25 30

Leu Ala Ala Val Ala Gln Xaa Val Arg Arg His Gly Arg Gly Gly Arg
35 40 45
Gly Ala Gly Arg Asp Pro Ala Ala Pro Arg Leu Pro Pro Asp Ala Leu
50 55 60
Ala Arg Arg Leu Gln Gly Arg Arg Thr Pro Ala Pro Arg Arg Leu His
65 70 75 80
Gly Gly Gly Arg Arg Xaa Thr Ser Pro Ala Gly Arg Ser Gly Thr Pro
85 90 95
Cys Ser Cys Tyr Pro Lys Leu Arg Asn Ser Pro Arg Phe Gly Met Ile
100 105 110
Cys Ala Leu Gly Thr
115

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1482221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Ala Val Ser Pro Gly Arg Gly Trp Gln Gln Trp Arg Xaa Lys
1 5 10 15
Ser Ala Ala Thr Ala Glu Glu Asp Glu Glu Leu Gly Val Thr Pro Gln
20 25 30
Leu Leu Asp Phe Leu Arg Thr Leu Ser Pro Asp Ala Phe Lys Ala Ala
35 40 45
Ala Leu Gln Leu Gln Gly Gly Ser Thr Glu Ala Ala Ala Xaa Arg Pro
50 55 60
His Gln Leu Ala Gly Ala Ala Arg Arg Ala Arg Ala Ile Gln Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..732

(D) OTHER INFORMATION: / Ceres Seq. ID 1482230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

taaaggcatc gacaaaatct ataagcagct gacaaaaagc catacacatc cactcggagg 60
aacagcatat ttaaattctag aaaatgaaga cgaaccgttt cttaatggaa tcaagtacac 120
agctatgcc a cctaccaagc ggtttagaga tatggaacag ttatccggtg gggagaagac 180
tggtgcagca ctggctttgc tttttgccat tcacagtttt aggccatcac cgttcttcat 240
attggacgaa ttagatgctg ctctggacaa tttaaatgtg gccaagggtg cggggtttat 300
cagatcaaaa tcatgtgaac gtgttggtga tgaacaaggc agcgatggcg agagtggttt 360
tcagagcata gttatatctc tgaaggacag tttctatgac aaggccgagg cacttggttg 420
tgtttatagg gactcagaac gaagttgctc gaggactctc accttcgacc tgagaaagta 480
tagggaatcg tgaagcagct tttgttgaat gtttgacta tgtgtgtagt tgcctgctcc 540
atcagcttgc tagatagctg tcgtgagcct tcgatgtttt aactatctgt atactcctag 600
tcctacataa gtgctagctg aacaaggacc ctgaaatatt catttggtag gtggataact 660
gatgtttcga acacgcataa actttttttac ctgttgatat aagccatttc tccgaattac 720
tataatctgt tt

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Lys Gly Ile Asp Lys Ile Tyr Lys Gln Leu Thr Lys Ser His Thr His
1 5 10 15
Pro Leu Gly Gly Thr Ala Tyr Leu Asn Leu Glu Asn Glu Asp Glu Pro
20 25 30
Phe Leu Asn Gly Ile Lys Tyr Thr Ala Met Pro Pro Thr Lys Arg Phe
35 40 45
Arg Asp Met Glu Gln Leu Ser Gly Gly Glu Lys Thr Val Ala Ala Leu
50 55 60
Ala Leu Leu Phe Ala Ile His Ser Phe Arg Pro Ser Pro Phe Phe Ile
65 70 75 80
Leu Asp Glu Val Asp Ala Ala Leu Asp Asn Leu Asn Val Ala Lys Val
85 90 95
Ala Gly Phe Ile Arg Ser Lys Ser Cys Glu Arg Val Gly Asp Glu Gln
100 105 110
Gly Ser Asp Gly Glu Ser Gly Phe Gln Ser Ile Val Ile Ser Leu Lys
115 120 125
Asp Ser Phe Tyr Asp Lys Ala Glu Ala Leu Val Gly Val Tyr Arg Asp
130 135 140
Ser Glu Arg Ser Cys Ser Arg Thr Leu Thr Phe Asp Leu Arg Lys Tyr
145 150 155 160
Arg Glu Ser

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Met Pro Pro Thr Lys Arg Phe Arg Asp Met Glu Gln Leu Ser Gly Gly
1 5 10 15
Glu Lys Thr Val Ala Ala Leu Ala Leu Phe Ala Ile His Ser Phe
20 25 30
Arg Pro Ser Pro Phe Phe Ile Leu Asp Glu Val Asp Ala Ala Leu Asp
35 40 45
Asn Leu Asn Val Ala Lys Val Ala Gly Phe Ile Arg Ser Lys Ser Cys
50 55 60
Glu Arg Val Gly Asp Glu Gln Gly Ser Asp Gly Glu Ser Gly Phe Gln
65 70 75 80
Ser Ile Val Ile Ser Leu Lys Asp Ser Phe Tyr Asp Lys Ala Glu Ala
85 90 95
Leu Val Gly Val Tyr Arg Asp Ser Glu Arg Ser Cys Ser Arg Thr Leu

100 105 110
Thr Phe Asp Leu Arg Lys Tyr Arg Glu Ser
115 120
(2) INFORMATION FOR SEQ ID NO:421:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1482233
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:
Met Glu Gln Leu Ser Gly Gly Glu Lys Thr Val Ala Ala Leu Ala Leu
1 5 10 15
Leu Phe Ala Ile His Ser Phe Arg Pro Ser Pro Phe Phe Ile Leu Asp
20 25 30
Glu Val Asp Ala Ala Leu Asp Asn Leu Asn Val Ala Lys Val Ala Gly
35 40 45
Phe Ile Arg Ser Lys Ser Cys Glu Arg Val Gly Asp Glu Gln Gly Ser
50 55 60
Asp Gly Glu Ser Gly Phe Gln Ser Ile Val Ile Ser Leu Lys Asp Ser
65 70 75 80
Phe Tyr Asp Lys Ala Glu Ala Leu Val Gly Val Tyr Arg Asp Ser Glu
85 90 95
Arg Ser Cys Ser Arg Thr Leu Thr Phe Asp Leu Arg Lys Tyr Arg Glu
100 105 110
Ser

(2) INFORMATION FOR SEQ ID NO:422:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 773 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..773
(D) OTHER INFORMATION: / Ceres Seq. ID 1482234
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:
ctccgccgcc aggacgacgg caaatvcgcc cagacagggg ggacgtcgac gccggcgcaat 60
cctgctcgga ttgcacacat caccgccacc cgtcgtgcgc cgacatctgt aggtcgccag 120
ccaacaacct tagactgagg caccctgaat ccatctgcta ttgttcagct tgggtgttcgg 180
gcaatccttg ttctgcctc agcacaaata gatcgccaag atgaatagaa gttggttgaa 240
tgggtacattg ttttcccctg aatatatcaa tgggtgtcaaa gaatttatga gctttattca 300
aagaaaattc ggtgaggatg aagatatttt gtgtccatgt agtagatgtc tcaacaaaaa 360
gtcctttcat caagcctttg tggagaagca tatattaatg aatgggatgg aaagtacata 420
tactcgatgg attcatcatg gagagaactt tgaggaagat gccggtcatt cgatacatgg 480
gacaggtgtg attgatgatg acagctatgg tgatgattgt tttgatggga tgttacaaga 540
cctatgcact gcataagagc aagataaaga ggatgggtgaa aatgaggatg gagacaatac 600
taatgatgac aatgagtcatt tttatagtgt rgtgctgaaa gaggcgaaac gtcatatatta 660
tcctggttgt accaaatttt caaggttrtc ctttgtwgta aagcttcttc atatgaagtc 720
attatatagg atcactaact ctgcatktac tgcarkatww aagttgttgg ttg
(2) INFORMATION FOR SEQ ID NO:423:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1482235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Pro	Pro	Pro	Gly	Arg	Arg	Gln	Xaa	Arg	Pro	Asp	Arg	Val	Asp	Val	Asp
1				5				10					15		
Ala	Gly	Glu	Ser	Cys	Ser	Asp	Cys	Thr	His	His	Arg	His	Pro	Ser	Cys
			20					25					30		
Ala	Asp	Ile	Cys	Arg	Ser	Pro	Ala	Asn	Asn	Leu	Arg	Leu	Arg	His	Pro
		35					40					45			
Glu	Ser	Ile	Cys	Tyr	Cys	Ser	Ala	Trp	Cys	Ser	Gly	Asn	Pro	Cys	Ser
	50					55					60				
Arg	Leu	Ser	Thr	Asn	Arg	Ser	Pro	Arg							
65				70											

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1482236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met	Asn	Arg	Ser	Trp	Leu	Asn	Gly	Thr	Leu	Phe	Ser	Pro	Glu	Tyr	Ile
1			5					10					15		
Asn	Gly	Val	Lys	Glu	Phe	Met	Ser	Phe	Ile	Gln	Arg	Lys	Phe	Gly	Glu
			20					25					30		
Asp	Glu	Asp	Ile	Leu	Cys	Pro	Cys	Ser	Arg	Cys	Leu	Asn	Gln	Lys	Ser
		35					40					45			
Phe	His	Gln	Ala	Phe	Val	Glu	Lys	His	Ile	Leu	Met	Asn	Gly	Met	Glu
	50					55				60					
Ser	Thr	Tyr	Thr	Arg	Trp	Ile	His	His	Gly	Glu	Asn	Phe	Glu	Glu	Asp
65				70						75				80	
Ala	Gly	His	Ser	Ile	His	Gly	Thr	Gly	Val	Ile	Asp	Asp	Asp	Ser	Tyr
			85					90						95	
Gly	Asp	Asp	Cys	Phe	Asp	Gly	Met	Leu	Gln	Asp	Leu	Cys	Thr	Ala	
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1482237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met	Ser	Phe	Ile	Gln	Arg	Lys	Phe	Gly	Glu	Asp	Glu	Asp	Ile	Leu	Cys
1			5					10					15		

Pro Cys Ser Arg Cys Leu Asn Gln Lys Ser Phe His Gln Ala Phe Val
 20 25 30
 Glu Lys His Ile Leu Met Asn Gly Met Glu Ser Thr Tyr Thr Arg Trp
 35 40 45
 Ile His His Gly Glu Asn Phe Glu Glu Asp Ala Gly His Ser Ile His
 50 55 60
 Gly Thr Gly Val Ile Asp Asp Asp Ser Tyr Gly Asp Asp Cys Phe Asp
 65 70 75 80
 Gly Met Leu Gln Asp Leu Cys Thr Ala
 85

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

cacggcgccc gtcctctgtc gttgaaggac agggagcggc ggctagggtt tcgcggtgct	60
gtggcgcccg acgcccgtcc tctactatcc gtggcgacca tcgtcggtta tccgcggast	120
gtggcgatcg gcctgtgtc ctatccgcgg ttgccgagga aagtactatg ttgttgatgc	180
tggatatcca aatagggatg agtacttggc cccgtacaaa ggacaactgt atcatgttcc	240
ggaatggaga aatgatcctc cacctaattg ctcactcgaa ggtgaagcat gggaaagtgar	300
tcacaggtcc aacgacctcc atgaaggtaa agcacatggc ttcaagtkag tcgcaagtcc	360
aatcgagtcc atgaaggtga agcatgggag gtccaagtra atctggaaag aataacgggtg	420
gaagtaggtt gggccttata ataggggagg agtagtagaa attattttcc gcgtagtctg	480
ggttttaatt atttagataa g	

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

His Gly Ala Arg Pro Leu Ser Leu Lys Asp Arg Glu Arg Arg Leu Gly	
1 5 10 15	
Phe Arg Gly Ala Val Ala Ala Asp Ala Arg Pro Leu Leu Ser Val Ala	
20 25 30	
Thr Ile Val Gly Tyr Pro Arg Xaa Val Ala Ile Gly Leu Cys Ser Tyr	
35 40 45	
Pro Arg Leu Pro Arg Lys Val Leu Cys Cys	
50 55	

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1482240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Arg Arg Pro Ser Ser Val Val Glu Gly Gln Gly Ala Ala Ala Arg Val
1 5 10 15
Ser Arg Cys Cys Gly Gly Arg Arg Pro Ser Ser Thr Ile Arg Gly Asp
20 25 30
His Arg Arg Leu Ser Ala Xaa Cys Gly Asp Arg Pro Val Leu Leu Ser
35 40 45
Ala Val Ala Glu Glu Ser Thr Met Leu Leu Met Leu Asp Ile Gln Ile
50 55 60
Gly Met Ser Thr Trp Pro Arg Thr Lys Asp Asn Cys Ile Met Phe Arg
65 70 75 80
Asn Gly Glu Met Ile Leu His Leu Met Ala His Ser Lys Val Lys His
85 90 95
Gly Lys

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..798
(D) OTHER INFORMATION: / Ceres Seq. ID 1482245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

aaccatagaa atcctccaat tattcgattc ccaagccact aaggcccttg gaggaacaac 60
agaatccaga aaccgaaaag argcctcact gctgccgcct gggccaagtc gtcgtcttgc 120
tttgccaatc cgtcgctcca cctgaacaca ccggcggaaga ggaggcgaag aagcgatggg 180
cgtgaccaag gaggacgtcg aggcggccat cacctctgct ctcagccctt ccaatctcgt 240
ggtgacggac acgtccggag ggtgtggcgc gagctacgag atcgagggtg tgtcggagaa 300
gttcgagggg aagcggctgc tggagaggca ccgcatgggtg aacaccgcgc tggcgtctca 360
catggcggag atccacgccc tctccatcaa gaaggcgctc accccggctc aggccagcc 420
ccagggccca gccggagccg gccgccgata agccccaggc ttaagtgtt aacaccccc 480
aaaacggttt gatcccatat gccgatgcac gattacattg gctatctgct tgaataatgc 540
gggcgggatgc acttgctaaa ttgcaggatg ttatccttga ctgattagaa acttctgcac 600
cgtgcattta acttctgtgt cactgtgtgt gtgttctgga tgcctctgcc ctggtcgttt 660
gctcgagact gtgtgttgca gttcatgctg ttaatgttct gccagggtgg ggttttcagt 720
cctggaattt ttatatattga ctgttgctat gtctttcctt gctttagagg gtaagggtt 780
tattctttaa ccttgtgg

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: / Ceres Seq. ID 1482246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Thr Ile Glu Ile Leu Gln Leu Phe Asp Ser Gln Ala Thr Lys Ala Leu
1 5 10 15
Gly Gly Thr Thr Glu Ser Arg Asn Arg Lys Xaa Ala Ser Leu Leu Pro

20 25 30
Pro Gly Pro Ser Arg Arg Leu Ala Leu Pro Ile Arg Arg Ser Thr
35 40 45

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met Gly Val Thr Lys Glu Asp Val Glu Ala Ala Ile Thr Ser Ala Leu
1 5 10 15
Ser Pro Ser Asn Leu Val Val Thr Asp Thr Ser Gly Gly Cys Gly Ala
20 25 30
Ser Tyr Glu Ile Glu Val Val Ser Glu Lys Phe Glu Gly Lys Arg Leu
35 40 45
Leu Glu Arg His Arg Met Val Asn Thr Ala Leu Ala Ser His Met Ala
50 55 60
Glu Ile His Ala Val Ser Ile Lys Lys Ala Leu Thr Pro Ala Gln Ala
65 70 75 80
Gln Pro Gln Gly Pro Ala Gly Ala Gly Arg Arg
85 90

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

atgggtggtc cgcactccgc accggtaccg cacaaccccc acaccgcgag catccccatt 60
tctccgtccc aaaaccctag gctagtcccc ccacacctgg atccatcggg tcggaggcca 120
tgacgacggc gaggtccga tcctcgccct cctccgcggg ggctctcctc cgccacttct 180
ccgtgggtcc cgcctcgact ccgcgcgcgc tctcccggtt ccagatttcc caggttcctc 240
agtctattat gtggaggcat ttcgcaacgt ccaggcctaa ttctcttgca agacgcgaca 300
actttggtct gatggcctgt ttgcacgctc agatacgatg cgcttcgcag gctgctgctg 360
tgaaagaaac cgaatccagt agcagcaaga taagcatcgg gcccaaacca aaacagatca 420
aggaggatga cgaggatgct aacctggtat accaagggcc aatatcatcg accataaaga 480
aagtgaagct tctctccctg tccacctgct gcctctccgt gtcgctgggg ccagtggttaa 540
cattcatgac ttgcctgac atgaatgtga tc

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1482249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Met Thr Thr Ala Arg Leu Arg Ser Ser Ala Ser Leu Arg Gly Ala Leu
1 5 10 15
Leu Arg His Phe Ser Val Gly Pro Ala Ser Thr Pro Arg Ala Val Ser
20 25 30
Arg Val Pro Asp Phe Gln Val Pro Gln Ser Ile Met Trp Arg His Phe
35 40 45
Ala Thr Ser Arg Pro Asn Ser Leu Ala Arg Arg Asp Asn Phe Gly Leu
50 55 60
Met Ala Cys Leu His Ala Gln Ile Arg Cys Ala Ser Gln Ala Ala Ala
65 70 75 80
Val Lys Glu Thr Glu Ser Ser Ser Ser Lys Ile Ser Ile Gly Pro Lys
85 90 95
Pro Lys Gln Ile Lys Glu Asp Asp Glu Asp Ala Asn Leu Val Tyr Gln
100 105 110
Gly Pro Ile Ser Ser Thr Ile Lys Lys Val Lys Leu Leu Ser Leu Ser
115 120 125
Thr Cys Cys Leu Ser Val Ser Leu Gly Pro Val Val Thr Phe Met Thr
130 135 140
Ser Pro Asp Met Asn Val Ile
145 150

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1482250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Trp Arg His Phe Ala Thr Ser Arg Pro Asn Ser Leu Ala Arg Arg
1 5 10 15
Asp Asn Phe Gly Leu Met Ala Cys Leu His Ala Gln Ile Arg Cys Ala
20 25 30
Ser Gln Ala Ala Ala Val Lys Glu Thr Glu Ser Ser Ser Ser Lys Ile
35 40 45
Ser Ile Gly Pro Lys Pro Lys Gln Ile Lys Glu Asp Asp Glu Asp Ala
50 55 60
Asn Leu Val Tyr Gln Gly Pro Ile Ser Ser Thr Ile Lys Lys Val Lys
65 70 75 80
Leu Leu Ser Leu Ser Thr Cys Cys Leu Ser Val Ser Leu Gly Pro Val
85 90 95
Val Thr Phe Met Thr Ser Pro Asp Met Asn Val Ile
100 105

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1482251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Ala Cys Leu His Ala Gln Ile Arg Cys Ala Ser Gln Ala Ala Ala
1 5 10 15
Val Lys Glu Thr Glu Ser Ser Ser Ser Lys Ile Ser Ile Gly Pro Lys
20 25 30
Pro Lys Gln Ile Lys Glu Asp Asp Glu Asp Ala Asn Leu Val Tyr Gln
35 40 45
Gly Pro Ile Ser Ser Thr Ile Lys Lys Val Lys Leu Leu Ser Leu Ser
50 55 60
Thr Cys Cys Leu Ser Val Ser Leu Gly Pro Val Val Thr Phe Met Thr
65 70 75 80
Ser Pro Asp Met Asn Val Ile
85

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

aaggctcact gctcagtgt cactgtcac tagctaaaaa catctccttt cttatccatg 60
gaganggcag cgctcacctc ccactccctg cagcgcccag cagcagcagc agctgtctcc 120
gcgcatggcc agcngcggag ggtcggagcg gcgggcctgc ggcaccggca gccgcgcgcc 180
ggcggcagga tccggggccct gccttcggcg gaggtcatca gcgagatcct gagccccaag 240
ctggtgcccc gctcgcccg cgacaccggc gacgtctcct cgctcgctcc ggtcagtgcc 300
ctgatgtgct tcttctactt cgtgtccaac tgggtggtgc ccgagctgct cctgaagggc 360
ctcaacgagc ccaagcccga ggacgaagcg tccacgtcct tcgccgcgtc cgcnacaac 420
gccgccgccg ctggcccagc agacgacggc ggcaccggta agatccgcct caaggtcaag 480
aagaagaaga acgggaaagc gaccatcgtc aaggtctag

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Gly Ser Leu Leu Ser Ala His Cys Ser Leu Ala Lys Asn Ile Ser Phe
1 5 10 15
Leu Ile His Gly Xaa Gly Ser Ala His Leu Pro Leu Pro Ala Ala Pro
20 25 30
Ser Ser Ser Ser Ser Cys Ser Arg Ala Trp Pro Xaa Ala Glu Gly Arg
35 40 45
Ser Gly Gly Pro Ala Ala Pro Ala Ala Arg Arg Arg Gln Asp Pro
50 55 60
Gly Pro Ala Phe Gly Gly Gly His Gln Arg Asp Pro Glu Pro Gln Ala
65 70 75 80
Gly Ala Arg Leu Ala Arg Arg His Arg Arg Arg Leu Leu Ala Arg Pro
85 90 95
Gly Gln Cys Pro Asp Ala Ala Leu Leu Leu Arg Val Gln Leu Gly Gly

100 105 110
Ala Arg Ala Ala Pro Glu Gly Pro Gln Arg Ala Gln Ala Arg Gly Arg
115 120 125
Ser Val His Val Leu Arg Arg Val Arg Xaa Gln Arg Arg Arg Arg Trp
130 135 140
Pro Ser Arg Arg Arg Arg His Arg
145 150

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met Glu Xaa Ala Ala Leu Thr Ser His Ser Leu Gln Arg Pro Ala Ala
1 5 10 15
Ala Ala Ala Ala Pro Ala His Gly Gln Xaa Arg Arg Val Gly Ala Ala
20 25 30
Gly Leu Arg His Arg Gln Pro Arg Ala Gly Gly Arg Ile Arg Ala Leu
35 40 45
Pro Ser Ala Glu Val Ile Ser Glu Ile Leu Ser Pro Lys Leu Val Pro
50 55 60
Gly Ser Pro Ala Asp Thr Gly Asp Val Ser Ser Leu Val Pro Val Ser
65 70 75 80
Ala Leu Met Leu Leu Phe Tyr Phe Val Ser Asn Trp Val Val Pro Glu
85 90 95
Leu Leu Leu Lys Gly Leu Asn Glu Pro Lys Pro Glu Asp Glu Ala Ser
100 105 110
Thr Ser Phe Ala Ala Ser Ala Xaa Asn Ala Ala Ala Gly Pro Ala
115 120 125
Asp Asp Gly Gly Thr Gly Lys Ile Arg Leu Lys Val Lys Lys Lys Lys
130 135 140
Asn Gly Lys Ala Thr Ile Val Lys Val
145 150

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

artgcaagca tatrgngcgc cgtgccagcc tgctcctcgc cgcrgcgtg ctgcgtgccg 60
tcgctgccgc ggcgggtgccs cgacgtgcga gcgcacgag tgcccggcgt acgaggtggt 120
ggacagcgcc aacgggttcg agatccggcg gtacacggac gccatgtgga tcaccacggc 180
gcccacgag gacatctcct tcgtcgccgc cagcgcacc ggcttcctac agctgttcga 240
ctacatcbag ggcaagaacg cgtacaacca gacgatcg

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Xaa	Ala	Ser	Ile	Xaa	Xaa	Ala	Val	Pro	Ala	Cys	Ser	Ser	Pro	Xaa	Arg	
1				5					10					15		
Cys	Ser	Ser	Pro	Ser	Leu	Pro	Arg	Arg	Cys	Xaa	Asp	Val	Arg	Ala	His	
			20					25					30			
Arg	Val	Pro	Gly	Val	Arg	Gly	Gly	Gly	Gln	Arg	Gln	Arg	Val	Arg	Asp	
			35				40					45				
Pro	Ala	Val	His	Gly	Arg	His	Val	Asp	His	His	Gly	Ala	His	Arg	Gly	
	50					55					60					
His	Leu	Leu	Arg	Arg	Arg	His	Ala	His	Arg	Leu	Pro	Thr	Ala	Val	Arg	
65				70					75						80	
Leu	His	Xaa	Gly	Gln	Glu	Arg	Val	Gln	Pro	Asp	Asp					
			85					90								

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Xaa	Gln	Ala	Tyr	Xaa	Ala	Pro	Cys	Gln	Pro	Ala	Pro	Arg	Arg	Xaa	Ala	
1				5				10						15		
Ala	Arg	Arg	Arg	Arg	Cys	Arg	Gly	Gly	Ala	Xaa	Thr	Cys	Glu	Arg	Ile	
			20					25					30			
Glu	Cys	Pro	Ala	Tyr	Glu	Val	Val	Asp	Ser	Ala	Asn	Gly	Phe	Glu	Ile	
			35				40					45				
Arg	Arg	Tyr	Thr	Asp	Ala	Met	Trp	Ile	Thr	Thr	Ala	Pro	Ile	Glu	Asp	
	50					55					60					
Ile	Ser	Phe	Val	Ala	Ala	Thr	Arg	Thr	Gly	Phe	Leu	Gln	Leu	Phe	Asp	
65				70					75						80	
Tyr	Ile	Xaa	Gly	Lys	Asn	Ala	Tyr	Asn	Gln	Thr	Ile					
			85					90								

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..92
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Cys	Lys	His	Xaa	Xaa	Arg	Arg	Ala	Ser	Leu	Leu	Ala	Xaa	Ala	Leu	
1				5				10						15	

Leu Val Ala Val Ala Ala Ala Val Xaa Arg Arg Ala Ser Ala Ser
20 25 30
Ser Ala Arg Arg Thr Arg Trp Trp Thr Ala Pro Thr Gly Ser Arg Ser
35 40 45
Gly Gly Thr Arg Thr Pro Cys Gly Ser Pro Arg Arg Pro Ser Arg Thr
50 55 60
Ser Pro Ser Ser Pro Pro Arg Ala Pro Ala Ser Tyr Ser Cys Ser Thr
65 70 75 80
Thr Xaa Arg Ala Arg Thr Arg Thr Thr Arg Arg Ser
85 90

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

gaattcctcg ccgccgtctt cgtccaccag aaccatggcc tccgacaccg cctcggcagt 60
tccgtcgtct gtggtctcag ctgccgagga gacgctcgga tataccgaat ccgtagggac 120
catctctccc atctgctcgc ggcggcggcg gcggaccccc acgccgtggc cgagctccca 180
ccccttctcc gggcgcgcgc ttctcttgcc ttggcgcagg ccgcgacctc ccttctcgga 240
gttcgtttaa ggtgttcggg agttgacctt gacgagcacc ccatacagaaa ggagtttgaa 300
aggttaagcc taatgcagga gaagttaa atcaatttga actgggacaa agcaccactt 360
cgcccttcta ctacactaaa tacacaagca gcagcaaggt tcattggaca ctcaatttcc 420
catctgacat ctgatcagaa gaggagcatg catgaaataa gtagaggaga aaggcggagt 480
tggtctgggc agaagagaaa gcctgaacct tcagtagaaa agaagtctgt tcgtgctgct 540
gcagaagagt tccttgcaaa ggcttctcag gaacttattg gacatagtga tagcagggtc 600
aagggtcctg ttatactcat ttctgatgaa gatgaggact agatcaaaaa aatgggcgct 660
taccagatta catgcctgat tcacgcgcta ggcaaaggaa ggtagaagtt cctggtgatg 720
aagataaact tacgtacatt gctgtggtga tgaagatgaa tttatctgca ttgctgtggt 780
gttctacatg taacagggaa tggagcaaaag ctgcataggc ttgcttaagt cccagttct 840
gggagcaatt ggctcgaat cttgagtgc aattatctga gtttctttcc ggaaagaatt 900
ttgacattct atttgctagt ggaactggag c

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Glu Phe Leu Ala Ala Val Phe Val His Gln Asn His Gly Leu Arg His
1 5 10 15
Arg Leu Gly Ser Ser Val Val Cys Gly Leu Ser Cys Arg Gly Asp Ala
20 25 30
Arg Ile Tyr Arg Ile Arg Arg Asp His Leu Ser His Leu Leu Ala Ala
35 40 45
Ala Ala Ala Asp Pro Asp Ala Val Ala Glu Leu Pro Pro Leu Leu Arg
50 55 60
Ala Arg Ala Phe Leu Ala Leu Ala Gln Ala Ala Thr Ser Leu Leu Gly

65		70		75		80									
Val	Arg	Leu	Arg	Cys	Ser	Gly	Val	Asp	Pro	Asp	Glu	His	Pro	Ile	Arg
				85					90					95	
Lys	Glu	Phe	Glu	Arg	Leu	Ser	Leu	Met	Gln	Glu	Lys	Leu	Asn	Gln	Phe
			100					105					110		
Glu	Asn	Trp	Asp	Lys	Ala	Pro	Leu	Arg	Pro	Ser	Thr	Thr	Leu	Asn	Thr
		115					120						125		
Gln	Ala	Ala	Ala	Arg	Phe	Ile	Gly	His	Ser	Leu	Ser	His	Leu	Thr	Ser
	130						135					140			
Asp	Gln	Lys	Arg	Ser	Met	His	Glu	Ile	Ser	Arg	Gly	Glu	Arg	Arg	Ser
145					150					155					160
Trp	Ser	Gly	Gln	Lys	Arg	Lys	Pro	Glu	Pro	Ser	Val	Glu	Lys	Lys	Ser
				165					170					175	
Val	Arg	Ala	Ala	Ala	Glu	Glu	Phe	Leu	Ala	Lys	Ala	Ser	Gln	Glu	Leu
		180						185					190		
Ile	Gly	His	Ser	Asp	Ser	Arg	Val	Lys	Gly	Pro	Val	Ile	Leu	Ile	Ser
	195					200						205			
Asp	Glu	Asp	Glu	Asp											
210															

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met	Gln	Glu	Lys	Leu	Asn	Gln	Phe	Glu	Asn	Trp	Asp	Lys	Ala	Pro	Leu
1				5					10					15	
Arg	Pro	Ser	Thr	Thr	Leu	Asn	Thr	Gln	Ala	Ala	Ala	Arg	Phe	Ile	Gly
			20					25					30		
His	Ser	Leu	Ser	His	Leu	Thr	Ser	Asp	Gln	Lys	Arg	Ser	Met	His	Glu
		35				40						45			
Ile	Ser	Arg	Gly	Glu	Arg	Arg	Ser	Trp	Ser	Gly	Gln	Lys	Arg	Lys	Pro
	50				55					60					
Glu	Pro	Ser	Val	Glu	Lys	Lys	Ser	Val	Arg	Ala	Ala	Ala	Glu	Glu	Phe
65					70				75						80
Leu	Ala	Lys	Ala	Ser	Gln	Glu	Leu	Ile	Gly	His	Ser	Asp	Ser	Arg	Val
			85					90						95	
Lys	Gly	Pro	Val	Ile	Leu	Ile	Ser	Asp	Glu	Asp	Glu	Asp			
		100						105							

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

actgacagct	cgccgarrrg	ccgcgccgcg	ctcgaraccc	gtcgatggcg	aggcggagct	60
ggcggtcgac	gcaaccgcag	gcgccgcac	ccgggttcg	ttcgcgccca	cctccaataa	120

cctgctcgtc	tcctcatggg	attcggggct	gcgggtgtac	gatgccgacg	agggcacgct	180
caggggtcaac	gtggagtcag	aggcggcatt	cctcgactgc	tgcttcgagg	atgagtctgc	240
agcgtttgcc	tgcggtctctg	atggatctgt	gagaaggtac	gacttcact	caggttcgca	300
ggatacgggtg	gggtcccatg	aagatgcact	agcctgcatt	gagttctctt	cactgaccgg	360
tcagattatg	acaggcagcc	ttgacaagaa	gctaaagctt	tgggattcaa	aaacaagaaa	420
tgtaaagccc	agcggcacca	taaccttaaa	ttcagatgtg	gcctcaattt	ctatatgcgg	480
catttacata	ttagctgcag	ttgagagaaa	tgtttatctt	tatgacatga	ggaatctaac	540
aagaccagtt	gatgaaaaaa	gactgtcctc	tggattatca	aattcgatgc	cttcatactt	600

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1482265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Leu Thr Ala Arg Arg Xaa Ala Ala Pro Arg Ser Xaa Pro Val Asp Gly
1 5 10 15
Glu Ala Glu Leu Ala Val Asp Ala Thr Ala Gly Ala Ala Ser Arg Val
20 25 30
Arg Phe Ala Pro Thr Ser Asn Asn Leu Leu Val Ser Ser Trp Asp Ser
35 40 45
Gly Leu Arg Leu Tyr Asp Ala Asp Glu Gly Thr Leu Arg Val Asn Val
50 55 60
Glu Ser Glu Ala Ala Phe Leu Asp Cys Cys Phe Glu Asp Glu Ser Ala
65 70 75 80
Ala Phe Ala Cys Gly Ser Asp Gly Ser Val Arg Arg Tyr Asp Phe His
85 90 95
Ser Gly Ser Gln Asp Thr Val Gly Leu His Glu Asp Ala Leu Ala Cys
100 105 110
Ile Glu Phe Ser Ser Leu Thr Gly Gln Ile Met Thr Gly Ser Leu Asp
115 120 125
Lys Lys Leu Lys Leu Trp Asp Ser Lys Thr Arg Asn Val Ser Pro Ser
130 135 140
Gly Thr Ile Thr Leu Asn Ser Asp Val Ala Ser Ile Ser Ile Cys Gly
145 150 155 160
Ile Tyr Ile Leu Ala Val Glu Arg Asn Val Tyr Leu Tyr Asp Met
165 170 175
Arg Asn Leu Thr Arg Pro Val Asp Glu Lys Arg Leu Ser Ser Gly Leu
180 185 190
Ser Asn Ser Met Pro Ser Tyr
195

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```
gcgtcaccat ccatttgacg aggcgggttta tccccagca ccccaaccaa cttttccacg      60
taccaccggg tttctgtccg cgccccgcc ttcaaaagca ggtccgcacg ccggccggcg      120
agacagacga caccaccacg ccgggacggg aggcacaggt gcggtctgcg tcgagagttg      180
gtccactggc aggccggaat gaagaagtgc gcgtcggagc tggagctgga ggcgttcac      240
cgggagagcg gcgaggacgc ccgcgccgcc gccggaggta gcagtccggg gtgcggtgga      300
tcaagcgatc ccggagggag cggcgtcttc tcacccggct tcggtttcgc cgactcggac      360
accatggatg gaggcagttg gtggtacggg aacgtccgca cgccgaacc agtcatgtcg      420
caggcggcgt ccatatccgc tagccccggg ctaaccacct cagccaatca tgctcttgaa      480
agcgagtcag actccgacag cgaatcactg tatgag
```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```
Arg His His Pro Phe Asp Glu Ala Val Tyr Pro Pro Ala Pro Gln Pro
1          5          10          15
Thr Phe Pro Arg Thr Thr Gly Phe Leu Ser Ala Pro Arg Pro Ser Lys
          20          25          30
Ala Gly Pro His Ala Gly Arg Arg Asp Arg Arg His His Ala Gly
          35          40          45
Thr Gly Gly Thr Gly Ala Val Cys Val Glu Ser Trp Ser Thr Gly Arg
50          55          60
Pro Glu
65
```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```
Val Thr Ile His Leu Thr Arg Arg Phe Ile Pro Gln His Pro Asn Gln
1          5          10          15
Pro Phe His Val Pro Pro Gly Phe Cys Pro Arg Pro Ala Leu Gln Lys
          20          25          30
Gln Val Arg Thr Pro Ala Gly Glu Thr Asp Asp Thr Thr Thr Pro Gly
          35          40          45
Arg Glu Ala Gln Val Arg Ser Ala Ser Arg Val Gly Pro Leu Ala Gly
50          55          60
Arg Asn Glu Glu Val Arg Val Gly Ala Gly Ala Gly Gly Val His Pro
65          70          75          80
Gly Glu Arg Arg Gly Arg Pro Arg Arg Arg Arg Arg
          85          90
```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```
Met Lys Lys Cys Ala Ser Glu Leu Glu Leu Glu Ala Phe Ile Arg Glu
1          5          10          15
Ser Gly Glu Asp Ala Arg Ala Ala Ala Gly Gly Ser Ser Pro Gly Cys
          20          25          30
Gly Gly Ser Ser Asp Pro Gly Gly Ser Gly Val Phe Ser Pro Gly Phe
          35          40          45
Gly Phe Ala Asp Ser Asp Thr Met Asp Gly Gly Ser Trp Trp Tyr Gly
          50          55          60
Asn Val Arg Thr Pro Asn Pro Val Met Ser Gln Ala Ala Ser Ile Ser
65          70          75          80
Ala Ser Pro Gly Leu Thr Thr Ser Ala Asn His Ala Leu Glu Ser Glu
          85          90          95
Ser Asp Ser Asp Ser Glu Ser Leu Tyr Glu
          100          105
```

- (2) INFORMATION FOR SEQ ID NO:452:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..561
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482274

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```
aagatggaca ggctctgtcg ccaactgctac accagtagac cctgcacgcg ctgcgggcgt      60
ttccgccggc tttgtgcctc ctctgccctc cccggggcgt cgccctccgt ccacgctcaa      120
gctcgctccg tcccggcgcc tcgaactcgt cgctcctcgt tccgctgtcg ccaccgcgaa      180
gcatgaggag gcgtcctggg atcactggct tgcagaatgt ggcggtact ctcgaactat      240
cagaaccagt tgggactggt cggggacaat atggccaagg tcgggaccga tgtcatgaag      300
aagcagcgac ttgggatggt ccgatcacag ctcgagaaat ttgcttgcaa gcataagggt      360
ttgagcaggt ttggtgcaat ctgattttga acctgctatg gacatcttcc actcaagttc      420
ttgtcaatgg agtgccctga cagcctataa atctcaagcg tgggttgcaa caagctgctc      480
tgaaacatcc attttctctg kgccatcaat ggatgcttag cacagatcgc ttccacatat      540
cacatgatca atcagtactg g
```

- (2) INFORMATION FOR SEQ ID NO:453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..61
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482275
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```
Lys Met Asp Arg Leu Cys Arg His Cys Tyr Thr Ser Thr Pro Cys Thr
1          5          10          15
Arg Cys Gly Arg Phe Arg Arg Leu Cys Ala Ser Ser Ala Leu Pro Gly
```

	20		25		30										
Arg	Ser	Pro	Ser	Val	His	Ala	Gln	Ala	Arg	Ser	Val	Pro	Ala	Pro	Arg
	35						40						45		
Thr	Arg	Arg	Pro	Arg	Phe	Arg	Cys	Arg	His	Arg	Glu	Ala			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1482276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Arg	Trp	Thr	Gly	Ser	Val	Ala	Thr	Ala	Thr	Pro	Val	His	Pro	Ala	Arg
1			5						10					15	
Ala	Ala	Gly	Val	Ser	Ala	Gly	Phe	Val	Pro	Pro	Leu	Pro	Ser	Pro	Gly
		20					25					30			
Ala	Arg	Pro	Pro	Ser	Thr	Leu	Lys	Leu	Ala	Pro	Ser	Arg	Arg	Leu	Glu
	35					40					45				
Leu	Val	Val	Leu	Ala	Ser	Ala	Val	Ala	Thr	Ala	Lys	His	Glu	Glu	Ala
	50				55						60				
Ser	Trp	Asp	His	Trp	Leu	Ala	Glu	Cys	Gly	Gly	Tyr	Ser	Arg	Thr	Ile
65					70					75					80
Arg	Thr	Ser	Trp	Asp	Trp	Ser	Gly	Thr	Ile	Trp	Pro	Arg	Ser	Gly	Pro
			85					90						95	

Met Ser

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1482277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Asp	Gly	Gln	Ala	Leu	Ser	Pro	Leu	Leu	His	Gln	Tyr	Thr	Leu	His	Ala
1				5					10					15	
Leu	Arg	Ala	Phe	Pro	Pro	Ala	Leu	Cys	Leu	Leu	Cys	Pro	Pro	Arg	Ala
		20					25					30			
Leu	Ala	Leu	Arg	Pro	Arg	Ser	Ser	Ser	Leu	Arg	Pro	Gly	Ala	Ser	Asn
	35					40						45			
Ser	Ser	Ser	Ser	Leu	Pro	Leu	Ser	Pro	Pro	Arg	Ser	Met	Arg	Arg	Arg
	50					55					60				
Pro	Gly	Ile	Thr	Gly	Leu	Gln	Asn	Val	Ala	Ala	Thr	Leu	Glu	Leu	Ser
65					70					75					80
Glu	Pro	Val	Gly	Thr	Gly	Arg	Gly	Gln	Tyr	Gly	Gln	Gly	Arg	Asp	Arg
			85					90						95	
Cys	His	Glu	Glu	Ala	Ala	Thr	Trp	Asp	Gly	Pro	Ile	Thr	Ala	Arg	Glu
			100					105						110	

Ile Cys Leu Gln Ala
115

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..578
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

acctcggctc	gggcgcagag	cgcgcggcgc	cggcgcgtcc	tctcctcctg	ctccgatctc	60
tctgcccagc	ccgcctgtg	cgcttcgcta	ctacgcttcc	tccatgcata	ccctcagcca	120
tgtacgcctg	tatttgggaa	gacattagcg	gagttgaatc	cagaagaaga	gccgaagagt	180
tatcttagcc	acagccaggt	cgcccgttag	ttgttcgcgg	aaatgtccct	ccgccagctg	240
cttcacaaa	cgcgctcgtg	gcgcgcgctt	gagcagccca	cgaagatgtc	ttgtctcctc	300
tccatcttcc	gtgcgtcttc	cattctccgt	tctgaaggct	cggctgagcc	actgcgccga	360
tcttcattctg	tgccagcccc	gctgccaa	agcttgccct	gctccagctc	tgacccccctt	420
ggccccagat	tcagcatcga	cgtggctgac	tcggaccatt	ggccctcgtc	atttgacttg	480
ktgtccgacg	ctgcacggag	caatgaatgc	ccagatgtct	ncgagcaaca	tgaggatgat	540
gaactgcmcg	actcttatga	tgagatagat	gacatgag			

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Thr	Ser	Ala	Arg	Gln	Ser	Ala	Arg	Arg	Arg	Val	Leu	Ser	Ser
1				5				10				15	
Cys	Ser	Asp	Leu	Ser	Ala	Gln	Pro	Arg	Leu	Cys	Ala	Ser	Leu
			20					25				30	Leu
Phe	Leu	His	Ala	Ser	Pro	Gln	Pro	Cys	Thr	Pro	Val	Phe	Gly
			35				40					45	Lys
Leu	Ala	Glu	Leu	Asn	Pro	Glu	Glu	Pro	Lys	Ser	Tyr	Leu	Ser
			50			55				60			His
Ser	Gln	Val	Ala	Arg									
65													

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met	Ser	Leu	Arg	Gln	Leu	Leu	His	Gln	Thr	Arg	Pro	Trp	Arg	Ala	Leu
1				5				10						15	
Glu	Gln	Pro	Thr	Lys	Met	Ser	Cys	Leu	Leu	Ser	Ile	Phe	Arg	Ala	Leu

20 25 30
Ser Ile Leu Arg Ser Glu Gly Ser Ala Glu Pro Leu Arg Arg Ser Ser
35 40 45
Ser Val Pro Ala Pro Leu Pro Arg Ser Leu Pro Cys Ser Ser Ser Asp
50 55 60
Pro Leu Gly Pro Arg Phe Ser Ile Asp Val Val Asp Ser Asp His Trp
65 70 75 80
Pro Ser Ser Phe Asp Leu Xaa Ser Asp Ala Arg Ser Asn Glu Cys
85 90 95
Pro Asp Val Xaa Glu Gln His Glu Asp Asp Glu Leu Xaa Asp Ser Tyr
100 105 110
Asp Glu Ile Asp Asp Met
115

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met Ser Cys Leu Leu Ser Ile Phe Arg Ala Leu Ser Ile Leu Arg Ser
1 5 10 15
Glu Gly Ser Ala Glu Pro Leu Arg Arg Ser Ser Ser Val Pro Ala Pro
20 25 30
Leu Pro Arg Ser Leu Pro Cys Ser Ser Ser Asp Pro Leu Gly Pro Arg
35 40 45
Phe Ser Ile Asp Val Val Asp Ser Asp His Trp Pro Ser Ser Phe Asp
50 55 60
Leu Xaa Ser Asp Ala Ala Arg Ser Asn Glu Cys Pro Asp Val Xaa Glu
65 70 75 80
Gln His Glu Asp Asp Glu Leu Xaa Asp Ser Tyr Asp Glu Ile Asp Asp
85 90 95
Met

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..881
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

tctctctttt ttccccagca atgcaattcc gcagacagac gcaggcggca rgcggcaggc 60
ggcggcgcac cgcaccgctt cttcctcttc tatctctcat ctacagcctt cgctgcgccg 120
ccatggccac caccgcttg ctgccgtgc tccgacgccg cctcgccgcc gcaatcgccg 180
gatcgccctgc tccctactcc ctccgaggac cctcatttcc tgcaccagca gctgcagggc 240
taaggctccct cctaacagtt gctggagcga gcgatactgc aacagaaccc caggaccaac 300
agcattccga aacaactccc ccgccggctt ctgtcccgcac accggagtcc ggtctcaaag 360
tcagggacac ctccaacctg aagatctcac caaggcatga cctcgccatg atctttacgt 420
gcaagggtgtg cgagaccagg tccatgaaga tggccagcag ggactcgtac gagaacggag 480

tcgtggtcgt gcgggtgcgggt ggctgcaaca acctccacct catggcggac aggcttggct 540
ggtttgggga gccagggagc atcgaggact tcctagcgac gcaaggggag gaggtgaaga 600
aaggttcgac agatactatc agctttactt tggacgactt ggctgggtct caggtcagtt 660
ctaaggggcc ttccgaacaa aattaatatg atagtgtttg gtccagtaag aacctgtaga 720
agcctctctt tactataaag aagatgcgcg tgtcacctgt gtgttgaaga aaaaaacgcc 780
tctagaagcc taccttaact gttgcacctg tagttctgct taacttcatg gcttttcatg 840
tgtagctttc gagcccatca aatatgcgat gttgttatc t

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Ser Leu Ser Ser Pro Ala Met Gln Phe Arg Arg Gln Thr Gln Ala Ala
1 5 10 15
Xaa Gly Arg Arg Arg Arg Thr Ala Pro Leu Leu Pro Leu Leu Ser Leu
20 25 30
Ile Tyr Ser Leu Arg Cys Ala Ala Met Ala Thr Thr Arg Leu Leu Pro
35 40 45
Leu Leu Arg Arg Arg Leu Ala Ala Ala Ile Ala Gly Ser Pro Ala Pro
50 55 60
Tyr Ser Leu Arg Gly Pro Ser Phe Pro Ala Pro Ala Ala Ala Gly Leu
65 70 75 80
Arg Ser Leu Leu Thr Val Ala Gly Ala Ser Asp Thr Ala Thr Glu Pro
85 90 95
Gln Asp Gln Gln His Ser Glu Thr Thr Pro Pro Pro Ala Ser Val Pro
100 105 110
Thr Pro Glu Ser Gly Leu Lys Val Arg Asp Thr Ser Asn Leu Lys Ile
115 120 125
Ser Pro Arg His Asp Leu Ala Met Ile Phe Thr Cys Lys Val Cys Glu
130 135 140
Thr Arg Ser Met Lys Met Ala Ser Arg Asp Ser Tyr Glu Asn Gly Val
145 150 155 160
Val Val Val Arg Cys Gly Gly Cys Asn Asn Leu His Leu Met Ala Asp
165 170 175
Arg Leu Gly Trp Phe Gly Glu Pro Gly Ser Ile Glu Asp Phe Leu Ala
180 185 190
Thr Gln Gly Glu Glu Val Lys Lys Gly Ser Thr Asp Thr Ile Ser Phe
195 200 205
Thr Leu Asp Asp Leu Ala Gly Ser Gln Val Ser Ser Lys Gly Pro Ser
210 215 220
Glu Gln Asn
225

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1482291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Gln Phe Arg Arg Gln Thr Gln Ala Ala Xaa Gly Arg Arg Arg Arg
1 5 10 15
Thr Ala Pro Leu Leu Pro Leu Leu Ser Leu Ile Tyr Ser Leu Arg Cys
20 25 30
Ala Ala Met Ala Thr Thr Arg Leu Leu Pro Leu Leu Arg Arg Arg Leu
35 40 45
Ala Ala Ala Ile Ala Gly Ser Pro Ala Pro Tyr Ser Leu Arg Gly Pro
50 55 60
Ser Phe Pro Ala Pro Ala Ala Ala Gly Leu Arg Ser Leu Leu Thr Val
65 70 75 80
Ala Gly Ala Ser Asp Thr Ala Thr Glu Pro Gln Asp Gln Gln His Ser
85 90 95
Glu Thr Thr Pro Pro Pro Ala Ser Val Pro Thr Pro Glu Ser Gly Leu
100 105 110
Lys Val Arg Asp Thr Ser Asn Leu Lys Ile Ser Pro Arg His Asp Leu
115 120 125
Ala Met Ile Phe Thr Cys Lys Val Cys Glu Thr Arg Ser Met Lys Met
130 135 140
Ala Ser Arg Asp Ser Tyr Glu Asn Gly Val Val Val Val Arg Cys Gly
145 150 155 160
Gly Cys Asn Asn Leu His Leu Met Ala Asp Arg Leu Gly Trp Phe Gly
165 170 175
Glu Pro Gly Ser Ile Glu Asp Phe Leu Ala Thr Gln Gly Glu Glu Val
180 185 190
Lys Lys Gly Ser Thr Asp Thr Ile Ser Phe Thr Leu Asp Asp Leu Ala
195 200 205
Gly Ser Gln Val Ser Ser Lys Gly Pro Ser Glu Gln Asn
210 215 220

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1482292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met Ala Thr Thr Arg Leu Leu Pro Leu Leu Arg Arg Arg Leu Ala Ala
1 5 10 15
Ala Ile Ala Gly Ser Pro Ala Pro Tyr Ser Leu Arg Gly Pro Ser Phe
20 25 30
Pro Ala Pro Ala Ala Ala Gly Leu Arg Ser Leu Leu Thr Val Ala Gly
35 40 45
Ala Ser Asp Thr Ala Thr Glu Pro Gln Asp Gln Gln His Ser Glu Thr
50 55 60
Thr Pro Pro Pro Ala Ser Val Pro Thr Pro Glu Ser Gly Leu Lys Val
65 70 75 80
Arg Asp Thr Ser Asn Leu Lys Ile Ser Pro Arg His Asp Leu Ala Met
85 90 95
Ile Phe Thr Cys Lys Val Cys Glu Thr Arg Ser Met Lys Met Ala Ser
100 105 110
Arg Asp Ser Tyr Glu Asn Gly Val Val Val Val Arg Cys Gly Gly Cys
115 120 125
Asn Asn Leu His Leu Met Ala Asp Arg Leu Gly Trp Phe Gly Glu Pro

130 135 140
Gly Ser Ile Glu Asp Phe Leu Ala Thr Gln Gly Glu Glu Val Lys Lys
145 150 155 160
Gly Ser Thr Asp Thr Ile Ser Phe Thr Leu Asp Asp Leu Ala Gly Ser
165 170 175
Gln Val Ser Ser Lys Gly Pro Ser Glu Gln Asn
180 185

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..671
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

gctctttccc ccttgcccc ttccagttc ccactctgag cactctcctc cgctctgctc 60
ctttgctccc cacggcaaac cgtaaaccct agcctgaggg gcacccctgt cgcagccatg 120
ggcgccascg gaagctgcag ggcgagatcg accgcgtcct gaagaaggtc caggagggcg 180
tcgatgtctt tgacagcatc tgggaataagg tctacgacac tgagaatgcc aaccagaagg 240
agaagttcga ggcgacacac aagaaggaga tcaagaagct gcagcggnnta cagggaccag 300
atcaagacgt ggattcagtc cagcgagatc aaggacaaga aggctctgat ggatgctcga 360
aagcagattg aacgagagat ggaacgattt aaagtatgtg agaaggaaac aaaaactaag 420
gcatttctcaa aagaagggtt aggtcagcaa ccaaaaacag atcccaaaga aaaggccaaa 480
gctgaaacaa gagactggct taataatgtg gtgtgttgga atcctgaatt gctactctta 540
tgctcttatg ttttcatatc tgttttttgg tatactaact gaaccacact gttaaactcg 600
aacatatgta tactattttg ttgagaata ccttgatctt ttaattcatt tccgaggaca 660
tggtttgtgt c

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met Ser Leu Thr Ala Ser Gly Ile Arg Ser Thr Thr Leu Arg Met Pro
1 5 10 15
Thr Arg Arg Arg Ser Ser Arg Arg Thr Ser Arg Arg Arg Ser Arg Ser
20 25 30
Cys Ser Xaa Tyr Arg Asp Gln Ile Lys Thr Trp Ile Gln Ser Ser Glu
35 40 45
Ile Lys Asp Lys Lys Ala Leu Met Asp Ala Arg Lys Gln Ile Glu Arg
50 55 60
Glu Met Glu Arg Phe Lys Val Cys Glu Lys Glu Thr Lys Thr Lys Ala
65 70 75 80
Phe Ser Lys Glu Gly Leu Gly Gln Gln Pro Lys Thr Asp Pro Lys Glu
85 90 95
Lys Ala Lys Ala Glu Thr Arg Asp Trp Leu Asn Asn Val Val Cys Trp
100 105 110
Asn Pro Glu Leu Leu Leu Leu Cys Ser Tyr Val Phe Ile Ser Val Phe
115 120 125

Trp Tyr Thr Asn
130

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```
Met Pro Thr Arg Arg Arg Ser Ser Arg Thr Ser Arg Arg Arg Ser
1      5      10      15
Arg Ser Cys Ser Xaa Tyr Arg Asp Gln Ile Lys Thr Trp Ile Gln Ser
      20      25      30
Ser Glu Ile Lys Asp Lys Lys Ala Leu Met Asp Ala Arg Lys Gln Ile
      35      40      45
Glu Arg Glu Met Glu Arg Phe Lys Val Cys Glu Lys Glu Thr Lys Thr
      50      55      60
Lys Ala Phe Ser Lys Glu Gly Leu Gly Gln Gln Pro Lys Thr Asp Pro
65      70      75      80
Lys Glu Lys Ala Lys Ala Glu Thr Arg Asp Trp Leu Asn Asn Val Val
      85      90      95
Cys Trp Asn Pro Glu Leu Leu Leu Leu Cys Ser Tyr Val Phe Ile Ser
      100      105      110
Val Phe Trp Tyr Thr Asn
115
```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```
Met Asp Ala Arg Lys Gln Ile Glu Arg Glu Met Glu Arg Phe Lys Val
1      5      10      15
Cys Glu Lys Glu Thr Lys Thr Lys Ala Phe Ser Lys Glu Gly Leu Gly
      20      25      30
Gln Gln Pro Lys Thr Asp Pro Lys Glu Lys Ala Lys Ala Glu Thr Arg
      35      40      45
Asp Trp Leu Asn Asn Val Val Cys Trp Asn Pro Glu Leu Leu Leu Leu
50      55      60
Cys Ser Tyr Val Phe Ile Ser Val Phe Trp Tyr Thr Asn
65      70      75
```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..868

(D) OTHER INFORMATION: / Ceres Seq. ID 1482297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

gtccatgcat	gggcatggaa	tggatggatg	tgaatgccac	gaacgattcc	gccccgccgg	60
ccaggtgaga	gatgagcctc	acggcggcct	tccgtgccac	caaaatcccg	cgcgtctctc	120
ctccaaagtg	cggtgagcct	gccgcctcct	cttcggcctc	ggcgtccggg	gatccgccgc	180
cggggggccgt	gaagagtact	aaggcgccgc	cgcgtgggtg	cgtgtacctt	atagcctcat	240
cccggatccg	ccgcacgtac	gtcggcgcta	ccaccgattt	ccctcgccgg	ctgcggcaac	300
ataatggtga	gttaaaagggt	ggtgcaaaag	cttcctctgc	cggcaggcct	tggaaatctcg	360
catgccttgt	tgaaggattt	gccaacagaa	gtgaagcctg	tgagtttgaa	tcgaaatgga	420
agatcgtctc	ccgaaaaatt	gcacggaaaa	gaactgagct	tagcatgaag	tcagtgtctg	480
aacatcgaga	agcagctttg	agcagagtgg	aaacattcat	ggattgtagc	cacctaaaaa	540
tcaaattggca	gtcaagttga	gaccatttaa	tcacttgcac	tatgcagggtg	gcaggcatct	600
aacttgagga	aacatcacca	cttaagaatc	ctcctgtctt	ctagcagctc	gtagcaaaaga	660
taacttataa	tcttctgctg	aaccatcaag	atggctgctg	ctatgctttc	ttaacatgaa	720
aaaccaagag	tagccccagt	ggaattctat	gtttgatttt	tttttctatg	aacaattggt	780
tccgaacaat	aatatggatc	atgcgacacc	cgtttgtaaa	tgtaaattat	acttatgtat	840
tgtaatcacc	tatatttctt	ctcattct				

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1482298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Met	Ser	Leu	Thr	Ala	Ala	Phe	Arg	Ala	Thr	Lys	Ile	Pro	Arg	Ala	Leu	
1				5					10					15		
Pro	Pro	Lys	Cys	Gly	Glu	Pro	Ala	Ala	Ser	Ser	Ser	Ala	Ser	Ala	Ser	
			20					25					30			
Gly	Asp	Pro	Pro	Pro	Gly	Ala	Val	Lys	Ser	Thr	Lys	Ala	Pro	Pro	Pro	
			35				40					45				
Trp	Cys	Val	Tyr	Leu	Ile	Ala	Ser	Ser	Arg	Ile	Arg	Arg	Thr	Tyr	Val	
			50			55				60						
Gly	Val	Thr	Thr	Asp	Phe	Pro	Arg	Arg	Leu	Arg	Gln	His	Asn	Gly	Glu	
65				70					75					80		
Leu	Lys	Gly	Gly	Ala	Lys	Ala	Ser	Ser	Ala	Gly	Arg	Pro	Trp	Asn	Leu	
			85					90						95		
Ala	Cys	Leu	Val	Glu	Gly	Phe	Ala	Asn	Arg	Ser	Glu	Ala	Cys	Glu	Phe	
			100				105						110			
Glu	Ser	Lys	Trp	Lys	Ile	Val	Ser	Arg	Lys	Ile	Ala	Arg	Lys	Arg	Thr	
			115			120					125					
Glu	Leu	Ser	Met	Lys	Ser	Val	Leu	Gln	His	Arg	Glu	Ala	Ala	Leu	Ser	
			130			135				140						
Arg	Val	Glu	Thr	Phe	Met	Asp	Cys	Ser	His	Leu	Lys	Ile	Lys	Trp	Gln	
145				150						155				160		
Ser	Ser															

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 642 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..642

(D) OTHER INFORMATION: / Ceres Seq. ID 1482299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

aaatttttct	ccagccgccg	cgctcctgat	ccttatctct	gcgcgcgctg	catcggcgcc	60
cgccgggagg	gagtcgccgc	cgctcgtcc	atgttggtgg	tccgcaatat	ccgccgcttc	120
gtcgacacgg	gcgcggcctt	cggatccgag	gccatcatgg	aactggagac	taaaaggata	180
ttgcttgaga	ttttcaagga	gcggcagcgn	gaagagtgcc	gaggctggtt	ccatcccaag	240
tttttacaag	aaacctgaag	aaggatccat	tagctctaga	gttcaaaggt	tggccaagta	300
caggtttcta	aagaaacaat	cagagcttct	gctgaatgct	gatgatcttg	atgccatgtg	360
ggtttgcttc	agagaaaatt	gtgttattga	tgatgctact	ggtgctgaaa	agatgaatta	420
tgaagatttc	tgccatatcg	ccacagtctg	cactgagtag	attggtcaga	aatgcaaacg	480
atttttcagc	ccttcaaact	tcatgaagtc	tgcacggagc	acttgcacag	attgtttggc	540
taattacaag	attatctcag	tgttttggtt	tgaatttaga	gtatacttat	gtatgaaata	600
ttgattggta	ctcatttata	ttatattaat	tatatatta	tt		

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1482300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Lys	Phe	Phe	Ser	Ser	Arg	Arg	Ala	Pro	Asp	Pro	Tyr	Leu	Cys	Ala	Arg	
1			5					10						15		
Cys	Ile	Gly	Ala	Arg	Arg	Glu	Gly	Val	Pro	Pro	Ala	Ser	Ser	Met	Leu	
			20					25						30		
Trp	Val	Arg	Asn	Ile	Arg	Arg	Phe	Val	Asp	Thr	Gly	Ala	Gly	Leu	Gly	
			35				40					45				
Ser	Glu	Ala	Ile	Met	Glu	Leu	Glu	Thr	Lys	Arg	Ile	Leu	Leu	Glu	Ile	
			50			55					60					
Phe	Lys	Glu	Arg	Gln	Xaa	Glu	Glu	Cys	Arg	Gly	Trp	Phe	His	Pro	Lys	
65				70					75						80	
Phe	Leu	Gln	Glu	Thr												
				85												

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1482301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Asn	Phe	Ser	Pro	Ala	Ala	Ala	Leu	Leu	Ile	Leu	Ile	Ser	Ala	Arg	Ala	
1			5						10					15		
Ala	Ser	Ala	Pro	Ala	Gly	Arg	Glu	Ser	Arg	Pro	Pro	Arg	Pro	Cys	Cys	
			20					25						30		
Gly	Ser	Ala	Ile	Ser	Ala	Ala	Ser	Ser	Thr	Arg	Ala	Pro	Ala	Ser	Asp	

35	40	45
Pro Arg Pro Ser Trp Asn Trp Arg Leu Lys Gly Tyr Cys Leu Arg Phe		
50	55	60
Ser Arg Ser Gly Ser Xaa Lys Ser Ala Glu Ala Gly Ser Ile Pro Ser		
65	70	75
Phe Tyr Lys Lys Pro Glu Glu Gly Ser Ile Ser Ser Arg Val Gln Arg		80
	85	90
Leu Ala Lys Tyr Arg Phe Leu Lys Lys Gln Ser Glu Leu Leu Leu Asn		95
	100	105
Ala Asp Asp Leu Asp Ala Met Trp Val Cys Leu Arg Glu Asn Cys Val		110
	115	120
Ile Asp Asp Ala Thr Gly Ala Glu Lys Met Asn Tyr Glu Asp Phe Cys		125
	130	135
His Ile Ala Thr Val Cys Thr Glu		140
145	150	

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..607
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

aagttcgatg	gaatagctgg	atccgtgacc	gtgcaaccac	ctcaaccgca	tttcaggggc	60
aaggtcttca	tcccgaatcc	tgcgcctcgt	ctcccatctc	gtgccctaca	taaaatccag	120
acgccccgct	ttaccccgtt	cacgacggct	ccgcgcttg	ggctgttgaa	gccgcctcca	180
gtggtgggcg	aggtgccgga	tgtgcgttg	tcagtctgcg	gccgccactg	tctccacact	240
ggtgtcgtgc	ttggtttggt	gacattgaag	attatctctg	gggcacgacg	atgtcgttca	300
tcgctgctgc	agcttggttg	cctccgatgg	ctgcttggtc	agcgccgggg	cctcacgcct	360
cgggacaact	tgcgcgtcgt	catcatccaa	ctccattccc	gtcgcagtca	cgcgtgaggt	420
cacgtgtaat	ttgaagatca	ttctcgtacc	tggaaatctaa	agtcccagg	caagaacagg	480
taccacagga	tgagggggcat	ggaggtggct	gcgatgtgtt	cgtgagargt	ctaggtcgtc	540
gtctcccaagt	caactttggg	ttgctggatc	gttgtctcct	tacgatgtat	ttatttat	600
yatatag						

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Lys Phe Asp Gly Ile Ala Gly Ser Val Thr Val Gln Pro Pro Gln Pro		
1	5	10
His Phe Arg Gly Lys Val Phe Ile Pro Asn Pro Arg Pro Arg Leu Pro		15
	20	25
Ser Arg Ala Leu His Lys Ile Gln Thr Pro Arg Phe Thr Pro Phe Thr		30
	35	40
Thr Ala Pro Arg Leu Gly Leu Leu Lys Pro Pro Pro Val Leu Gly Glu		45
	50	55
Val Pro Asp Val Arg Trp Ser Val Cys Gly Arg His Cys Leu His Thr		60

65 70 75 80
Gly Val Val Leu Gly Leu Val Thr Leu Lys Ile Ile Ser Gly Ala Arg
85 90 95
Arg Cys Arg Ser Ser Leu Leu Gln Leu Gly Cys Leu Arg Trp Leu Leu
100 105 110
Val Lys Arg Arg Gly Leu Thr Pro Arg Asp Asn Leu Arg Val Val Ile
115 120 125
Ile Gln Leu His Ser Arg Arg Ser His Ala
130 135

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..546
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

aaaccctagc cattttcttt tcttatcccc agccgccaca aagacagccg gccgcctggg 60
aacttttttt tcttttcttc ttcctggccg accgcacctc ccacttctct ctattttttt 120
tccttgacc atggcttggc aaacggatct aggctggctt cctctctttc tgttcttctc 180
ctgctctgtt ctttgcttct ttcttcccca ccgaacagct caaaccggtg agctagccgc 240
tgcctgagcg cgcagcsggc tcacatatcc gaggatgacc ggattaatgt tcaggggcat 300
gcgggtttta ccgccggtgt gcgcgtcccc tcggtagggc gcgccgccgt cggtaaaccg 360
ccgacagatg tccctgttga cagcagagaa aaggggtcga cctcttggtc gacttctgtg 420
actgtgcacg cccagatctt atctccctta cctctttgac tcgatctcgt tctctgtgat 480
gtatgagatg gatctaattg aatattcggg atcgagttat gagttgatag aacgtagatt 540
ttctgc

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Asn Pro Ser His Phe Leu Phe Leu Ser Pro Ala Ala Thr Lys Thr Ala
1 5 10 15
Gly Arg Leu Gly Thr Phe Phe Ser Phe Leu Leu Pro Gly Arg Pro His
20 25 30
Leu Pro Leu Leu Ser Ile Phe Phe Pro Cys Thr Met Ala Trp Gln Thr
35 40 45
Asp Leu Gly Trp Leu Pro Leu Phe Leu Phe Phe Ser Cys Ser Val Leu
50 55 60
Cys Phe Phe Leu Pro His Arg Thr Ala Gln Thr Gly Glu Leu Ala Ala
65 70 75 80
Ala

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..49
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```
Thr Leu Ala Ile Phe Phe Ser Tyr Pro Gln Pro Pro Gln Arg Gln Pro
1           5           10           15
Ala Ala Trp Glu Leu Phe Phe Leu Phe Phe Phe Leu Ala Asp Arg Thr
          20           25           30
Ser His Phe Ser Leu Phe Phe Phe Leu Ala Pro Trp Leu Gly Lys Arg
        35           40           45
Ile
```

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 742 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..742
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482322
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```
atttgctcac cagccccagc accgcagcta gtccattgca ttgacgcctc gatcagggct      60
agcgacggac gaaagaaagc tctgcatgca gcgcctcgcc gccgccgtcg tccccagcct      120
ggtgccgccg ctctacctgt ccatggccgc ctccgccgct gccggctggt ttccagcaga      180
agcagccggc agtagtagcc ggacgacgac gtcgacgccg acgccgacgc ggcggccatt      240
attagcgcas cgccgtggcg ggtggtgcta ctgacgtccc tgctgctggc gccgagctgc      300
tgccaggcga cgcgagggcat gcagccgttc aggggcaagc cgctgcggcc aggcaccgcc      360
aaccatttcc tggggttctt gccgcgggga ccggcgccctc cgtccggccc ctgcggcag      420
cacaactcca tcggagcgca ggcataaagc catccctgac ggcgaccgca ggactgaagc      480
gtggaagaag cagggccgcc gtcgtgtcga tgctcgatc cgaggagtaa gatctccacc      540
aatcaagag agttcgcata accatggatt aggttccttg tcaaaagggtt aagctcgtag      600
tattgattat ttagctagtt tcgtagcact agcagcaata gatgtatact cggagagggga      660
acgaagaaaa ggcacgttct ttgtaggacg atgtacatga ggctatatatt tttttgttgg      720
ggatgggtgt ggtggcgtct cg
```

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..64
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482323
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```
Ile Cys Ser Pro Arg Pro Ala Pro Gln Leu Val His Cys Ile Asp Ala
1           5           10           15
Ser Ile Arg Ala Ser Asp Gly Arg Lys Lys Ala Leu His Ala Ala Pro
          20           25           30
Arg Arg Arg Arg Arg Pro Gln Pro Gly Ala Ala Ala Leu Pro Val His
        35           40           45
```

Gly Arg Leu Arg Arg Cys Arg Leu Phe Ser Ser Arg Ser Ser Arg Gln
50 55 60

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1482324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Met Gln Arg Leu Ala Ala Val Val Pro Ser Leu Val Pro Pro Leu
1 5 10 15
Tyr Leu Ser Met Ala Ala Ser Ala Ala Ala Gly Cys Phe Pro Ala Glu
20 25 30
Ala Ala Gly Ser Ser Ser Arg Thr Thr Thr Ser Thr Pro Thr Pro Thr
35 40 45
Arg Arg Pro Leu Leu Ala Xaa Arg Arg Gly Gly Trp Cys Tyr
50 55 60

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1482325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Met Gln Pro Phe Arg Gly Lys Pro Leu Arg Pro Gly Thr Ala Asn His
1 5 10 15
Phe Leu Gly Phe Leu Pro Arg Gly Pro Ala Pro Pro Ser Gly Pro Ser
20 25 30
Arg Gln His Asn Ser Ile Gly Ala Gln Asp Gln Ser His Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1482334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

acgacccaca cgcgtgccgc caccgctgcc gacgtakbca cggccgctcc cggacccaca	60
cctcgacta tgtsscccc accgcgcgcg cctcccctct agatcctcaa tgcactgcta	120
ggtcccgtcc acagccgctc actgcgcgca cctctaacgc gcctaggacc atcgccacct	180
ccacatctag cttctggagt cgagatccat ggctcactcc cctggaggag cccgcatctg	240
gcctaccggg caggtctcgc agcttttaggc gtctcagcag gcagcgcggt gtactccgtc	300

atcgcccaat ggagcagccg accaagcaag aactctatcc gtgctcgtgc cgaggcgctg 360
tctctactct ctactccatc tgttctgttc ccgcgcctgc gcgtcgtcct ctacggatcc 420
gtccaccgcc gcgccasacc atgtgaactg agacacgcct cmacctatgc atccaagaca 480
casctctgca tctgcgtccg tgcactggct acactggatc gattacggag tggagggtgt 540
tctttacaaa gaaagcttgt accttaaac aggaggatag aagaagt

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1482335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Asp Pro His Arg Cys Arg His Arg Cys Arg Arg Xaa His Gly Arg Ser
1 5 10 15
Pro Thr His Thr Ser His Tyr Xaa Xaa Pro Thr Ala Ala Ala Ser Pro
20 25 30
Leu Asp Pro Gln Cys Thr Ala Arg Ser Arg Pro Gln Pro Leu Thr Ala
35 40 45
Ala Thr Ser Asn Ala Pro Arg Thr Ile Ala Thr Ser Thr Ser Ser Phe
50 55 60
Trp Ser Arg Asp Pro Trp Ser Thr Pro Leu Glu Glu Pro Gly Ser Gly
65 70 75 80
Leu Pro Gly Thr Val Ser Ser Phe Arg Arg Leu Ser Arg Gln Arg Gly
85 90 95
Val Leu Arg His Arg Pro Met Glu Gln Pro Thr Lys Gln Glu Leu Tyr
100 105 110
Pro Cys Ser Cys Arg Gly Ala Val Ser Thr Leu Tyr Ser Ile Cys Ser
115 120 125
Val Pro Ala Pro Ala Arg Arg Pro Leu Arg Ile Arg Pro Pro Pro Arg
130 135 140
Xaa Thr Met
145

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1482336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

gcttgtagaag acagaaaacg attcctctcc cctccctccc agctctggac gcgtgamgct 60
cggcggcggc cgcacccctc gctcctcgcc tcacctcccg gtccatcctc gccgctctgc 120
gcgtgccctca cctcgacacc agccttccct cgtgacacga ctgcaacctc gctgacggag 180
agtacgtcct cgtgccggag caaggtattg ctcaggagggt agcccccaga tccagcacca 240
gagcctgcac cagaggatct gcctgccact gctttggaag gttctttgga ggacatggtt 300
gctggagtga cttggccgct catcttgcca ccgggttgga cagtcgagtg ggatcctgcc 360
tcggctgagg aggagcatga ggagtgatgg gacaggcttc cccatccctc catttaatta 420
tcgttagttt tattgccgct gcacttcgaa caatgatggc aacttttgaa aaactccgat 480
ggtgatgtaa taatttagta ctccttgatg tatgatttta tgtcttattg tatttgctct 540
gtg

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Ala Cys Glu Asp Arg Lys Arg Phe Leu Ser Pro Pro Ser Gln Leu Trp
1 5 10 15
Thr Arg Xaa Ala Arg Arg Arg Pro His Pro Arg Leu Leu Ala Ser Pro
20 25 30
Pro Gly Pro Ser Ser Pro Leu Cys Ala Cys Leu Thr Ser Thr Pro Ala
35 40 45
Phe Pro Arg Asp Thr Thr Ala Thr Ser Leu Thr Glu Ser Thr Ser Ser
50 55 60
Cys Arg Ser Lys Val Leu Leu Arg Arg
65 70

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Leu Val Lys Thr Glu Asn Asp Ser Ser Pro Leu Pro Pro Ser Ser Gly
1 5 10 15
Arg Val Xaa Leu Gly Gly Gly Arg Ile Leu Gly Ser Ser Pro His Leu
20 25 30
Pro Val His Pro Arg Arg Ser Ala Arg Ala Ser Pro Arg His Gln Pro
35 40 45
Ser Leu Val Thr Arg Leu Gln Pro Arg
50 55

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..633
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

acgccgagca ctccttctcc tcctcctctg tcggcggtcg tgggagacgt acacggcgat	60
taggaggcac gtcgtccacc agtctcctcg cagggatgtc gaagagcacg gaaatcgag	120
ataaagcaat catcttgatg caggatcatg ccaagcatat ctatcgtatt tgcaatgaga	180
agctaataatt gggtaaagga ttgactgcat ttgaggtcaa agaacttcgt gaagcacttg	240
aattcgccgc cgaaggattg gaccagggct cccttttttg ccaagaggaa ttggatgcaa	300


```
ctgttaagga ggaacaattg gagcatgacg agaaggtggc ttcacagatg attgaaagcc 360
cacttccttc tcctgattcg gactgcttcc tatcccttga agagcacatt gagaagtttt 420
ggggcggttg ttacaactcg gaccagatgc ctagctactc cgactaggct cagagtttat 480
ggtgctgtga aattctagat gtttgggtgt aatggtatatt tggatgtgta tgtgaactgt 540
aattctggat gtgtggatgt aatggtgaac tgactgaatg gtgtcttgtg taatggtatt 600
ttggatgtct atgtgaactc tagctctggg ttt
```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1482340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```
Ala Glu His Ser Phe Ser Ser Ser Ser Val Gly Gly Arg Gly Arg Arg
1           5           10           15
Thr Arg Arg Leu Gly Gly Thr Ser Ser Thr Ser Leu Leu Ala Gly Met
20           25           30
Ser Lys Ser Thr Glu Ile Ala Asp Lys Ala Ile Ile Leu Met Gln Asp
35           40           45
His Ala Lys His Ile Tyr Arg Ile Cys Asn Glu Lys Leu Ile Leu Gly
50           55           60
Lys Gly Leu Thr Ala Phe Glu Val Lys Glu Leu Arg Glu Ala Leu Glu
65           70           75           80
Phe Ala Ala Glu Gly Leu Asp Gln Gly Ser Leu Phe Cys Gln Glu Glu
85           90           95
Leu Asp Ala Thr Val Lys Glu Glu Gln Leu Glu His Asp Glu Lys Val
100          105          110
Ala Ser Gln Met Ile Glu Ser Pro Leu Pro Ser Pro Asp Ser Asp Cys
115          120          125
Phe Leu Ser Leu Glu Glu His Ile Glu Lys Phe Trp Gly Val Asp Tyr
130          135          140
Asn Ser Asp Gln Met Pro Ser Tyr Ser Asp
145          150
```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1482341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```
Met Ser Lys Ser Thr Glu Ile Ala Asp Lys Ala Ile Ile Leu Met Gln
1           5           10           15
Asp His Ala Lys His Ile Tyr Arg Ile Cys Asn Glu Lys Leu Ile Leu
20           25           30
Gly Lys Gly Leu Thr Ala Phe Glu Val Lys Glu Leu Arg Glu Ala Leu
35           40           45
Glu Phe Ala Ala Glu Gly Leu Asp Gln Gly Ser Leu Phe Cys Gln Glu
50           55           60
Glu Leu Asp Ala Thr Val Lys Glu Glu Gln Leu Glu His Asp Glu Lys
```

65 70 75 80
Val Ala Ser Gln Met Ile Glu Ser Pro Leu Pro Ser Pro Asp Ser Asp
85 90 95
Cys Phe Leu Ser Leu Glu Glu His Ile Glu Lys Phe Trp Gly Val Asp
100 105 110
Tyr Asn Ser Asp Gln Met Pro Ser Tyr Ser Asp
115 120

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Gln Asp His Ala Lys His Ile Tyr Arg Ile Cys Asn Glu Lys Leu
1 5 10 15
Ile Leu Gly Lys Gly Leu Thr Ala Phe Glu Val Lys Glu Leu Arg Glu
20 25 30
Ala Leu Glu Phe Ala Ala Glu Gly Leu Asp Gln Gly Ser Leu Phe Cys
35 40 45
Gln Glu Glu Leu Asp Ala Thr Val Lys Glu Glu Gln Leu Glu His Asp
50 55 60
Glu Lys Val Ala Ser Gln Met Ile Glu Ser Pro Leu Pro Ser Pro Asp
65 70 75 80
Ser Asp Cys Phe Leu Ser Leu Glu Glu His Ile Glu Lys Phe Trp Gly
85 90 95
Val Asp Tyr Asn Ser Asp Gln Met Pro Ser Tyr Ser Asp
100 105

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..827
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

cctaatacgaa aaatcgaaaa cccaccgcac cctttcatca gcctgcctgt ccactgttgg 60
cttgggtgact tctccgctc cgctccgctc ccctccgctc ccgaacggtc gatctttgca 120
tggcagcagc agctggctcc aaggggcggg cgatcgctgg aagcttcgtc agccgcgtcc 180
tcgccggcaa ggccgcctcg ccgaggaggg ccgtgcacgc ctccggcgta gacaagaacc 240
tggaggacca ggtgcgccc ggcgttcgtgc cggacgatgt gatcggcagc gccggnagac 300
cccgacaagt actggagccc ccaccccaag accggcgctc tcggcccggc ggcggtggac 360
cccaagctgg ccgctggtgg cgccgccgga cgccggcgcg gawtgctgca ggaggcacgg 420
tgctggacca gaaggtgtgg ttccgcccgc tcgaggacgt cgagaagccg cccccgccg 480
cgtgagccgc gcgccgctgc taggccagcc cacactgctg ctccgtcata aaaagggcgg 540
cgggagagcc tggcagtggc aggcaactctg ctccgtgctc gccgggctgg gctccctgct 600
tatatcactg caatattata ctactagtag tgggtgctga tagcagtgtg tggctgtgct 660
aataccagta taatactggt tctactataa tacagtcgta tcaggcatgg cgtgcatcag 720
gactggttgt gatagtagca acgtgatgct cgtgcctgta ataagaacaa gcaggcagatg 780
tgtgcctgtg atgtaccggt gtcgtcagtg ttataagtac ttgggggc

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Leu Ile Glu Lys Ser Lys Thr His Arg Thr Leu Ser Ser Ala Cys Leu
1 5 10 15
Ser Thr Val Gly Leu Val Thr Ser Ser Ala Pro Leu Arg Ser Pro Pro
20 25 30
Leu Pro Asn Gly Arg Ser Leu His Gly Ser Ser Ser Trp Leu Gln Gly
35 40 45
Ala Gly Asp Arg Trp Lys Leu Arg Gln Pro Arg Pro Arg Arg Gln Gly
50 55 60
Arg Leu Ala Glu Glu Gly Arg Ala Arg Leu Gly Val Arg Gln Glu Pro
65 70 75 80
Gly Gly Pro Gly Ala Pro Gly Val Arg Ala Gly Arg Cys Asp Arg Gln
85 90 95
Arg Arg Xaa Ala Pro Thr Ser Thr Gly Ala Pro Thr Pro Arg Pro Ala
100 105 110
Ser Ser Ala Arg Arg Arg Trp Thr Pro Ser Trp Pro Leu Val Ala Pro
115 120 125
Pro Asp Ala Gly Ala Xaa Cys Cys Arg Arg His Gly Ala Gly Pro Glu
130 135 140
Gly Val Val Pro Pro Ala Arg Gly Arg Arg Glu Ala Ala Pro Arg Arg
145 150 155 160
Val Ser Arg Ala Ala Leu Leu Gly Gln Pro Thr Leu Leu Leu Ala His
165 170 175
Lys Lys Gly Gly Arg Ala Trp Gln Trp Gln Ala Leu Cys Ser Cys
180 185 190
Ser Ala Gly Leu Gly Ser Leu Leu Ile Ser Leu Gln Tyr Tyr Thr Thr
195 200 205
Ser Ser Gly Ala
210

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Met Ala Ala Ala Gly Ser Lys Gly Arg Ala Ile Ala Gly Ser Phe
1 5 10 15
Val Ser Arg Val Leu Ala Gly Lys Ala Ala Ser Pro Arg Arg Ala Val
20 25 30
His Ala Ser Ala Tyr Asp Lys Asn Leu Glu Asp Gln Val Arg Pro Ala
35 40 45
Phe Val Pro Asp Asp Val Ile Gly Ser Ala Xaa Glu Pro Arg Gln Val

50 55 60
Leu Glu Pro Pro Pro Gln Asp Arg Arg Leu Arg Pro Gly Gly Gly Gly
65 70 75 80
Pro Gln Ala Gly Arg Trp Trp Arg Arg Arg Thr Pro Ala Arg Xaa Ala
85 90 95
Ala Gly Gly Thr Val Leu Asp Gln Lys Val Trp Phe Arg Pro Leu Glu
100 105 110
Asp Val Glu Lys Pro Pro Pro Ala Ala
115 120

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

awrcctgcac	cgcgctccttc	tcttcccaac	ttcctcgcgt	tcatttcttc	acccaccccg	60
cccccaaacg	ccaaatctaa	cagcaaaggt	ccggaacctt	ctagccgcac	ctagggtttg	120
gattggcgcc	gagcatggcg	tacgtcgacc	acgccttctc	catctccgac	gaggacgacc	180
tcgtcggmgt	cgccatgggg	ggcccgcgcg	ggcgcmcg	gaaggagatc	gccttcgccg	240
ccgcgtgct	cgmcttcggg	gcgbtcggt	ccatcagggt	gcctgcta	ggctgtcaac	300
cgcgtcggag	gggaccgcgc	gcacggaatt	ttcttcatga	tggtgggcat	tgtaatgttc	360
atccctgggt	tctactacac	aaggatcgcc	tactatgctt	acaaagggt	caagggtttc	420
tctttttcga	acatcccacc	gatctgaagg	agtgtgctgc	ctgcctggct	ggatcatgaag	480
tggtgtcgct	ggtttaagag	tttgcgact	ctgtcgaatg	gctctgtaga	cacccttggt	540
ctacatcttt	ctgtggccac	attctctttg	aacactctag	aatgaactgg	tggatgtgta	600
cagataaatg	cagccatagt	tgtgtcccat	cgctgtttgg	ccgattggaa	gggtgtttgt	660
tgtgctagt	tgaccatgtt	caactgatac	gcattgctac	ttgtgcatta	ctatcgtttt	720
tgtcaggac	cttaa	atcat	tatatgggaa	taagatctcg	tcgttcc	

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Xaa	Ser	His	Arg	Val	Leu	Leu	Phe	Pro	Thr	Ser	Ser	Arg	Ser	Phe	Leu	
1					5				10					15		
His	Pro	Thr	Arg	Pro	Gln	Thr	Pro	Asn	Leu	Thr	Ala	Lys	Val	Arg	Asn	
				20				25					30			
Leu	Leu	Ala	Ala	Pro	Arg	Val	Trp	Ile	Gly	Ala	Glu	His	Gly	Val	Arg	
				35			40					45				
Arg	Pro	Arg	Leu	Leu	His	Leu	Arg	Arg	Gly	Arg	Pro	Arg	Arg	Xaa	Arg	
			50			55			60							
His	Gly	Gly	Pro	Ala	Arg	Gly	Xaa	Arg	Glu	Gly	Asp	Arg	Leu	Arg	Arg	
65					70				75					80		
Arg	Ala	Ala	Xaa	Leu	Arg	Gly	Xaa	Arg	Tyr	His	Gln	Val	Ala	Cys		
				85				90						95		

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Met	Ala	Tyr	Val	Asp	His	Ala	Phe	Ser	Ile	Ser	Asp	Glu	Asp	Asp	Leu
1				5				10					15		
Val	Xaa	Gly	Ala	Met	Gly	Gly	Pro	Arg	Gly	Ala	Xaa	Val	Lys	Glu	Ile
		20					25					30			
Ala	Phe	Ala	Ala	Ala	Leu	Leu	Xaa	Phe	Gly	Ala	Xaa	Gly	Thr	Ile	Arg
		35					40					45			
Trp	Pro	Ala	Asn	Gly	Cys	Gln	Pro	Arg	Arg	Arg	Gly	Pro	Arg	Ala	Arg
	50					55					60				
Asn	Phe	Leu	His	Asp	Val	Gly	His	Cys	Asn	Val	His	Pro	Trp	Val	Leu
65					70				75					80	
Leu	His	Lys	Asp	Arg	Leu	Leu	Cys	Leu	Gln	Arg	Leu	Gln	Gly	Phe	Leu
			85					90						95	
Phe	Phe	Glu	His	Pro	Thr	Asp	Leu	Lys	Glu	Cys	Ala	Ala	Cys	Leu	Ala
			100					105						110	
Gly	His	Glu	Val	Val	Ser	Leu	Val								
		115					120								

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Met	Gly	Gly	Pro	Arg	Gly	Ala	Xaa	Val	Lys	Glu	Ile	Ala	Phe	Ala	Ala
1			5					10					15		
Ala	Leu	Leu	Xaa	Phe	Gly	Ala	Xaa	Gly	Thr	Ile	Arg	Trp	Pro	Ala	Asn
		20					25					30			
Gly	Cys	Gln	Pro	Arg	Arg	Arg	Gly	Pro	Arg	Ala	Arg	Asn	Phe	Leu	His
		35					40					45			
Asp	Val	Gly	His	Cys	Asn	Val	His	Pro	Trp	Val	Leu	Leu	His	Lys	Asp
	50					55				60					
Arg	Leu	Leu	Cys	Leu	Gln	Arg	Leu	Gln	Gly	Phe	Leu	Phe	Phe	Glu	His
65				70					75					80	
Pro	Thr	Asp	Leu	Lys	Glu	Cys	Ala	Ala	Cys	Leu	Ala	Gly	His	Glu	Val
			85					90						95	
Val	Ser	Leu	Val												
			100												

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1072

(D) OTHER INFORMATION: / Ceres Seq. ID 1482353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

acatcacaaa	ccgaaaaaarg	ccgcgacgag	ccgacgatct	ctactgcccc	cttccggcct	60
tcggcgaccg	tgacgagcaa	cgacgacgac	ggcgacgatg	gccgcttcct	ccctctgcca	120
cgggcacttg	ctcctgtttc	tcctcgtgtc	cgtcacatcg	gcctgcctcg	gtaccgcggc	180
asscantcaa	gccgggtctg	gagagggcta	cacgatcgcc	ggccgcgtca	agatcgatgg	240
catgagttag	aagggctatg	gtcttccagc	caagacatca	aacacaaaag	tgatacttaa	300
tggcggccaa	agggttacat	ttgccaggcc	agacggctac	tttgcatctc	acaacgtgcc	360
agctggaact	catctgattg	aggtctcctc	aattgggttac	ttcttttccc	ctgtccgagt	420
tgatataagt	gcaaggaatc	ctggatatat	tcaagcagca	ttgactgaaa	ccagaagagt	480
tctgaatgag	cttgttcttg	aacctctgaa	agaagagcag	tactttgagg	ttagggagcc	540
gttctccgtc	atgtcacttt	tgaagagccc	catgggggta	atgggttggt	ttatggtctt	600
aatggtcttc	gtgatgcccc	agatgatgga	gaacatagat	cccgaggaga	tgaagcaagc	660
tcaagwacaa	atgaggaaca	accctgtatc	attctctggc	ttgctcgcca	gagcgcaggg	720
ctagagaagt	agactgtaga	catgaggata	ctgcaaaggt	caaacattct	agaatgtgag	780
taagagcact	attaaagtgc	ttggcacgtc	actcactcgg	ggcaatttcc	tggggataag	840
aaggaaatcc	tttccccctg	tttttaccgt	atttttagggc	tagtttgga	acaccaattt	900
tccaaaggat	ttatattttc	ccatgggaaa	atgaactaat	tttccttggg	aaaatgaaaa	960
tctcttgga	aattgggggt	ccaaactagy	ccttaagtta	taatttgtct	gcggtgtaga	1020
accttctgaa	acctctgagc	tagtgatgcg	tcagattgag	atattttgtt	cg	

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1482354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Met	Ala	Ala	Ser	Ser	Leu	Cys	His	Gly	His	Leu	Leu	Leu	Phe	Leu	Leu
1				5					10					15	
Val	Ser	Val	Thr	Ser	Ala	Cys	Leu	Gly	Thr	Ala	Ala	Xaa	Xaa	Gln	Ala
			20						25				30		
Gly	Ser	Gly	Glu	Gly	Tyr	Thr	Ile	Ala	Gly	Arg	Val	Lys	Ile	Asp	Gly
		35				40						45			
Met	Ser	Glu	Lys	Gly	Tyr	Gly	Leu	Pro	Ala	Lys	Thr	Ser	Asn	Thr	Lys
	50					55					60				
Val	Ile	Leu	Asn	Gly	Gly	Gln	Arg	Val	Thr	Phe	Ala	Arg	Pro	Asp	Gly
65				70						75				80	
Tyr	Phe	Ala	Phe	His	Asn	Val	Pro	Ala	Gly	Thr	His	Leu	Ile	Glu	Val
			85						90					95	
Ser	Ser	Ile	Gly	Tyr	Phe	Phe	Ser	Pro	Val	Arg	Val	Asp	Ile	Ser	Ala
		100						105					110		
Arg	Asn	Pro	Gly	Tyr	Ile	Gln	Ala	Ala	Leu	Thr	Glu	Thr	Arg	Arg	Val
		115				120						125			
Leu	Asn	Glu	Leu	Val	Leu	Glu	Pro	Leu	Lys	Glu	Glu	Gln	Tyr	Phe	Glu
	130					135						140			
Val	Arg	Glu	Pro	Phe	Ser	Val	Met	Ser	Leu	Leu	Lys	Ser	Pro	Met	Gly
145					150					155				160	
Leu	Met	Val	Gly	Phe	Met	Val	Leu	Met	Val	Phe	Val	Met	Pro	Lys	Met
			165					170						175	
Met	Glu	Asn	Ile	Asp	Pro	Glu	Glu	Met	Lys	Gln	Ala	Gln	Xaa	Gln	Met

	180		185		190										
Arg	Asn	Asn	Pro	Val	Ser	Phe	Ser	Gly	Leu	Leu	Ala	Arg	Ala	Gln	Gly
	195						200					205			

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Met	Ser	Glu	Lys	Gly	Tyr	Gly	Leu	Pro	Ala	Lys	Thr	Ser	Asn	Thr	Lys
1				5					10					15	
Val	Ile	Leu	Asn	Gly	Gly	Gln	Arg	Val	Thr	Phe	Ala	Arg	Pro	Asp	Gly
			20				25					30			
Tyr	Phe	Ala	Phe	His	Asn	Val	Pro	Ala	Gly	Thr	His	Leu	Ile	Glu	Val
	35					40					45				
Ser	Ser	Ile	Gly	Tyr	Phe	Phe	Ser	Pro	Val	Arg	Val	Asp	Ile	Ser	Ala
	50					55					60				
Arg	Asn	Pro	Gly	Tyr	Ile	Gln	Ala	Ala	Leu	Thr	Glu	Thr	Arg	Arg	Val
65				70					75				80		
Leu	Asn	Glu	Leu	Val	Leu	Glu	Pro	Leu	Lys	Glu	Glu	Gln	Tyr	Phe	Glu
			85						90				95		
Val	Arg	Glu	Pro	Phe	Ser	Val	Met	Ser	Leu	Leu	Lys	Ser	Pro	Met	Gly
		100					105					110			
Leu	Met	Val	Gly	Phe	Met	Val	Leu	Met	Val	Phe	Val	Met	Pro	Lys	Met
	115					120					125				
Met	Glu	Asn	Ile	Asp	Pro	Glu	Met	Lys	Gln	Ala	Gln	Xaa	Gln	Met	
	130					135				140					
Arg	Asn	Asn	Pro	Val	Ser	Phe	Ser	Gly	Leu	Leu	Ala	Arg	Ala	Gln	Gly
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..803
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

accaacctca	cctactgttc	tgggttgaaa	tcttgcggaa	agtctgccaa	aacaaaaaac	60
aaaagtcctt	gcaggtgggt	tggcaggcta	aacttgacgt	ttgcgttggc	aggaagccgt	120
ggctgctgta	atctaattctg	ctgctgcaat	ctccgacccg	tctcccagac	ttgactgtac	180
ctgaaaccac	tattgaaaca	atcggtgaga	gcgagagaga	aaattaaaga	gaaaccgcac	240
aaaaaccaac	caaccaagca	gctctccgtt	ccatatagcc	gctgcatcag	atccattcaa	300
gaactagagc	caagccacca	acaataaatt	cctctggccg	gcctgcctca	tcagctcggt	360
tcaaaaaaaaa	caaaaaaaaa	agaagtcgca	gcggcagtag	taaactgcag	tgacatacgg	420
agcactactg	tactgtactg	tagtaacata	ctactactgc	tgctgctcac	agcaagaaca	480

aggatacgcgta aaaaaagaac caaggcaaaa agctaagggtc ctgtttggga acaaagtttt 540
tgaaaaccac agtttttgaa atactatact atactttagt tataacaata ccgtagttta 600
taataccgca gttttgaaaa ctgaggtcca gagctaagtt tagaatgcct taaaacaact 660
atagtatttg caatacttca gttttgaaaa cagagatttt acctagcttg ccaaacacca 720
ttatgtatat aatactgcag tatttgagaa tactgcagta ttcttccaaa actgcagaaa 780
aactttgttc ccaaacaccc cct

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1482357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

Thr Asn Leu Thr Tyr Cys Ser Gly Leu Lys Ser Cys Gly Lys Ser Ala
1 5 10 15
Lys Thr Lys Asn Lys Ser Pro Cys Arg Trp Phe Gly Arg Leu Asn Leu
20 25 30
Thr Phe Ala Leu Ala Gly Ser Arg Gly Cys Cys Asn Leu Ile Cys Cys
35 40 45
Cys Asn Leu Arg Pro Val Ser Gln Thr
50 55

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1482358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

Gln Pro His Leu Leu Phe Trp Val Glu Ile Leu Arg Lys Val Cys Gln
1 5 10 15
Asn Lys Lys Gln Lys Ser Leu Gln Val Val Trp Gln Ala Lys Leu Asp
20 25 30
Val Cys Val Gly Arg Lys Pro Trp Leu Leu
35 40

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..517

(D) OTHER INFORMATION: / Ceres Seq. ID 1482359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

gtagacgacg tgcattgtgtr gccggccaat ttacgcgcgc ccacatgctc tgctcgccca 60
tcgctttcga gctttgtgta aatggactag agcggaaggc atagcatgca taggaatagg 120
agcaactaac caccggcctc tcgctccctc gctgcgccat aaggctgcga ctgcgagagc 180


```
cagccgcacc cgcaccagtc cataggccgg cctcctctct taccttccca cacccttct 240
cgaccgtacg tagcctagtt gtgcttggtta gccagccaga aggtcgtcgg ccgatgatgg 300
gaggaagaac agtggtcccg ccgctcgtcc tcgcgctggt gaccatcatc gccatcggcg 360
gcggccgarg gggacgaggt gaagtgtggc gggtrctctc cgtrcrgcgg crccgactgc 420
mcggtgctgt acccgthnmm gcscrcrcg ccgtactact actacagcmc tmccccaccc 480
gcgacctacc ccggggagtc ctgctcatatc taccagc
```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```
Met Cys Xaa Arg Pro Ile Tyr Ala Pro Pro His Ala Leu Leu Ala His
1           5           10           15
Arg Phe Arg Ala Leu Cys Lys Trp Thr Arg Ala Glu Gly Ile Ala Cys
20           25           30
Ile Gly Ile Gly Ala Thr Asn His Arg Pro Leu Ala Pro Ser Leu Arg
35           40           45
His Lys Ala Ala Thr Ala Arg Ala Ser Arg Thr Arg Thr Ser Pro
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```
Met Met Gly Gly Arg Thr Val Ala Pro Pro Leu Val Leu Ala Leu Val
1           5           10           15
Thr Ile Ile Ala Ile Gly Gly Gly Arg Xaa Gly Arg Gly Glu Val Trp
20           25           30
Arg Xaa Leu Ser Xaa Xaa Arg Xaa Arg Leu Xaa Gly Ala Val Pro Xaa
35           40           45
Xaa Xaa Pro Xaa Ala Val Leu Leu Leu Gln Xaa Xaa Pro Thr Arg Asp
50           55           60
Leu Pro Arg Gly Val Leu Val Ile Leu Pro
65           70
```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

```
Met Gly Gly Arg Thr Val Ala Pro Pro Leu Val Leu Ala Leu Val Thr
1           5           10           15
Ile Ile Ala Ile Gly Gly Gly Arg Xaa Gly Arg Gly Glu Val Trp Arg
20           25           30
Xaa Leu Ser Xaa Xaa Arg Xaa Arg Leu Xaa Gly Ala Val Pro Xaa Xaa
35           40           45
Xaa Pro Xaa Ala Val Leu Leu Leu Gln Xaa Xaa Pro Thr Arg Asp Leu
50           55           60
Pro Arg Gly Val Leu Val Ile Leu Pro
65           70
```

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```
aaagagaaag tttattacga ttaggtgca tattcaaggc ccgttgatgg atgaactttt      60
gtagtgtggg tccaaagggtg tacgtatgtg ggacgggcat aaaaaatatg attttgatct      120
acgtgctttg ttattggcga acaggcgagt gagtgaagag agaagccatg cctctttcgt      180
gtgaggcaag cgatgaacga gtagatgctg ccattcaaca agggattcag ggtctgcacc      240
tattgtttag atgagatcgg tatcttgtat ctacatcatt gtagagaagt tatttacatg      300
ggccatcgtc gatttcttgt aaacaccaaa taagaagaaa aggcaagcat tgaaatgcac      360
aagtagacca tcgtgccaaa gcctattccc caaaggagca accttgattt ccagatggta      420
tagaacttaa atgtagtgtg tgggaatcg
```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```
Met Asn Phe Cys Ser Cys Gly Pro Lys Val Tyr Val Cys Gly Thr Gly
1           5           10           15
Ile Lys Asn Met Ile Leu Ile Tyr Val Leu Cys Tyr Trp Arg Thr Gly
20           25           30
Glu
```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1482365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```
Met Trp Asp Gly His Lys Lys Tyr Asp Phe Asp Leu Arg Ala Leu Leu
1           5           10          15
Leu Ala Asn Arg Arg Val Ser Glu Glu Arg Ser His Ala Ser Phe Val
20          25          30
```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1482366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```
Met Leu Pro Phe Asn Lys Gly Phe Arg Val Cys Thr Tyr Cys Leu Asp
1           5           10          15
Glu Ile Gly Ile Leu Tyr Leu His His Cys Arg Glu Val Ile Tyr Met
20          25          30
Gly His Arg Arg Phe Leu Val Asn Thr Lys
35          40
```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..757

(D) OTHER INFORMATION: / Ceres Seq. ID 1482371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```
tgattggttt gatgaacagc tagagaacta cttagatgat gattatcttg tgtttgattg      60
ccctggccag attgaactct tcacacatgt tccagttctg cggaactttg tcgagcacct      120
gaaacgaaaa aatttcaacg tttgcgctgt ttaccttctt gattcacagt ttgtcagcga      180
tgtaacaaaa tacatcagtg gttgcatggc ttctctatct gctatgattc agcttgaact      240
tcctcatatc aacatccttt caaagatgga tcttggtctcc aacaaaaaag atgtagaaga      300
gtacctggac ccgaatgcac aggttcttct ttcacagctg aatcggcaga tggcacctcg      360
gtttggcaag ttgaacaagt gtttagctga actggttgat gattacagca tggttaattt      420
cattccactt gatttgagaa aggaaagcag catacaatat gtgctatctt ctatcgacac      480
ctgtatccag tatggggaag atgcagatgt gaaggtcagg gacttcgaag aagacgaaga      540
ctaaccactg gcaactggatg ctgtaggagg tgcaaactgg ttgctagcag tcgtgtagtg      600
cggagtgaga ctttgggact gtgtakggtg gcgcaggcat gcaaaaacgt cgtaggatgc      660
tgatgacagc tawctggcct atgtaagacg aactaawgca gatatttggc aagtcctagt      720
aaaatgtgtg wgcrccttga tggctmyctrw tctcccc
```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1482372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```
Asp Trp Phe Asp Glu Gln Leu Glu Asn Tyr Leu Asp Asp Asp Tyr Leu
1          5          10          15
Val Phe Asp Cys Pro Gly Gln Ile Glu Leu Phe Thr His Val Pro Val
          20          25          30
Leu Arg Asn Phe Val Glu His Leu Lys Arg Lys Asn Phe Asn Val Cys
          35          40          45
Ala Val Tyr Leu Leu Asp Ser Gln Phe Val Ser Asp Val Thr Lys Tyr
          50          55          60
Ile Ser Gly Cys Met Ala Ser Leu Ser Ala Met Ile Gln Leu Glu Leu
          65          70          75          80
Pro His Ile Asn Ile Leu Ser Lys Met Asp Leu Val Ser Asn Lys Lys
          85          90          95
Asp Val Glu Glu Tyr Leu Asp Pro Asn Ala Gln Val Leu Leu Ser Gln
          100          105          110
Leu Asn Arg Gln Met Ala Pro Arg Phe Gly Lys Leu Asn Lys Cys Leu
          115          120          125
Ala Glu Leu Val Asp Asp Tyr Ser Met Val Asn Phe Ile Pro Leu Asp
          130          135          140
Leu Arg Lys Glu Ser Ser Ile Gln Tyr Val Leu Ser Ser Ile Asp Thr
          145          150          155          160
Cys Ile Gln Tyr Gly Glu Asp Ala Asp Val Lys Val Arg Asp Phe Glu
          165          170          175
Glu Asp Glu Asp
          180
```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1482373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```
Met Ala Ser Leu Ser Ala Met Ile Gln Leu Glu Leu Pro His Ile Asn
1          5          10          15
Ile Leu Ser Lys Met Asp Leu Val Ser Asn Lys Lys Asp Val Glu Glu
          20          25          30
Tyr Leu Asp Pro Asn Ala Gln Val Leu Leu Ser Gln Leu Asn Arg Gln
          35          40          45
Met Ala Pro Arg Phe Gly Lys Leu Asn Lys Cys Leu Ala Glu Leu Val
          50          55          60
Asp Asp Tyr Ser Met Val Asn Phe Ile Pro Leu Asp Leu Arg Lys Glu
          65          70          75          80
Ser Ser Ile Gln Tyr Val Leu Ser Ser Ile Asp Thr Cys Ile Gln Tyr
          85          90          95
Gly Glu Asp Ala Asp Val Lys Val Arg Asp Phe Glu Glu Asp Glu Asp
          100          105          110
```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met	Ile	Gln	Leu	Leu	Pro	His	Ile	Asn	Ile	Leu	Ser	Lys	Met	Asp	
1			5					10					15		
Leu	Val	Ser	Asn	Lys	Lys	Asp	Val	Glu	Glu	Tyr	Leu	Asp	Pro	Asn	Ala
			20					25					30		
Gln	Val	Leu	Leu	Ser	Gln	Leu	Asn	Arg	Gln	Met	Ala	Pro	Arg	Phe	Gly
			35				40					45			
Lys	Leu	Asn	Lys	Cys	Leu	Ala	Glu	Leu	Val	Asp	Asp	Tyr	Ser	Met	Val
			50			55					60				
Asn	Phe	Ile	Pro	Leu	Asp	Leu	Arg	Lys	Glu	Ser	Ser	Ile	Gln	Tyr	Val
65				70					75					80	
Leu	Ser	Ser	Ile	Asp	Thr	Cys	Ile	Gln	Tyr	Gly	Glu	Asp	Ala	Asp	Val
			85					90						95	
Lys	Val	Arg	Asp	Phe	Glu	Glu	Asp	Glu	Asp						
			100				105								

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..617
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

agaatcccc	gtmgacgcgc	acggcagagc	tccgcatccg	caccggccgc	cggcggstgg	60
atggggaagc	tctccgccct	gaagcgggaa	gcggtcggag	tggactaggc	gctcggtgac	120
ttcctagttt	agaagcggta	rgtggaggcg	atgcggggcg	gggcgatgaa	ggccctgcgg	180
cgatccagca	cctcctcggc	gccatcgcca	aggggtgccg	cttccccgcg	gtcttattcg	240
tggatccacc	gccggtcgct	tctcgttacc	tygccggcct	cgccggmgmc	gtcctctgtg	300
tctgaatcgg	cgaatttgcc	cgcggagggt	tcggattcag	cgccagcktc	agtggtgga	360
gcttcctcgt	cgccctcgct	ggctgcttcg	tctccgaaca	tggaatggtg	gggctatcct	420
gtccggattt	ctcctcgtgc	tgcattgggtc	gcttcaaaat	ggggaataat	tggtgggcta	480
cttgatattt	cccaacaacg	attcgcgcac	ttattcccaa	aattatgctg	ttctggtagc	540
acagtgggaag	tggtagtttg	ttcgggtacta	ttattcttat	aagatttgct	ttagtctctt	600
agattaaaaa	aaagctg					

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Arg Gly Gly Ala Met Lys Ala Leu Arg Arg Ser Ser Thr Ser Ser

1	5	10	15												
Ala	Pro	Ser	Pro	Arg	Val	Pro	Ser	Ser	Pro	Arg	Ser	Tyr	Ser	Trp	Ile
	20							25					30		
His	Arg	Arg	Ser	Leu	Leu	Val	Thr	Xaa	Pro	Ala	Ser	Pro	Xaa	Xaa	Ser
	35						40					45			
Ser	Val	Ser	Glu	Ser	Ala	Asn	Leu	Pro	Ala	Glu	Gly	Ser	Asp	Ser	Ala
	50					55					60				
Pro	Xaa	Ser	Val	Val	Ala	Ala	Ser	Ser	Ser	Pro	Ser	Leu	Ala	Ala	Ser
65					70					75					80
Ser	Pro	Asn	Met	Glu	Trp	Trp	Gly	Tyr	Pro	Val	Arg	Ile	Ser	Pro	Arg
		85						90					95		
Ala	Ala	Trp	Val	Ala	Ser	Lys	Trp	Gly	Ile	Ile	Val	Gly	Leu	Leu	Asp
	100							105					110		
Ile	Ser	Gln	Gln	Arg	Phe	Ala	His	Leu	Phe	Pro	Lys	Leu	Cys	Cys	Ser
	115						120					125			
Gly	Ser	Thr	Val	Glu	Val	Val	Cys	Ser	Val	Leu	Leu	Phe	Leu		
130					135					140					

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

Met	Lys	Ala	Leu	Arg	Arg	Ser	Ser	Thr	Ser	Ser	Ala	Pro	Ser	Pro	Arg
1			5					10				15			
Val	Pro	Ser	Ser	Pro	Arg	Ser	Tyr	Ser	Trp	Ile	His	Arg	Arg	Ser	Leu
	20						25				30				
Leu	Val	Thr	Xaa	Pro	Ala	Ser	Pro	Xaa	Xaa	Ser	Ser	Val	Ser	Glu	Ser
	35					40					45				
Ala	Asn	Leu	Pro	Ala	Glu	Gly	Ser	Asp	Ser	Ala	Pro	Xaa	Ser	Val	Val
	50				55					60					
Ala	Ala	Ser	Ser	Ser	Pro	Ser	Leu	Ala	Ala	Ser	Ser	Pro	Asn	Met	Glu
65					70					75				80	
Trp	Trp	Gly	Tyr	Pro	Val	Arg	Ile	Ser	Pro	Arg	Ala	Ala	Trp	Val	Ala
		85						90					95		
Ser	Lys	Trp	Gly	Ile	Ile	Val	Gly	Leu	Leu	Asp	Ile	Ser	Gln	Gln	Arg
	100						105						110		
Phe	Ala	His	Leu	Phe	Pro	Lys	Leu	Cys	Cys	Ser	Gly	Ser	Thr	Val	Glu
	115					120							125		
Val	Val	Val	Cys	Ser	Val	Leu	Leu	Phe	Leu						
130					135										

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..585
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```
aattcattac cggaagagaa aaaaataact cggaaaagaa ggagacgccg aaaattcgaa      60
aggggagggg aaagcaaagc tgatggcgga ggaccagggg aaagcaaagc aaatggcgga      120
ggccccgagc aagatcgaat ccatgaggaa gtgggtcgtc gagcacaagc tccgagccgt      180
aggttgccctc tggctagggtg ggatcagcag ttcgatcgcc tacaactggt cgcggcccaa      240
tatgaagcct agcgtcaaga tcatccacgc aaggttgcac gctcaagctc taaccctggc      300
tgcattagtt ggttctgcat gcgtggagta ctatgatcag aagtatggtt cttctgggcc      360
aaaggtggac aaatacacaa gccaatatct ggcccattcg cataaagatt aaaggtcgcc      420
atggttggttc ctgcatgccg gattaatttt gggtcatctc cgggttgctc atgaccgcc      480
catggatgct ggatgtttat tctttttttg tcttcataat tacaaaatgg tgggtgtactt      540
gccaggcaaa tgtaatatgag ggtataatgc agatattgtc gtcgc
```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

```
Met Ala Glu Asp Gln Gly Lys Ala Lys Gln Met Ala Glu Ala Pro Ser
1          5          10          15
Lys Ile Glu Ser Met Arg Lys Trp Val Val Glu His Lys Leu Arg Ala
20          25          30
Val Gly Cys Leu Trp Leu Gly Gly Ile Ser Ser Ser Ile Ala Tyr Asn
35          40          45
Trp Ser Arg Pro Asn Met Lys Pro Ser Val Lys Ile Ile His Ala Arg
50          55          60
Leu His Ala Gln Ala Leu Thr Leu Ala Ala Leu Val Gly Ser Ala Cys
65          70          75          80
Val Glu Tyr Tyr Asp Gln Lys Tyr Gly Ser Ser Gly Pro Lys Val Asp
85          90          95
Lys Tyr Thr Ser Gln Tyr Leu Ala His Ser His Lys Asp
100         105
```

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```
Met Ala Glu Ala Pro Ser Lys Ile Glu Ser Met Arg Lys Trp Val Val
1          5          10          15
Glu His Lys Leu Arg Ala Val Gly Cys Leu Trp Leu Gly Gly Ile Ser
20          25          30
Ser Ser Ile Ala Tyr Asn Trp Ser Arg Pro Asn Met Lys Pro Ser Val
35          40          45
Lys Ile Ile His Ala Arg Leu His Ala Gln Ala Leu Thr Leu Ala Ala
50          55          60
Leu Val Gly Ser Ala Cys Val Glu Tyr Tyr Asp Gln Lys Tyr Gly Ser
65          70          75          80
Ser Gly Pro Lys Val Asp Lys Tyr Thr Ser Gln Tyr Leu Ala His Ser
```

85

90

95

His Lys Asp

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1482381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```
Met Arg Lys Trp Val Val Glu His Lys Leu Arg Ala Val Gly Cys Leu
1          5          10          15
Trp Leu Gly Gly Ile Ser Ser Ser Ile Ala Tyr Asn Trp Ser Arg Pro
20          25          30
Asn Met Lys Pro Ser Val Lys Ile Ile His Ala Arg Leu His Ala Gln
35          40          45
Ala Leu Thr Leu Ala Ala Leu Val Gly Ser Ala Cys Val Glu Tyr Tyr
50          55          60
Asp Gln Lys Tyr Gly Ser Ser Gly Pro Lys Val Asp Lys Tyr Thr Ser
65          70          75          80
Gln Tyr Leu Ala His Ser His Lys Asp
85
```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..769

(D) OTHER INFORMATION: / Ceres Seq. ID 1482382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

```
caaaaaaaaaac caatcggacg gaaacgaaaa aggcctcact catctccgtc cgtccgccgc 60
accgtcgccg agcgccgctc cgcgccggag acgtcctgtt tttttgccgc ctacgagcgc 120
tgtccctctt ttctttccgc ggttctgccc caacttctgc atccgaatct cccacgaagt 180
tgtcacggcg atggcagcga ccggcgccgt ttcaactgac gatatcccga tcctgcaagc 240
agagaacctc accagcaacg tcaagtccgt ccactacagt cgaacattct tgatgatcat 300
tggtggagtt gttgctggaa tctggggatt cacaggcttg acgggatttg tcttctactt 360
tctgataatg atggttgcat ctatcgggct cttagcaaag tcaaagtttt cagtgcagac 420
atacttcgat agttggacca ggatttcaat tgaaggagtt tttggtggcc ttatgtcatt 480
cgtgctgttc tggacatttg cttatgacat tggtcatatc ttctgatgga cgtagaaaga 540
gctaccctcc aaagaaaata tggaatttca tctgatgtcg aacattccca atgggctctt 600
tgtacactca gtttttattt tggttaattgt tgatataata ttttgatgata ctatatcggt 660
ggacctaaagc agagctcata aactgatgta gcaactcctt cgcttgatg atctgtagca 720
gttgtgattt gtcatttcca gtaatgaatg taaactttga ttgatggac
```

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Lys	Lys	Asn	Gln	Ser	Asp	Gly	Asn	Glu	Lys	Gly	Leu	Thr	His	Leu	Arg
1				5				10						15	
Pro	Ser	Ala	Ala	Pro	Ser	Pro	Ser	Ala	Pro	Arg	Arg	Arg	Arg	Pro	
			20					25				30			
Val	Phe	Leu	Pro	Pro	Thr	Ser	Ala	Val	Pro	Leu	Phe	Phe	Pro	Arg	Phe
		35					40					45			
Cys	Pro	Asn	Phe	Cys	Ile	Arg	Ile	Ser	His	Glu	Val	Val	Thr	Ala	Met
	50					55					60				
Ala	Ala	Thr	Gly	Gly	Val	Ser	Thr	Asp	Asp	Ile	Pro	Ile	Leu	Gln	Ala
65					70					75				80	
Glu	Asn	Leu	Thr	Ser	Asn	Val	Lys	Ser	Val	His	Tyr	Ser	Arg	Thr	Phe
				85					90					95	
Leu	Ser	Ile	Ile	Gly	Gly	Val	Val	Ala	Gly	Ile	Trp	Gly	Phe	Thr	Gly
			100					105					110		
Leu	Thr	Gly	Phe	Val	Phe	Tyr	Phe	Leu	Ile	Met	Met	Val	Ala	Ser	Ile
		115					120					125			
Gly	Leu	Leu	Ala	Lys	Ser	Lys	Phe	Ser	Val	Gln	Thr	Tyr	Phe	Asp	Ser
	130					135					140				
Trp	Thr	Arg	Ile	Ser	Ile	Glu	Gly	Val	Phe	Gly	Gly	Leu	Met	Ser	Phe
145					150					155					160
Val	Leu	Phe	Trp	Thr	Phe	Ala	Tyr	Asp	Ile	Val	His	Ile	Phe		
				165					170						

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Lys	Lys	Thr	Asn	Arg	Thr	Glu	Thr	Lys	Lys	Ala	Ser	Leu	Ile	Ser	Val
1				5				10						15	
Arg	Pro	Pro	His	Arg	Arg	Arg	Ala	Pro	Leu	Arg	Ala	Gly	Asp	Val	Leu
			20					25					30		
Phe	Phe	Cys	Arg	Leu	Arg	Ala	Leu	Ser	Leu	Phe	Ser	Phe	Arg	Gly	Ser
		35					40					45			
Ala	Pro	Thr	Ser	Ala	Ser	Glu	Ser	Pro	Thr	Lys	Leu	Ser	Arg	Arg	Trp
	50					55					60				
Gln	Arg	Pro	Ala	Ala	Phe	Gln	Leu	Thr	Ile	Ser	Arg	Ser	Cys	Lys	Gln
65					70					75				80	
Arg	Thr	Ser	Pro	Ala	Thr	Ser	Ser	Pro	Ser	Thr	Thr	Val	Glu	His	Ser
				85					90					95	
Cys	Arg	Ser	Leu	Val	Glu	Leu	Leu	Leu	Glu	Ser	Gly	Asp	Ser	Gln	Ala
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..111
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482385
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

Met	Ala	Ala	Thr	Gly	Gly	Val	Ser	Thr	Asp	Asp	Ile	Pro	Ile	Leu	Gln
1				5				10						15	
Ala	Glu	Asn	Leu	Thr	Ser	Asn	Val	Lys	Ser	Val	His	Tyr	Ser	Arg	Thr
		20						25					30		
Phe	Leu	Ser	Ile	Ile	Gly	Gly	Val	Val	Ala	Gly	Ile	Trp	Gly	Phe	Thr
		35					40						45		
Gly	Leu	Thr	Gly	Phe	Val	Phe	Tyr	Phe	Leu	Ile	Met	Met	Val	Ala	Ser
	50					55					60				
Ile	Gly	Leu	Leu	Ala	Lys	Ser	Lys	Phe	Ser	Val	Gln	Thr	Tyr	Phe	Asp
65					70					75					80
Ser	Trp	Thr	Arg	Ile	Ser	Ile	Glu	Gly	Val	Phe	Gly	Gly	Leu	Met	Ser
			85						90					95	
Phe	Val	Leu	Phe	Trp	Thr	Phe	Ala	Tyr	Asp	Ile	Val	His	Ile	Phe	
			100						105					110	

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 767 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..767
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482386
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

agtcagacat	agagaatcct	tctagacaca	gcgatgtgcc	ggtgccccag	caattcattg	60
tggcatttcg	caccacatc	aacccttca	cacacgaacc	agatcagaaa	agccactact	120
gctttctctc	tctctctcac	acacacacag	acacaaataa	aagaaatcag	tagttcgatt	180
tctcctctca	cctttattta	cacatatctc	tgtattttaca	aattagggtg	ttgatgtagg	240
ctgtacgcac	ctgctagttt	gctactcgat	cctatatatc	gtccaatcct	atctgacctc	300
tgcacatctg	gtccttgatt	actcgctcct	tttgcttggt	tatatcgctc	ccccggcgcg	360
ttgagctagc	ttcctctagt	tctcgcgcgc	gtcgtcgatc	ggttggttgc	atagcccacg	420
gcgagccgaa	ggaataatgt	cgctcggcgc	cctgcagatc	gcgcccgtgc	cgggagcatg	480
tgtgctacgt	gcactgcaac	ttctgcaaca	caattctcgc	ggtaaacacc	ctcatctctc	540
tgtttgtccc	cctccctcct	ttgaattccc	agttctcgat	cggcgatgat	gcctctgaag	600
tgcagatcta	caaaggggag	atgcacatga	aatgattgst	gcgcgcgcgc	atgcatcata	660
cagttttattt	tgtaggattt	ggctgtcccc	tcttgctgga	tttcttcttc	ttcttcttta	720
tttttttgct	ctataaattg	ttttgtaaag	gttgaatgaa	atttctg		

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482387
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Ser Asp Ile Glu Asn Pro Ser Arg His Ser Asp Val Pro Val Pro Gln
1 5 10 15
Gln Phe Ile Val Ala Phe Arg Thr His Ile Asn Pro Phe Thr His Glu
20 25 30
Pro Asp Gln Lys Ser His Tyr Cys Phe Leu Ser Leu Ser His Thr His
35 40 45
Thr Asp Thr Asn Lys Arg Asn Gln
50 55

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1482388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

Met Cys Arg Cys Pro Ser Asn Ser Leu Trp His Phe Ala Pro Thr Ser
1 5 10 15
Thr Pro Ser His Thr Asn Gln Ile Arg Lys Ala Thr Thr Ala Phe Ser
20 25 30
Leu Ser Leu Thr His Thr Gln Thr Gln Ile Lys Glu Ile Ser Ser Ser
35 40 45
Ile Ser Pro Leu Thr Phe Ile Tyr Thr Tyr Leu Cys Ile Tyr Lys Leu
50 55 60
Gly Cys
65

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1482389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met Ser Ser Ala Pro Leu Gln Ile Ala Pro Val Pro Gly Ala Cys Val
1 5 10 15
Leu Arg Ala Leu Gln Leu Leu Gln His Asn Ser Arg Gly Lys His Pro
20 25 30
His Leu Ser Val Cys Pro Pro Pro Ser Phe Glu Phe Pro Val Leu Asp
35 40 45
Arg His Ala Cys Leu
50

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1023 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1023

(D) OTHER INFORMATION: / Ceres Seq. ID 1482398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

atttgcctat	ttccggtgca	ggcagtcctgg	cagagcgagc	aggcarrcaa	ctggggccaga	60
rtcagacagg	cctgcccgcc	acgccgtccc	gacggccatg	gcccgaccct	tctcttcccc	120
acacatcccc	tcttcacctt	gggtgactcg	ccgccctcct	ccctggacct	cctcaccgtc	180
cgtctccacc	acgagaacta	gcgcctcgtc	tattaccgcg	tgacagaccgc	gccgcagggc	240
agtcgcgccg	gcggcctccc	tccacctcgg	cccgggggag	atcgccgagc	tcgcgcgcaa	300
caaggttttr	attgcggcga	cagtrgcgag	cgcgatcggg	cagctgtcca	agcccttcac	360
ctcgttcaag	aatggggggc	tcggcgccgg	ccttgacctc	aggaccgtct	tccgctccgg	420
agggatgccc	tccayycact	ccgcgagtg	tggttcagtt	gctacttcgc	ttgggctaga	480
aaggggggtt	rcagactcca	tatttggaat	gtcagtrgw	tttkcagcaa	ttgtaatgta	540
tgatgctcag	ggagtaagaa	gagaaktggg	caaccacgcc	aagatcttga	acaggttttg	600
gatcctcaaa	gagaaggtac	ctctggagta	ttctgaagt	gacatggcag	ctcctgggtt	660
tgtttcggtc	accgaggaag	cgagctccaa	cgcgagcccc	tccttgaagc	gcggttctag	720
caccgaatca	ccaaggggtg	atgggctccg	tggttcagag	cctgagctga	cagagctgaa	780
gcaggttgc	gtagaggagg	attaccggtt	gagtgaatct	ggtggccaca	cggagcttca	840
ggtcacagtc	ggcgccctgt	tggtttttgc	tgtaagctta	gcagtgtatg	caacactgta	900
acggaccttt	tcatatcacg	tccttgattg	attacacatt	tacacttttt	tttacacaga	960
aacaatacat	gcggttttatt	gttcccaccg	tttaaatacag	aaatgcctat	gctagctcgt	1020
ttc						

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..299

(D) OTHER INFORMATION: / Ceres Seq. ID 1482399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Phe	Ala	Tyr	Phe	Arg	Cys	Arg	Gln	Ser	Gly	Arg	Ala	Ser	Arg	Xaa	Xaa
1			5				10							15	
Thr	Gly	Pro	Xaa	Ser	Asp	Arg	Pro	Ala	Arg	His	Ala	Val	Pro	Thr	Ala
			20					25					30		
Met	Ala	Arg	Pro	Phe	Ser	Ser	Pro	His	Ile	Pro	Ser	Ser	Ser	Trp	Val
			35				40					45			
Thr	Arg	Arg	Pro	Pro	Pro	Trp	Thr	Ser	Ser	Pro	Ser	Val	Ser	Thr	Thr
			50			55					60				
Arg	Thr	Ser	Ala	Ser	Ser	Ile	Thr	Ala	Cys	Arg	Pro	Arg	Arg	Arg	Ala
65					70				75					80	
Val	Ala	Pro	Ala	Ala	Ser	Leu	His	Leu	Gly	Pro	Gly	Glu	Ile	Ala	Glu
			85					90						95	
Leu	Ala	Arg	Asn	Lys	Val	Xaa	Ile	Ala	Ala	Thr	Xaa	Ala	Ser	Ala	Ile
			100					105					110		
Gly	Gln	Leu	Ser	Lys	Pro	Phe	Thr	Ser	Val	Lys	Asn	Gly	Gly	Val	Gly
		115				120						125			
Ala	Gly	Leu	Asp	Leu	Arg	Thr	Val	Phe	Arg	Ser	Gly	Gly	Met	Pro	Ser
		130				135					140				
Xaa	His	Ser	Ala	Ser	Val	Val	Ala	Val	Ala	Thr	Ser	Leu	Gly	Leu	Glu
145					150					155				160	
Arg	Gly	Phe	Xaa	Asp	Ser	Ile	Phe	Gly	Met	Ser	Xaa	Xaa	Phe	Xaa	Ala
			165					170						175	
Ile	Val	Met	Tyr	Asp	Ala	Gln	Gly	Val	Arg	Arg	Glu	Xaa	Gly	Asn	His
			180				185						190		
Ala	Lys	Ile	Leu	Asn	Arg	Phe	Trp	Ile	Leu	Lys	Glu	Lys	Val	Pro	Leu
		195					200						205		

Glu Tyr Ser Glu Val Asp Met Ala Ala Pro Gly Phe Val Ser Val Thr
210 215 220
Glu Glu Ala Ser Ser Asn Ala Ser Pro Ser Leu Lys Arg Gly Ser Ser
225 230 235 240
Thr Glu Ser Pro Arg Val Asn Gly Leu Arg Gly Ser Glu Pro Glu Leu
245 250 255
Thr Glu Leu Lys Gln Ala Cys Val Glu Glu Asp Tyr Arg Leu Ser Glu
260 265 270
Ser Val Gly His Thr Glu Leu Gln Val Thr Val Gly Ala Leu Leu Gly
275 280 285
Phe Ala Val Ser Leu Ala Val Tyr Ala Thr Leu
290 295

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1482400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Met Ala Arg Pro Phe Ser Ser Pro His Ile Pro Ser Ser Ser Trp Val
1 5 10 15
Thr Arg Arg Pro Pro Pro Trp Thr Ser Ser Pro Ser Val Ser Thr Thr
20 25 30
Arg Thr Ser Ala Ser Ser Ile Thr Ala Cys Arg Pro Arg Arg Arg Ala
35 40 45
Val Ala Pro Ala Ala Ser Leu His Leu Gly Pro Gly Glu Ile Ala Glu
50 55 60
Leu Ala Arg Asn Lys Val Xaa Ile Ala Ala Thr Xaa Ala Ser Ala Ile
65 70 75 80
Gly Gln Leu Ser Lys Pro Phe Thr Ser Val Lys Asn Gly Gly Val Gly
85 90 95
Ala Gly Leu Asp Leu Arg Thr Val Phe Arg Ser Gly Gly Met Pro Ser
100 105 110
Xaa His Ser Ala Ser Val Val Ala Val Ala Thr Ser Leu Gly Leu Glu
115 120 125
Arg Gly Phe Xaa Asp Ser Ile Phe Gly Met Ser Xaa Xaa Phe Xaa Ala
130 135 140
Ile Val Met Tyr Asp Ala Gln Gly Val Arg Arg Glu Xaa Gly Asn His
145 150 155 160
Ala Lys Ile Leu Asn Arg Phe Trp Ile Leu Lys Glu Lys Val Pro Leu
165 170 175
Glu Tyr Ser Glu Val Asp Met Ala Ala Pro Gly Phe Val Ser Val Thr
180 185 190
Glu Glu Ala Ser Ser Asn Ala Ser Pro Ser Leu Lys Arg Gly Ser Ser
195 200 205
Thr Glu Ser Pro Arg Val Asn Gly Leu Arg Gly Ser Glu Pro Glu Leu
210 215 220
Thr Glu Leu Lys Gln Ala Cys Val Glu Glu Asp Tyr Arg Leu Ser Glu
225 230 235 240
Ser Val Gly His Thr Glu Leu Gln Val Thr Val Gly Ala Leu Leu Gly
245 250 255
Phe Ala Val Ser Leu Ala Val Tyr Ala Thr Leu
260 265

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482401
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met Pro Ser Xaa His Ser Ala Ser Val Val Ala Val Ala Thr Ser Leu
1 5 10 15
Gly Leu Glu Arg Gly Phe Xaa Asp Ser Ile Phe Gly Met Ser Xaa Xaa
 20 25 30
Phe Xaa Ala Ile Val Met Tyr Asp Ala Gln Gly Val Arg Arg Glu Xaa
 35 40 45
Gly Asn His Ala Lys Ile Leu Asn Arg Phe Trp Ile Leu Lys Glu Lys
50 55 60
Val Pro Leu Glu Tyr Ser Glu Val Asp Met Ala Ala Pro Gly Phe Val
65 70 75 80
Ser Val Thr Glu Glu Ala Ser Ser Asn Ala Ser Pro Ser Leu Lys Arg
 85 90 95
Gly Ser Ser Thr Glu Ser Pro Arg Val Asn Gly Leu Arg Gly Ser Glu
 100 105 110
Pro Glu Leu Thr Glu Leu Lys Gln Ala Cys Val Glu Glu Asp Tyr Arg
 115 120 125
Leu Ser Glu Ser Val Gly His Thr Glu Leu Gln Val Thr Val Gly Ala
130 135 140
Leu Leu Gly Phe Ala Val Ser Leu Ala Val Tyr Ala Thr Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:535:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..524
(D) OTHER INFORMATION: / Ceres Seq. ID 1482402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

ttccggctcc gctcagtcag gcctcagatc ggtcgaatcc agcaccacct ccagatttgc 60
gtcaccaatc ttctttttct tccgccgcgc ccgccgctcc cccacaagga ggtagctgc 120
tatcccaaaa tcgattcatc aatcatccgt gtccttccat ttcattccag tcggtcgccg 180
cagcacggac cgagaacaga gcatcacgtc acatcaaact aacctaacca gcctcgtccc 240
tcgctgcgta tctgctgcac tttcatcaac accagtcttt ctctccttg attgcattgc 300
ccaggcaaga gaacgcacgc acaccgaccg gaatagccat gatcttctga tccaatccaa 360
gatgggcctc aaggagcagc agctagacgc cactgaccaa actcgtgatg ccgccaaactc 420
cctcgcttct gtttctgacg agcaccacga gggaccctgt gtctcaagct gcagcaccga 480
caaggattct ggccttccaa gttgccgagt ctgccattgc gtgg

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1482403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

```
Ser Gly Ser Ala Gln Ser Gly Leu Arg Ser Val Glu Ser Ser Thr Pro
1          5          10          15
Ser Arg Phe Ala Ser Pro Ile Phe Phe Phe Arg Arg Arg Arg Arg
20          25          30
Ser Pro Thr Arg Arg Leu Ala Ala Ile Pro Lys Ser Ile His Gln Ser
35          40          45
Ser Val Ser Phe His Phe Ile Pro Val Gly Arg Arg Ser Thr Asp Arg
50          55          60
Glu Gln Ser Ile Thr Ser His Gln Thr Asn Leu Thr Ser Leu Val Pro
65          70          75          80
Arg Cys Val Ser Ala Leu Ser Ser Thr Pro Val Phe Leu Leu Leu
85          90          95
Asp Cys Ile Ala Gln Ala Arg Glu Arg Thr His Thr Asp Arg Asn Ser
100         105         110
His Asp Leu Leu Ile Gln Ser Lys Met Gly Leu Lys Glu Gln Gln Leu
115         120         125
Asp Ala Thr Asp Gln Thr Arg Asp Ala Ala Asn Ser Leu Ala Ser Val
130         135         140
Ser Asp Glu His His Glu Gly Pro Arg Val Ser Ser Cys Ser Thr Asp
145         150         155         160
Lys Asp Ser Gly Leu Pro Ser Cys Arg Val Cys His Cys Val
165         170
```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..451

(D) OTHER INFORMATION: / Ceres Seq. ID 1482404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

```
gtggacgact ggcgcggtgg tgatacgctt gttactctcc caggtcgccc gtcgagtcga      60
gcttctgcgt ggagtcgctt ctgcctctgc acaccgccac cgccggtgca cgcattgacgt      120
ccatgctcgc cgctcctggc caaggcctcg gctggctcac ccaaggatct gatgaaacta      180
gatgaagagc agccggggaa agctgaaact gacggagtat aacgccccct gcgggtactt      240
taggaaccag gacatcaatt gtgcttcgag ttcttgtgtg cctggaggaa acaggaagag      300
ttgattggaa aaagaaaaaa tgggatgtgt ttttcttttt gttcatgtga actgagatac      360
gacttaataa actagatctt cgaatgatgc tctgaccccc cccccccctt tttgttaatg      420
ctttttcatt gactaaaacg gttatgtaat g
```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1482405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Val Asp Asp Trp Arg Gly Gly Asp Thr Leu Val Thr Leu Pro Gly Arg
1 5 10 15
Pro Ser Ser Arg Ala Ser Ala Trp Ser Arg Phe Cys Leu Cys Thr Pro
20 25 30
Pro Pro Pro Val His Ala
35

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Trp Thr Thr Gly Ala Val Val Ile Arg Leu Leu Leu Ser Gln Val Ala
1 5 10 15
Arg Arg Val Glu Leu Leu Arg Gly Val Ala Ser Ala Ser Ala His Arg
20 25 30
His Arg Arg Cys Thr His Asp Val His Ala Arg Arg Ser Trp Pro Arg
35 40 45
Pro Arg Leu Ala His Pro Arg Ile
50 55

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met Lys Ser Ser Arg Gly Lys Leu Lys Leu Thr Glu Tyr Asn Ala Pro
1 5 10 15
Cys Gly Tyr Phe Arg Asn Gln Asp Ile Asn Cys Ala Ser Ser Ser Cys
20 25 30
Val Pro Gly Gly Asn Arg Lys Ser
35 40

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..553
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

aaagacgaag gtaatttgat cagcaccggg agacgagacg agagagagag aacgggggaa 60
acaacaccgc cgccaggagt gtccaccggg gggaaatgat ggcgggagca ttgccaaggt 120
ctcgccgtgc ttctccggct gcaggatggg tccgccgtgg agcatggaca gcctcgtaag 180

tgccttcac	gccggttaga	aattctcttt	agagttcgta	catgtattag	cttcatacca	240
caccgtgtga	gggggaaagg	caccatcacg	ccccgcgtgt	ngttggtcgg	caatggcacc	300
gctacctgcg	ctgccgggcta	gctatacccg	aggaagaaga	atagtgccag	ccaatgatct	360
agaaaaagag	ggccccggatt	agagactagg	tgaccgcttt	ggctcgggtca	agctggaccg	420
ttgattttct	gttaaaccgt	catgtgtgca	tacctgtgcg	caatagaatg	tgagccattg	480
atctgtgac	cgaggatcta	cagatcatac	cgtttggtga	ccctggagat	ctaatatgtg	540
ccatccgtgc	gtg					

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Lys	Asp	Glu	Gly	Asn	Leu	Ile	Ser	Thr	Gly	Arg	Arg	Asp	Glu	Arg	Glu
1				5					10				15		
Arg	Thr	Gly	Glu	Thr	Thr	Pro	Pro	Pro	Gly	Val	Phe	Thr	Gly	Gly	Lys
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

Met	Cys	Ala	Tyr	Leu	Cys	Ala	Ile	Glu	Cys	Glu	Pro	Leu	Ile	Cys	Asp
1				5				10					15		
Pro	Arg	Ile	Tyr	Arg	Ser	Tyr	Arg	Leu	Val	Thr	Leu	Glu	Ile		
			20				25					30			

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..809
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

aagtgcatta	attagtgcc	actgcagtag	ctactagcta	gcacagttca	tcgacctcgc	60
tcgtggcccg	caagcaatcg	ctcaagctaa	gccatggcgc	ctcgagccg	cctcctcgac	120
ctggagaggc	acgacgtgct	cttcttctac	ggcgatgggtg	cctaccacca	gagcgagagc	180
kncgtcgtcc	ttgtcgtcgt	cgtcgccgcc	ctgctcctcc	tcctcgtcgc	gccgctcccg	240
cacgccgctg	ccgtctgcgg	ggcgctctac	gtcgccctact	gcttccctct	cgaccgcgca	300
gcraagngcg	agcagctcca	gctcgtcgtg	tccttccact	gacactgccg	cgccgccggc	360

```
ggcagacgcc tctcgcccca ctactcgggg cacggtggca ggctatatga tctgtgcagaa      420
gcagaattga agtcgcaatg gtcagcatgc ttatatattacc agttaccatg cttaattgca      480
tagttgcact gtagtgatca ccgcaggaag atggctctgt gtggaataga gtagtaggct      540
taagcacatt tctgtattaca ggaaaagagt ttgtgggtcag aggtcttccc acgtatatag      600
ctgtctcttg agactctgca tggactctgc aatckggata tgcatgcact ataatacactt      660
cgaaataggg ccacagttga caaatcagcc aggaaacata tgtaatctgg attcttttca      720
aaaaaaaaatt gtaatacggc tactcttctc aggaatatat atgaatggac tgcacgggtt      780
tctttcagtc tgttgccctgt tcttcagcc
```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

```
Met Ala Pro Arg Ser Arg Leu Leu Asp Leu Glu Arg His Asp Val Leu
1           5           10           15
Phe Phe Tyr Gly Asp Gly Ala Tyr His Gln Ser Glu Ser Xaa Val Val
          20          25          30
Leu Val Val Val Val Ala Ala Leu Leu Leu Leu Val Ala Pro Leu
          35          40          45
Pro His Ala Ala Ala Val Cys Gly Ala Leu Tyr Val Ala Tyr Cys Phe
          50          55          60
Leu Leu Asp Arg Ala Xaa Lys Xaa Glu Gln Leu Gln Leu Val Val Ser
65          70          75          80
Phe His
```

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

```
Met Val Pro Thr Thr Arg Ala Arg Xaa Xaa Ser Ser Leu Ser Ser Ser
1           5           10           15
Ser Pro Pro Cys Ser Ser Ser Ser Ser Arg Arg Ser Arg Thr Pro Leu
          20          25          30
Pro Ser Ala Gly Arg Ser Thr Ser Pro Thr Ala Ser Ser Thr Ala
          35          40          45
Gln Xaa Xaa Ala Ser Ser Ser Ser Ser Cys Pro Ser Thr Asp Thr
          50          55          60
Ala Ala Pro Pro Ala Ala Asp Ala Ser Arg Pro Thr Thr Arg Gly Thr
65          70          75          80
Val Ala Gly Tyr Met Ile Val Gln Lys Gln Asn
          85          90
```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1482414
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:
Met Asp Ser Ala Ile Xaa Ile Cys Met His Tyr Asn His Phe Glu Ile
1 5 10 15
Gly Pro Gln Leu Thr Asn Gln Pro Gly Asn Ile Cys Asn Leu Asp Ser
20 25 30
Phe Gln Lys Lys Ile Val Ile Arg Leu Leu Phe Ser Gly Ile Tyr Met
35 40 45
Asn Gly Leu His Gly Phe Leu Ser Val Cys Cys Leu Phe Phe Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..871
(D) OTHER INFORMATION: / Ceres Seq. ID 1482415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

atatatacgc acacgcggtg ggagtrggag ggggagactc tgccctgacc acagcaaaca 60
acctcctctt tcctttccat ccatcggacc atcgatcaca attttcatgg cggtaagga 120
ctgcr gcggg cacaagggt gcgagtgcga gcgggagcgr ctgtaccggc ggtgctgcgc 180
ggcggtcgtg gctctgatcc tcctggctct cttcatcggt ctcgtcgtgt ggtggtgct 240
gcgccccac aagccccggt tctacctgca ggacctgtcg gtgctgtgcc tgaacgtgac 300
gccgcggst ccacgtacct gttcacgacg atgcaggcga cggtggcggc gcgcaaccgc 360
aacgagcgcg tgggcgtgta ctacgaccag gcgagcgcgt acgcggaggt acaagggcgt 420
ggcgatcacg gtgccgacgc ggctgcccgt gcagtaccag gggccccggg acgcgtccgt 480
gtggtccccg ttcctgcgcg ccccggaagg cggcgtgcag ytcccgcgcg agctggccgt 540
ggcstggcgc aggacgagac ggcgggctac gtgcntstcg acgtccgcgt cgacggctgg 600
gtccgctgga aggtcggtac cagctggatc tccgggtcact accacctccg cgtcaactgc 660
cncgcgctgc tcaccgtcaa cgacggcagg ggcagctacg gcgccaacac cggcgggcgc 720
accggatact tccgcttcca gcaggcagsg catgcgccgt agacgtctag cagtgtctc 780
tctctctctg taccagctag ctgtgtttgc caattcgctg atcgaatcaa aggacgatgc 840
ttccttcgtc ggtgttcac actcacgcac t

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..290
(D) OTHER INFORMATION: / Ceres Seq. ID 1482416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

Tyr Ile Arg Thr Arg Gly Gly Ser Xaa Arg Gly Arg Leu Cys Pro Asp
1 5 10 15
His Ser Lys Gln Pro Pro Leu Ser Phe Pro Ser Ile Gly Pro Ser Ile

Met	Ala	Val	Lys	Asp	Cys	Xaa	Gly	His	Lys	Gly	Cys	Glu	Cys	Glu	Arg
1				5					10					15	
Glu	Xaa	Leu	Tyr	Arg	Arg	Cys	Cys	Ala	Ala	Val	Val	Ala	Leu	Ile	Leu
			20					25					30		
Leu	Val	Leu	Phe	Ile	Val	Leu	Val	Val	Trp	Leu	Val	Leu	Arg	Pro	His
			35				40					45			
Lys	Pro	Arg	Phe	Tyr	Leu	Gln	Asp	Leu	Ser	Val	Leu	Cys	Leu	Asn	Val
	50					55					60				
Thr	Pro	Pro	Xaa	Pro	Arg	Thr	Cys	Ser	Arg	Arg	Cys	Arg	Arg	Arg	Trp
65				70					75					80	
Arg	Arg	Ala	Thr	Arg	Thr	Ser	Ala	Trp	Ala	Cys	Thr	Thr	Thr	Arg	Arg
				85					90					95	

Thr Arg Thr Arg Arg Tyr Lys Gly Val Ala Ile Thr Val Pro Thr Arg
100 105 110
Leu Pro Val Gln Tyr Gln Gly Pro Arg Asp Ala Ser Val Trp Ser Pro
115 120 125
Phe Leu Arg Ala Pro Glu Gly Gly Val Gln Xaa Pro Pro Gln Leu Ala
130 135 140
Val Xaa Trp Arg Arg Thr Arg Arg Arg Ala Thr Cys Xaa Ser Thr Ser
145 150 155 160
Ala Ser Thr Ala Gly Ser Ala Gly Arg Ser Val Pro Ala Gly Ser Arg
165 170 175
Val Thr Thr Thr Ser Ala Ser Thr Ala Xaa Arg Cys Ser Pro Ser Thr
180 185 190
Thr Ala Gly Ala Ala Thr Ala Pro Thr Pro Ala Ala Ala Pro Asp Thr
195 200 205
Ser Ala Ser Ser Arg Gln Xaa Met Arg Arg Arg Arg Leu Ala Val Leu
210 215 220
Ser Leu Ser Leu Tyr Gln Leu Ala Val Phe Ala Asn Ser Ser Ile Glu
225 230 235 240
Ser Lys Asp Asp Ala Ser Phe Val Gly Val His His Ser Arg Thr
245 250 255

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..725
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

aggaacttgt aacctggctc gcagcggtgc gtgaaggacc tcgcgcgcgc tctcctctac	60
tgcttggtcg tctcggttgc ccggccgaac atccaagcct ctccatgtct ggcccttcga	120
aggagcagcg cgnccatgcc gcaactgggt gctggctaata ggctgtcggc acctccgct	180
tggccttcac ctggctcgtc ttcttcggct ccgggttgct ctgctcagcc acctactccg	240
agatacaggt gatcggcggt catggggcgca cgggttcgggt gtggacgctg ctgtcgtgca	300
ccctctgctt cctgtgcgcc ttcaacctca ccagcanagc cgctgtacgc ggccaccttc	360
ctgtccttcg tctacgcctt cgggtacctg agcaccgagt gcatgggtgta ccacaccatg	420
agtgcagcta gtctcgtccc gttcaccttc atcgtgtgta catccatggt ctggatgctg	480
attcaatgga actcggatgg tcacggcccc cgtcttcctt atgggtctac tgcttccaag	540
cagccatgac ttcgcaggtt ctctcaccta tggcttcctt caactacata cggttcagtg	600
catgcaagca ccatggaatt atggaatata tgtaataatc gtttctatgt	660
ccgcagggct agtgaatgaa actagcaagc tatcatctgt gataaatttg taattttacc	720
actct	

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Glu Leu Val Thr Trp Leu Ala Ala Leu Arg Glu Gly Pro Arg Ala Arg
1 5 10 15

Ser Pro Leu Leu Leu Gly Arg Leu Val Ala Pro Ala Glu His Pro Ser
20 25 30
Leu Ser Met Ser Gly Pro Ser Lys Glu Gln Arg Xaa Met Pro Ala Leu
35 40 45
Gly Cys Trp Leu Met Ala Val Gly Thr Phe Arg Leu Ala Phe Thr Trp
50 55 60
Ser Cys Phe Phe Gly Ser Gly Xaa Leu Cys Ser Ala Thr Tyr Ser Glu
65 70 75 80
Ile Gln Val Ile Gly Val His Gly Arg Thr Val Ala Val Trp Thr Leu
85 90 95
Leu Ser Cys Thr Leu Cys Phe Leu Cys Ala Phe Asn Leu Thr Ser Xaa
100 105 110
Ala Ala Val Arg Gly His Leu Pro Val Leu Arg Leu Arg Leu Arg Val
115 120 125
Pro Glu His Arg Val His Gly Val Pro His His Glu Cys Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Met Ser Gly Pro Ser Lys Glu Gln Arg Xaa Met Pro Ala Leu Gly Cys
1 5 10 15
Trp Leu Met Ala Val Gly Thr Phe Arg Leu Ala Phe Thr Trp Ser Cys
20 25 30
Phe Phe Gly Ser Gly Xaa Leu Cys Ser Ala Thr Tyr Ser Glu Ile Gln
35 40 45
Val Ile Gly Val His Gly Arg Thr Val Ala Val Trp Thr Leu Leu Ser
50 55 60
Cys Thr Leu Cys Phe Leu Cys Ala Phe Asn Leu Thr Ser Xaa Ala Ala
65 70 75 80
Val Arg Gly His Leu Pro Val Leu Arg Leu Arg Leu Arg Val Pro Glu
85 90 95
His Arg Val His Gly Val Pro His His Glu Cys Ser
100 105

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met Pro Ala Leu Gly Cys Trp Leu Met Ala Val Gly Thr Phe Arg Leu
1 5 10 15
Ala Phe Thr Trp Ser Cys Phe Phe Gly Ser Gly Xaa Leu Cys Ser Ala
20 25 30
Thr Tyr Ser Glu Ile Gln Val Ile Gly Val His Gly Arg Thr Val Ala

35 40 45
Val Trp Thr Leu Leu Ser Cys Thr Leu Cys Phe Leu Cys Ala Phe Asn
50 55 60
Leu Thr Ser Xaa Ala Ala Val Arg Gly His Leu Pro Val Leu Arg Leu
65 70 75 80
Arg Leu Arg Val Pro Glu His Arg Val His Gly Val Pro His His Glu
85 90 95
Cys Ser

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

aaccgcaagc tcaagcaaaa acacaaagcg cttaaaccac actcaaacca accgccagcc 60
aacaacagg cctcctagtc ccgaccagaa ctgcgtcgta gccccgagaa cccgacagc

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Thr Ala Ser Ser Lys Asn Thr Lys Arg Leu Asn His Thr Gln Thr
1 5 10 15
Asn Arg Gln Pro Thr Asn Arg Pro Pro Ser Pro Asp Gln Asn Ser Leu
20 25 30
Val Ala Pro Arg Thr Arg Gln
35

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

atctttcgcc cgccgcccc agtcccgatc cgaagctgtg cctcgtagca ttctgatcca 60
atggcgccga cgtcgaagct gtcgacgggc atcaagcgcg ctctcgcggtc gcacgcgtac 120
catcgccgtg ggctgtgggc catgatgaac ttgagcgcaa gaagagtata ccgctttag 180
ttactctgta acgtacgcag gcagagagcg cgcgttccag cgtatacgta cacgtagacg 240
tagtacgtac atgtactacc cgttacttgc tctccaatcg agttgcagtt gcagccc

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482425
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:
Ile Phe Arg Pro Pro Pro Pro Val Pro Ile Arg Ser Cys Ala Ser Tyr
1 5 10 15
His Phe Asp Pro Met Ala Pro Thr Ser Lys Leu Ser Thr Gly Ile Lys
 20 25 30
Arg Ala Ser Arg Ser His Ala Tyr His Arg Arg Gly Leu Trp Ala Met
 35 40 45
Met Asn Leu Ser Ala Arg Arg Val Tyr Arg Leu
50 55

(2) INFORMATION FOR SEQ ID NO:559:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..47
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482426
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:
Phe Phe Ala Arg Arg Pro Gln Ser Arg Ser Glu Ala Val Pro Arg Thr
1 5 10 15
Ile Ser Ile Gln Trp Arg Arg Arg Arg Ser Cys Arg Arg Ala Ser Ser
 20 25 30
Ala Leu Arg Gly Arg Thr Arg Thr Ile Ala Val Gly Cys Gly Pro
 35 40 45

(2) INFORMATION FOR SEQ ID NO:560:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..62
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482427
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:
Phe Ser Pro Ala Ala Pro Ser Pro Asp Pro Lys Leu Cys Leu Val Pro
1 5 10 15
Phe Arg Ser Asn Gly Ala Asp Val Glu Ala Val Asp Gly His Gln Ala
 20 25 30
Arg Phe Ala Val Ala Arg Val Pro Ser Pro Trp Ala Val Gly His Asp
 35 40 45
Glu Leu Glu Arg Lys Lys Ser Ile Pro Leu Val Val Thr Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:561:
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..606
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

gtctcacaaa ctttttttta gtctatcggg aacccgcttc agctagcgag cattgagcag	60
tctgcagtcg ccgagccgcg tgtccgcccg gccggcggtt accaagctca ccaaaaatct	120
ttccagggttc gaggcgccc atgttcgcct gcaggctctt cctcgcaagg gatcatattg	180
tcgaaataag ttggcctcat tcgtgatgga aggggcgcaa ggatcaagca ttgtgacaaa	240
acacaataaa aggcagtctc ctgtgcagag atggaggcca gtttcaacag aagcagttcc	300
ccagcatcac caagatgaca ttattgagac atcaaattct ggaagcaaga aaattataga	360
ggattgcata gcttctagtg agaatttgcc accagatgga acaaccaatg ttgttgaagt	420
taccgccaat gatgcttcat cgtcaaaaaa taattttaagt tttgggtaca gttcaactaa	480
agtagttata gaagaccatg cggagttatc tggcttcaat aaggatctag ctgggtccaa	540
tgtcttcggg acacattcct yctctgttga ggcggtkcaa agtcgacagc ttgactactc	600
tcattt	

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

Met	Glu	Gly	Ala	Gln	Gly	Ser	Ser	Ile	Val	Thr	Lys	His	Asn	Lys	Arg
1				5					10					15	
Gln	Ser	Pro	Val	Gln	Arg	Trp	Arg	Pro	Val	Ser	Thr	Glu	Ala	Val	Pro
			20					25					30		
Gln	His	His	Gln	Asp	Asp	Ile	Ile	Glu	Thr	Ser	Asn	Ser	Gly	Ser	Lys
			35				40				45				
Lys	Ile	Ile	Glu	Asp	Cys	Ile	Ala	Ser	Ser	Glu	Asn	Leu	Pro	Pro	Asp
	50					55				60					
Gly	Thr	Thr	Asn	Val	Val	Glu	Val	Thr	Ala	Asn	Asp	Ala	Ser	Ser	Ser
65				70					75					80	
Lys	Asn	Asn	Leu	Ser	Phe	Gly	Tyr	Ser	Ser	Thr	Lys	Val	Val	Ile	Glu
			85					90						95	
Asp	His	Ala	Glu	Leu	Ser	Gly	Phe	Asn	Lys	Asp	Leu	Ala	Gly	Ser	Asn
		100						105				110			
Val	Phe	Gly	Thr	His	Ser	Xaa	Ser	Val	Glu	Ala	Xaa	Gln	Ser	Arg	Gln
		115					120					125			
Leu	Asp	Tyr	Ser	His											
	130														

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..451

(D) OTHER INFORMATION: / Ceres Seq. ID 1482430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

gaaaaacggcg	atgttggccg	tcccattttg	taagctcccc	ttccccgtct	ggccgtctcg	60
actgccccag	tcctttctca	gatccatgtc	taccagaat	ctgctaactg	gcgcgtgcac	120
gagctccgcc	ccgaccccg	ccgagggcga	ggaaggggac	aggacgcctt	tggctgacgc	180
tgcgaacgcg	gcggaagagc	tgtaccgcct	ccgtgacacc	tttttccgcg	gggacccttc	240
cgagaaagtc	gccgcactcc	gcgcccgcgc	cgacgccgcc	ctcgcgctcc	tcgacgcctt	300
cccgtccgaa	caaaagaagt	ctcgacaact	gcgtggtgtt	tatgaatttt	tgaggggaaa	360
aatactggat	gtctttcctg	attatcataa	ggaggctgaa	gatcatttat	ccaaagcagt	420
aaagttgaac	ccatctcttg	tagatgcatg	g			

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1482431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

Lys	Thr	Ala	Met	Leu	Ala	Val	Pro	Phe	Cys	Lys	Leu	Pro	Phe	Pro	Val
1			5						10					15	
Trp	Pro	Ser	Arg	Leu	Pro	Gln	Ser	Phe	Leu	Arg	Ser	Met	Ser	Thr	Gln
			20					25					30		
Asn	Leu	Leu	Thr	Gly	Ala	Cys	Thr	Ser	Ser	Ala	Pro	Thr	Pro	Ser	Glu
			35				40					45			
Ala	Glu	Glu	Gly	Asp	Arg	Thr	Pro	Leu	Ala	Asp	Ala	Ala	Asn	Ala	Ala
			50			55				60					
Glu	Glu	Leu	Tyr	Arg	Leu	Arg	Asp	Thr	Phe	Phe	Pro	Arg	Asp	Pro	Ser
65				70					75					80	
Glu	Lys	Val	Ala	Ala	Leu	Arg	Ala	Arg	Ala	Asp	Ala	Ala	Leu	Ala	Leu
			85					90					95		
Leu	Asp	Ala	Phe	Pro	Ser	Glu	Gln	Lys	Lys	Ser	Arg	Gln	Leu	Arg	Gly
			100					105					110		
Val	Tyr	Glu	Phe	Leu	Arg	Gly	Lys	Ile	Leu	Asp	Val	Phe	Pro	Asp	Tyr
			115				120					125			
His	Lys	Glu	Ala	Glu	Asp	His	Leu	Ser	Lys	Ala	Val	Lys	Leu	Asn	Pro
			130				135					140			
Ser	Leu	Val	Asp	Ala	Trp										
145					150										

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1482432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

Met	Leu	Ala	Val	Pro	Phe	Cys	Lys	Leu	Pro	Phe	Pro	Val	Trp	Pro	Ser
1			5					10					15		
Arg	Leu	Pro	Gln	Ser	Phe	Leu	Arg	Ser	Met	Ser	Thr	Gln	Asn	Leu	Leu

	20							25						30				
Thr	Gly	Ala	Cys	Thr	Ser	Ser	Ala	Pro	Thr	Pro	Ser	Glu	Ala	Glu	Glu			
		35						40					45					
Gly	Asp	Arg	Thr	Pro	Leu	Ala	Asp	Ala	Ala	Asn	Ala	Ala	Glu	Glu	Leu			
	50						55					60						
Tyr	Arg	Leu	Arg	Asp	Thr	Phe	Phe	Pro	Arg	Asp	Pro	Ser	Glu	Lys	Val			
65					70					75					80			
Ala	Ala	Leu	Arg	Ala	Arg	Ala	Asp	Ala	Ala	Leu	Ala	Leu	Leu	Asp	Ala			
					85					90				95				
Phe	Pro	Ser	Glu	Gln	Lys	Lys	Ser	Arg	Gln	Leu	Arg	Gly	Val	Tyr	Glu			
			100						105				110					
Phe	Leu	Arg	Gly	Lys	Ile	Leu	Asp	Val	Phe	Pro	Asp	Tyr	His	Lys	Glu			
		115					120					125						
Ala	Glu	Asp	His	Leu	Ser	Lys	Ala	Val	Lys	Leu	Asn	Pro	Ser	Leu	Val			
	130						135					140						
Asp	Ala	Trp																
145																		

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Met	Ser	Thr	Gln	Asn	Leu	Leu	Thr	Gly	Ala	Cys	Thr	Ser	Ser	Ala	Pro			
1				5					10					15				
Thr	Pro	Ser	Glu	Ala	Glu	Glu	Gly	Asp	Arg	Thr	Pro	Leu	Ala	Asp	Ala			
			20					25					30					
Ala	Asn	Ala	Ala	Glu	Glu	Leu	Tyr	Arg	Leu	Arg	Asp	Thr	Phe	Phe	Pro			
	35						40					45						
Arg	Asp	Pro	Ser	Glu	Lys	Val	Ala	Ala	Leu	Arg	Ala	Arg	Ala	Asp	Ala			
	50						55					60						
Ala	Leu	Ala	Leu	Leu	Asp	Ala	Phe	Pro	Ser	Glu	Gln	Lys	Lys	Ser	Arg			
65					70					75				80				
Gln	Leu	Arg	Gly	Val	Tyr	Glu	Phe	Leu	Arg	Gly	Lys	Ile	Leu	Asp	Val			
				85					90					95				
Phe	Pro	Asp	Tyr	His	Lys	Glu	Ala	Glu	Asp	His	Leu	Ser	Lys	Ala	Val			
		100						105					110					
Lys	Leu	Asn	Pro	Ser	Leu	Val	Asp	Ala	Trp									
	115						120											

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

ataccgggat	gggcgccatg	ggcatcgctc	gcagagcgtg	ggcgccctccc	gctcttgccg	60
ccgcggccgc	gccggcacc	tccggctcca	gggacaccgg	tcaggcccag	cggaggagca	120

```
agccctcgag gaccggccgc gtgcgcgtgc tcggcgccac tggccgtgtc ggaggatcca 180
cgccaccgc actctccaaa ctccgcccc agettgcat cctcgtcggt ggcaggaacc 240
gggagaaagg cgagtccatt gcagccaagc ttgggggcca gtctgagttc gtccaggtcg 300
acaccgcaa cacaggcatg ttggaggaag cgctgcaggt ggtagctgtt cgcggagttg 360
ccaaaccgga ggcagctgcg acgccggcga ggcgctcgcg ccccatccct ctggcttccg 420
tggccgtgtg gagtctggtt gccactggcg ccgcaaatgc tgc
```

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

```
Thr Gly Met Gly Ala Met Gly Ile Val Val Arg Ala Trp Ala Pro Pro
1          5          10          15
Ala Leu Ala Ala Ala Ala Pro Ala Pro Ser Gly Ser Arg Asp Thr
20          25          30
Gly Gln Ala Gln Arg Arg Ser Lys Pro Ser Arg Thr Gly Arg Val Arg
35          40          45
Val Leu Gly Gly Thr Gly Arg Val Gly Gly Ser Thr Ala Thr Ala Leu
50          55          60
Ser Lys Leu Arg Pro Lys Leu Gly Ile Leu Val Gly Gly Arg Asn Arg
65          70          75          80
Glu Lys Gly Glu Ser Ile Ala Ala Lys Leu Gly Gly Gln Ser Glu Phe
85          90          95
Val Gln Val Asp Thr Arg Asn Thr Gly Met Leu Glu Glu Ala Leu Gln
100         105         110
Val Val Ala Val Arg Gly Val Ala Lys Pro Glu Ala Ala Thr Pro
115         120         125
Ala Arg Arg Ser Arg Pro Ile Pro Leu Ala Ser Val Ala Val Trp Ser
130         135         140
Leu Val Ala Thr Gly Ala Ala Asn Ala
145         150
```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1482436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

```
Met Gly Ala Met Gly Ile Val Val Arg Ala Trp Ala Pro Pro Ala Leu
1          5          10          15
Ala Ala Ala Ala Ala Pro Ala Pro Ser Gly Ser Arg Asp Thr Gly Gln
20          25          30
Ala Gln Arg Arg Ser Lys Pro Ser Arg Thr Gly Arg Val Arg Val Leu
35          40          45
Gly Gly Thr Gly Arg Val Gly Gly Ser Thr Ala Thr Ala Leu Ser Lys
50          55          60
Leu Arg Pro Lys Leu Gly Ile Leu Val Gly Gly Arg Asn Arg Glu Lys
```

(2) INFORMATION FOR SEQ ID NO:570:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1482437

[illegible]

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1482438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

aaacgacgcc	gagggtttct	aacaacgtaa	aaagaagaag	gaaagaacag	catttggtct	60
cgtccgtacg	tacaggggaa	aggacaaaag	gcttcgggcg	gtggcgggcg	cgctggtcga	120
cgatcgttca	gagcgcgggg	agggagaaga	ggtcgymgyc	kscsatgtmt	sykrarcsgc	180
agccgtcgac	tcctggccac	atcgggaggc	tgccgaggtc	gagcgcgggg	tcsgcggcsa	240

```
ggtagtcgag gccgagctgc ggmgtgggca agtcgtcgtc gaacgggacg ccgccgtaaa      300
gagaacgcgt cctcgccgag ctggggcagg agcgcgtcat cggcggaraa cgggkwkagg      360
ccgccsgggc cgtcgggcgc ktctttcttg gtcgcacaac cggmggcggm gtycgyykat      420
tttyggcggc agartckcac gcgccgtctc gtcgggcatt gcccggagga cggagaccgg      480
cgagccnacc accakctggg actcgtcgca g
```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```
Thr Thr Pro Arg Val Ser Asn Asn Val Lys Arg Arg Arg Lys Glu Gln
1          5          10          15
His Leu Ala Pro Ser Val Arg Thr Gly Glu Arg Thr Lys Gly Phe Gly
          20          25          30
Arg Trp Arg Pro Arg Trp Ser Thr Ile Val Gln Ser Ala Gly Arg Glu
          35          40          45
Lys Arg Ser Xaa Xaa Xaa Met Xaa Xaa Xaa Xaa Gln Pro Ser Thr Pro
          50          55          60
Gly His Ile Gly Arg Leu Pro Arg Ser Ser Ala Gly Xaa Ala Xaa Arg
          65          70          75          80
```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..613
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```
mrgtsccaag aatgtttctca cgaagctgat taaatcattg aaccttagat taactgctgt      60
gcaactaatt gattcccatac tatgttgtga tcccgggaac tacgtaagtt cgctacttct      120
ctccttatcc acaatgcttc acatgggaact cccacatgtc aatatattgt ctaaaatcga      180
tctgattgga agctacggga agctagcttt caatttagat ttctataaccg atgttcaaga      240
cttgtcatac ttggagcacc atcttagtca agatcctcgc tctgctaagt acagaaaact      300
aacaaaagag ctatgtagtg tcattgaaga ttacagtctt gttaatttta caaccttgga      360
tattcaggat aaagaaagtg ttgggggatct agtaaagctc atcgacaaga gcaatggata      420
catatttgcc ggcattgatg caagtgtggt tgaatacagc aagattgcaa ttggtcaaac      480
tgattgggat tataacagag tcgcagctgt acaggagaag tacatggaag atgaggaaat      540
acaagactga gaacagtgtc tgaaacttta tatagaagag agctggtcta aaatatctct      600
gaaccaaacc att
```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1482445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Xaa Xaa Lys Asn Val Leu Thr Lys Leu Ile Lys Ser Leu Asn Leu Arg
1 5 10 15
Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys Cys Asp Pro Gly
20 25 30
Asn Tyr Val Ser Ser Leu Leu Leu Ser Leu Ser Thr Met Leu His Met
35 40 45
Glu Leu Pro His Val Asn Ile Leu Ser Lys Ile Asp Leu Ile Gly Ser
50 55 60
Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr Asp Val Gln Asp
65 70 75 80
Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro Arg Ser Ala Lys
85 90 95
Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile Glu Asp Tyr Ser
100 105 110
Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys Glu Ser Val Gly
115 120 125
Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr Ile Phe Ala Gly
130 135 140
Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala Ile Gly Gln Thr
145 150 155 160
Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu Lys Tyr Met Glu
165 170 175
Asp Glu Glu Ile Gln Asp
180

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1482446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Met Leu His Met Glu Leu Pro His Val Asn Ile Leu Ser Lys Ile Asp
1 5 10 15
Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr
20 25 30
Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro
35 40 45
Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile
50 55 60
Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys
65 70 75 80
Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr
85 90 95
Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala
100 105 110
Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu
115 120 125
Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp
130 135

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Glu Leu Pro His Val Asn Ile Leu Ser Lys Ile Asp Leu Ile Gly
1 5 10 15
Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr Asp Val Gln
20 25 30
Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro Arg Ser Ala
35 40 45
Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile Glu Asp Tyr
50 55 60
Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys Glu Ser Val
65 70 75 80
Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr Ile Phe Ala
85 90 95
Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala Ile Gly Gln
100 105 110
Thr Asp Trp Asp Tyr Asn Arg Val Ala Val Gln Glu Lys Tyr Met
115 120 125
Glu Asp Glu Glu Ile Gln Asp
130 135

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

gatttttgaga aaaccatctc actgattagc caagatgtcg tcggctcggt ctgcgatcac 60
aaagctaaag ctggctcgat cctttgggga gagtcagatt ggtgcatcgc gttcgggtggt 120
atcgactcga ggaccggcga ttcggtactt cagtgcgat aaaggtcgtg tgctcagcga 180
agaggaacgc gcgaaagaga gcatgtatat ccagaaaatg gagagggaaa gactggagaa 240
gaagaagaaa ctcgagcaag ataagctaga tggtagagaaa ggaagtgcc acaagaaacc 300
tgagacaagc aagccatgag tttatcactc acagtataca gaatccggtc ataaggcaag 360
cagtagtgaa aaacaataat gcctttgacc tatgttctct cttggtatga gagatcttgt 420
acttgtacag agatctttta ccttctgatg tgtgtgtttg tatgttctaa gaaatcaagt 480
ttaaataat cgaaaaaac aaccatattg cttgattc

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1482458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

Asp Phe Glu Lys Thr Ile Ser Leu Ile Ser Gln Asp Val Val Gly Ser
1 5 10 15
Phe Cys Asp His Lys Ala Lys Ala Gly Ser Ile Leu Trp Gly Glu Ser
20 25 30
Asp Trp Cys Ile Ala Phe Gly Gly Ile Asp Ser Arg Thr Gly Asp Ser
35 40 45
Val Leu Gln
50

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1482459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met Ser Ser Ala Arg Ser Ala Ile Thr Lys Leu Lys Leu Ala Arg Ser
1 5 10 15
Phe Gly Glu Ser Gln Ile Gly Ala Ser Arg Ser Val Val Ser Thr Arg
20 25 30
Gly Pro Ala Ile Arg Tyr Phe Ser Asp Asp Lys Gly Arg Val Leu Ser
35 40 45
Glu Glu Glu Arg Ala Lys Glu Ser Met Tyr Ile Gln Lys Met Glu Arg
50 55 60
Glu Arg Leu Glu Lys Lys Lys Leu Glu Gln Asp Lys Leu Asp Gly
65 70 75 80
Glu Lys Gly Ser Ala Asn Lys Lys Pro Glu Thr Ser Lys Pro
85 90

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1116
(D) OTHER INFORMATION: / Ceres Seq. ID 1482460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

atagaacatc	ctaatacgaaa	aacattagtt	ttgctgcggt	tagtattcaa	tttcatcgac	60
ccaaatcaaa	atatatagga	tactagataa	agagtgaactg	aaggagagaa	aaacaaaaat	120
ggcgattggt	tccgtctcta	actcttttct	cactttcaat	tctcccaatc	agctccgatt	180
tagccgaaga	agattctctg	ccatggcttc	ttcaactact	ggagtgaag	tcgctgaagg	240
agaaggcaat	ttgccaaaac	tagtccttac	ttctcctcag	aacagcgagg	ctgagatata	300
tctcttcgga	ggctgcatta	cttcttgga	agttgcgagc	ggtaaagatc	ttctttttgt	360
cagaccagat	gctgtcttca	ataagattaa	gcccattagc	ggagggattc	cacattgttt	420
tccacagtgt	ggacctgggc	taattcaaca	gcatgggttt	ggaaggaaca	tggaactggtc	480
tggtgtcgat	tcccagaatg	cagatgacaa	tgctgctgtt	actcttgagc	ttaaggatgg	540
tccctatagt	cgagccatgt	gggactttgc	tttccaggct	ctatacaagg	tcattgttgg	600
cgcggactcc	ctttccactg	agctaaaagt	tacaaacaca	gacgataaac	cattttcttt	660

```
cagcactgcg ctgcatactt acttccgtgc ttcttctgcg ggggcctccg tgagaggtct 720
aaaggggtgt aaaaccctca ataaggatcc agaccctaag aacccaatag agggtaaaga 780
agacagggat gcagtcactt ttcctggatt tgtggatacc gtctatcttg atgctcccaa 840
tgaattgcag tttgataatg gcttgggtga taaaataatc atcaaaaaca caaattggtc 900
ggatgcggtc ttgtggaacc cgcatactca gatggaggct tgttacagag actttgtgtg 960
cgtggaaaat gcaaagcttg gggatgtcaa gctagagccg ggacagtctt ggactgcaac 1020
acaacttctc agcatcagtt gaaaacattg tactttaaac ttataatgtc cagtggatcc 1080
attttcttaa gcaataaaaag ttttatttcc tctccc
```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1482461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

```
Met Ala Ile Val Ser Val Ser Asn Ser Phe Leu Thr Phe Asn Ser Pro
1          5          10          15
Asn Gln Leu Arg Phe Ser Arg Arg Arg Phe Ser Ala Met Ala Ser Ser
          20          25          30
Thr Thr Gly Val Arg Val Ala Glu Gly Glu Gly Asn Leu Pro Lys Leu
          35          40          45
Val Leu Thr Ser Pro Gln Asn Ser Glu Ala Glu Ile Tyr Leu Phe Gly
          50          55          60
Gly Cys Ile Thr Ser Trp Lys Val Ala Ser Gly Lys Asp Leu Leu Phe
65          70          75          80
Val Arg Pro Asp Ala Val Phe Asn Lys Ile Lys Pro Ile Ser Gly Gly
          85          90          95
Ile Pro His Cys Phe Pro Gln Phe Gly Pro Gly Leu Ile Gln Gln His
          100          105          110
Gly Phe Gly Arg Asn Met Asp Trp Ser Val Val Asp Ser Gln Asn Ala
          115          120          125
Asp Asp Asn Ala Ala Val Thr Leu Glu Leu Lys Asp Gly Pro Tyr Ser
          130          135          140
Arg Ala Met Trp Asp Phe Ala Phe Gln Ala Leu Tyr Lys Val Ile Val
          145          150          155          160
Gly Ala Asp Ser Leu Ser Thr Glu Leu Lys Ile Thr Asn Thr Asp Asp
          165          170          175
Lys Pro Phe Ser Phe Ser Thr Ala Leu His Thr Tyr Phe Arg Ala Ser
          180          185          190
Ser Ala Gly Ala Ser Val Arg Gly Leu Lys Gly Cys Lys Thr Leu Asn
          195          200          205
Lys Asp Pro Asp Pro Lys Asn Pro Ile Glu Gly Lys Glu Asp Arg Asp
          210          215          220
Ala Val Thr Phe Pro Gly Phe Val Asp Thr Val Tyr Leu Asp Ala Pro
          225          230          235          240
Asn Glu Leu Gln Phe Asp Asn Gly Leu Gly Asp Lys Ile Ile Ile Lys
          245          250          255
Asn Thr Asn Trp Ser Asp Ala Val Leu Trp Asn Pro His Thr Gln Met
          260          265          270
Glu Ala Cys Tyr Arg Asp Phe Val Cys Val Glu Asn Ala Lys Leu Gly
          275          280          285
Asp Val Lys Leu Glu Pro Gly Gln Ser Trp Thr Ala Thr Gln Leu Leu
          290          295          300
Ser Ile Ser
```

305

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met	Ala	Ser	Ser	Thr	Thr	Gly	Val	Arg	Val	Ala	Glu	Gly	Glu	Gly	Asn	
1				5				10					15			
Leu	Pro	Lys	Leu	Val	Leu	Thr	Ser	Pro	Gln	Asn	Ser	Glu	Ala	Glu	Ile	
			20					25				30				
Tyr	Leu	Phe	Gly	Gly	Cys	Ile	Thr	Ser	Trp	Lys	Val	Ala	Ser	Gly	Lys	
		35				40					45					
Asp	Leu	Leu	Phe	Val	Arg	Pro	Asp	Ala	Val	Phe	Asn	Lys	Ile	Lys	Pro	
	50					55				60						
Ile	Ser	Gly	Gly	Ile	Pro	His	Cys	Phe	Pro	Gln	Phe	Gly	Pro	Gly	Leu	
65					70					75					80	
Ile	Gln	Gln	His	Gly	Phe	Gly	Arg	Asn	Met	Asp	Trp	Ser	Val	Val	Asp	
			85						90				95			
Ser	Gln	Asn	Ala	Asp	Asp	Asn	Ala	Ala	Val	Thr	Leu	Glu	Leu	Lys	Asp	
		100						105					110			
Gly	Pro	Tyr	Ser	Arg	Ala	Met	Trp	Asp	Phe	Ala	Phe	Gln	Ala	Leu	Tyr	
		115					120					125				
Lys	Val	Ile	Val	Gly	Ala	Asp	Ser	Leu	Ser	Thr	Glu	Leu	Lys	Ile	Thr	
	130					135					140					
Asn	Thr	Asp	Asp	Lys	Pro	Phe	Ser	Phe	Ser	Thr	Ala	Leu	His	Thr	Tyr	
145					150					155					160	
Phe	Arg	Ala	Ser	Ser	Ala	Gly	Ala	Ser	Val	Arg	Gly	Leu	Lys	Gly	Cys	
			165						170					175		
Lys	Thr	Leu	Asn	Lys	Asp	Pro	Asp	Pro	Lys	Asn	Pro	Ile	Glu	Gly	Lys	
		180						185					190			
Glu	Asp	Arg	Asp	Ala	Val	Thr	Phe	Pro	Gly	Phe	Val	Asp	Thr	Val	Tyr	
	195						200					205				
Leu	Asp	Ala	Pro	Asn	Glu	Leu	Gln	Phe	Asp	Asn	Gly	Leu	Gly	Asp	Lys	
	210					215					220					
Ile	Ile	Ile	Lys	Asn	Thr	Asn	Trp	Ser	Asp	Ala	Val	Leu	Trp	Asn	Pro	
225				230						235					240	
His	Thr	Gln	Met	Glu	Ala	Cys	Tyr	Arg	Asp	Phe	Val	Cys	Val	Glu	Asn	
			245						250					255		
Ala	Lys	Leu	Gly	Asp	Val	Lys	Leu	Glu	Pro	Gly	Gln	Ser	Trp	Thr	Ala	
		260						265					270			
Thr	Gln	Leu	Leu	Ser	Ile	Ser										

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1482463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met Asp Trp Ser Val Val Asp Ser Gln Asn Ala Asp Asp Asn Ala Ala
1 5 10 15
Val Thr Leu Glu Leu Lys Asp Gly Pro Tyr Ser Arg Ala Met Trp Asp
20 25 30
Phe Ala Phe Gln Ala Leu Tyr Lys Val Ile Val Gly Ala Asp Ser Leu
35 40 45
Ser Thr Glu Leu Lys Ile Thr Asn Thr Asp Asp Lys Pro Phe Ser Phe
50 55 60
Ser Thr Ala Leu His Thr Tyr Phe Arg Ala Ser Ser Ala Gly Ala Ser
65 70 75 80
Val Arg Gly Leu Lys Gly Cys Lys Thr Leu Asn Lys Asp Pro Asp Pro
85 90 95
Lys Asn Pro Ile Glu Gly Lys Glu Asp Arg Asp Ala Val Thr Phe Pro
100 105 110
Gly Phe Val Asp Thr Val Tyr Leu Asp Ala Pro Asn Glu Leu Gln Phe
115 120 125
Asp Asn Gly Leu Gly Asp Lys Ile Ile Ile Lys Asn Thr Asn Trp Ser
130 135 140
Asp Ala Val Leu Trp Asn Pro His Thr Gln Met Glu Ala Cys Tyr Arg
145 150 155 160
Asp Phe Val Cys Val Glu Asn Ala Lys Leu Gly Asp Val Lys Leu Glu
165 170 175
Pro Gly Gln Ser Trp Thr Ala Thr Gln Leu Leu Ser Ile Ser
180 185 190

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1430
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

ccwagaamca	tcctaatacaa	aaaacaattc	ccgaaattct	ctcaaatacac	agatccctttt	60
aggggtttttc	cactgttttct	aggtttttttt	tattgtctcaa	atctgatcaa	tggatagttg	120
tctctctaata	caaacggcgc	ttcagtttct	cccgtcgcgt	tccaggagac	agagcggcga	180
tggaggcgggt	ggttttggtta	ttccggcgaa	gaggaagatc	cagtatagtt	cgatggttgt	240
ggttgcgggcg	gcgggacaga	gtcgggtgtga	gcctggaagc	agtctaaacg	cgccgcttga	300
gccacgatcg	gcgcagggga	ggtttctgag	aagcgtgttg	ctaaacaaac	ggcagctatt	360
tcattacgcc	gccgctgatg	agctaaagca	actggctgat	gatagggaag	ctgcttttagc	420
tcgtatgtct	ctcagctctg	gttccgatga	ggcttctctc	cacagaagga	tagctgaact	480
caaggaacgc	tactgtaaaa	ctgcagtcca	agacataatg	tacatgttaa	tctttttacaa	540
atactccgag	ataagagtcc	ctcttggtcc	aaagctatcc	agatgcatct	ataatggaag	600
actcgagatc	tggccttcaa	aagactggga	gttagagtca	atttacagct	gcgataccct	660
tgagatcatc	aaagaacacg	ttagcgcagt	catcggatta	cgggtcaact	catgtgtgac	720
tgacaattgg	gcaacaacgc	agatacagaa	actgcattct	aggaaagtat	atgctgcctc	780
gatcttgtag	ggttacttct	tgaaatcagc	ttccctaagg	caccagcttg	agtgttccct	840
atcagatatt	catggaagcg	gatattctgaa	aagtcccatc	tttggtatgct	cattcacaa	900
gggcactgca	cagatctcca	acaagcagca	gctgagacat	tacatctcag	actttgatcc	960
cgagacattg	cagagatgcg	caaaaccaag	gacagaggag	gcaaggaatc	tgatagagaa	1020
gcaaagtttg	gctctttttg	gcacggaaga	gagtgatgag	accatagtga	catcgttttc	1080
gagtcgtgaag	cggtttggtc	tcgaggctgt	ggcgtttggg	acattcctgt	gggacacgga	1140
attgtatgta	gatggtgcat	ataagctgaa	ggagaatggg	aatgcagaag	aacaagaagg	1200
aaagaaaagc	atatgatgaa	caagtctggt	tagaagaaaa	gcttcatgat	cttctggtag	1260

tgtatatata gagaaatgta tctgccgaat ctctcaggca gttgttcagt tcaatgtata 1320
gatcttgctt agaaatattt tgatttctga ataagaatgt ggtgtgggta taaggaataa 1380
gagatactgt agttgggttc aattttatgt tatgtgttaa gtttccttgt

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

Met	Asp	Ser	Cys	Leu	Ser	Asn	Gln	Thr	Ala	Leu	Gln	Phe	Leu	Pro	Ser	
1			5				10							15		
Arg	Ser	Arg	Arg	Gln	Ser	Gly	Asp	Gly	Gly	Gly	Gly	Phe	Val	Ile	Pro	
			20				25						30			
Ala	Lys	Arg	Lys	Ile	Gln	Tyr	Ser	Ser	Met	Val	Val	Val	Ala	Ala	Ala	
			35				40					45				
Gly	Gln	Ser	Arg	Cys	Glu	Pro	Gly	Ser	Ser	Leu	Asn	Ala	Pro	Leu	Glu	
			50				55				60					
Pro	Arg	Ser	Ala	Gln	Gly	Arg	Phe	Leu	Arg	Ser	Val	Leu	Leu	Asn	Lys	
65						70				75					80	
Arg	Gln	Leu	Phe	His	Tyr	Ala	Ala	Ala	Asp	Glu	Leu	Lys	Gln	Leu	Ala	
				85					90					95		
Asp	Asp	Arg	Glu	Ala	Ala	Leu	Ala	Arg	Met	Ser	Leu	Ser	Ser	Gly	Ser	
			100					105					110			
Asp	Glu	Ala	Ser	Leu	His	Arg	Arg	Ile	Ala	Glu	Leu	Lys	Glu	Arg	Tyr	
			115				120					125				
Cys	Lys	Thr	Ala	Val	Gln	Asp	Ile	Met	Tyr	Met	Leu	Ile	Phe	Tyr	Lys	
			130			135					140					
Tyr	Ser	Glu	Ile	Arg	Val	Pro	Leu	Val	Pro	Lys	Leu	Ser	Arg	Cys	Ile	
145					150					155					160	
Tyr	Asn	Gly	Arg	Leu	Glu	Ile	Trp	Pro	Ser	Lys	Asp	Trp	Glu	Leu	Glu	
				165				170						175		
Ser	Ile	Tyr	Ser	Cys	Asp	Thr	Leu	Glu	Ile	Ile	Lys	Glu	His	Val	Ser	
			180					185					190			
Ala	Val	Ile	Gly	Leu	Arg	Val	Asn	Ser	Cys	Val	Thr	Asp	Asn	Trp	Ala	
			195				200					205				
Thr	Thr	Gln	Ile	Gln	Lys	Leu	His	Leu	Arg	Lys	Val	Tyr	Ala	Ala	Ser	
			210			215					220					
Ile	Leu	Tyr	Gly	Tyr	Phe	Leu	Lys	Ser	Ala	Ser	Leu	Arg	His	Gln	Leu	
225					230					235					240	
Glu	Cys	Ser	Leu	Ser	Asp	Ile	His	Gly	Ser	Gly	Tyr	Leu	Lys	Ser	Pro	
				245				250						255		
Ile	Phe	Gly	Cys	Ser	Phe	Thr	Thr	Gly	Thr	Ala	Gln	Ile	Ser	Asn	Lys	
			260					265					270			
Gln	Gln	Leu	Arg	His	Tyr	Ile	Ser	Asp	Phe	Asp	Pro	Glu	Thr	Leu	Gln	
			275				280					285				
Arg	Cys	Ala	Lys	Pro	Arg	Thr	Glu	Glu	Ala	Arg	Asn	Leu	Ile	Glu	Lys	
			290			295					300					
Gln	Ser	Leu	Ala	Leu	Phe	Gly	Thr	Glu	Glu	Ser	Asp	Glu	Thr	Ile	Val	
305					310					315					320	
Thr	Ser	Phe	Ser	Ser	Leu	Lys	Arg	Leu	Val	Leu	Glu	Ala	Val	Ala	Phe	
				325				330						335		
Gly	Thr	Phe	Leu	Trp	Asp	Thr	Glu	Leu	Tyr	Val	Asp	Gly	Ala	Tyr	Lys	
			340					345					350			

Leu Lys Glu Asn Gly Asn Ala Glu Glu Gln Glu Gly Lys Lys Ser Ile
355 360 365

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..327
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met Val Val Val Ala Ala Ala Gly Gln Ser Arg Cys Glu Pro Gly Ser
1 5 10 15
Ser Leu Asn Ala Pro Leu Glu Pro Arg Ser Ala Gln Gly Arg Phe Leu
20 25 30
Arg Ser Val Leu Leu Asn Lys Arg Gln Leu Phe His Tyr Ala Ala Ala
35 40 45
Asp Glu Leu Lys Gln Leu Ala Asp Asp Arg Glu Ala Ala Leu Ala Arg
50 55 60
Met Ser Leu Ser Ser Gly Ser Asp Glu Ala Ser Leu His Arg Arg Ile
65 70 75 80
Ala Glu Leu Lys Glu Arg Tyr Cys Lys Thr Ala Val Gln Asp Ile Met
85 90 95
Tyr Met Leu Ile Phe Tyr Lys Tyr Ser Glu Ile Arg Val Pro Leu Val
100 105 110
Pro Lys Leu Ser Arg Cys Ile Tyr Asn Gly Arg Leu Glu Ile Trp Pro
115 120 125
Ser Lys Asp Trp Glu Leu Glu Ser Ile Tyr Ser Cys Asp Thr Leu Glu
130 135 140
Ile Ile Lys Glu His Val Ser Ala Val Ile Gly Leu Arg Val Asn Ser
145 150 155 160
Cys Val Thr Asp Asn Trp Ala Thr Thr Gln Ile Gln Lys Leu His Leu
165 170 175
Arg Lys Val Tyr Ala Ala Ser Ile Leu Tyr Gly Tyr Phe Leu Lys Ser
180 185 190
Ala Ser Leu Arg His Gln Leu Glu Cys Ser Leu Ser Asp Ile His Gly
195 200 205
Ser Gly Tyr Leu Lys Ser Pro Ile Phe Gly Cys Ser Phe Thr Thr Gly
210 215 220
Thr Ala Gln Ile Ser Asn Lys Gln Gln Leu Arg His Tyr Ile Ser Asp
225 230 235 240
Phe Asp Pro Glu Thr Leu Gln Arg Cys Ala Lys Pro Arg Thr Glu Glu
245 250 255
Ala Arg Asn Leu Ile Glu Lys Gln Ser Leu Ala Leu Phe Gly Thr Glu
260 265 270
Glu Ser Asp Glu Thr Ile Val Thr Ser Phe Ser Ser Leu Lys Arg Leu
275 280 285
Val Leu Glu Ala Val Ala Phe Gly Thr Phe Leu Trp Asp Thr Glu Leu
290 295 300
Tyr Val Asp Gly Ala Tyr Lys Leu Lys Glu Asn Gly Asn Ala Glu Glu
305 310 315 320
Gln Glu Gly Lys Lys Ser Ile
325

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..263
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482484
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met Ser Leu Ser Ser Gly Ser Asp Glu Ala Ser Leu His Arg Arg Ile
1 5 10 15
Ala Glu Leu Lys Glu Arg Tyr Cys Lys Thr Ala Val Gln Asp Ile Met
 20 25 30
Tyr Met Leu Ile Phe Tyr Lys Tyr Ser Glu Ile Arg Val Pro Leu Val
 35 40 45
Pro Lys Leu Ser Arg Cys Ile Tyr Asn Gly Arg Leu Glu Ile Trp Pro
 50 55 60
Ser Lys Asp Trp Glu Leu Glu Ser Ile Tyr Ser Cys Asp Thr Leu Glu
65 70 75 80
Ile Ile Lys Glu His Val Ser Ala Val Ile Gly Leu Arg Val Asn Ser
 85 90 95
Cys Val Thr Asp Asn Trp Ala Thr Thr Gln Ile Gln Lys Leu His Leu
 100 105 110
Arg Lys Val Tyr Ala Ala Ser Ile Leu Tyr Gly Tyr Phe Leu Lys Ser
 115 120 125
Ala Ser Leu Arg His Gln Leu Glu Cys Ser Leu Ser Asp Ile His Gly
 130 135 140
Ser Gly Tyr Leu Lys Ser Pro Ile Phe Gly Cys Ser Phe Thr Thr Gly
145 150 155 160
Thr Ala Gln Ile Ser Asn Lys Gln Gln Leu Arg His Tyr Ile Ser Asp
 165 170 175
Phe Asp Pro Glu Thr Leu Gln Arg Cys Ala Lys Pro Arg Thr Glu Glu
 180 185 190
Ala Arg Asn Leu Ile Glu Lys Gln Ser Leu Ala Leu Phe Gly Thr Glu
 195 200 205
Glu Ser Asp Glu Thr Ile Val Thr Ser Phe Ser Ser Leu Lys Arg Leu
 210 215 220
Val Leu Glu Ala Val Ala Phe Gly Thr Phe Leu Trp Asp Thr Glu Leu
225 230 235 240
Tyr Val Asp Gly Ala Tyr Lys Leu Lys Glu Asn Gly Asn Ala Glu Glu
 245 250 255
Gln Glu Gly Lys Lys Ser Ile
 260

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 662 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..662
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482490
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

atcgaaaaag atcgaaaaaa aatcgagaag cgaatagcgg aagaacagaa aaagggaaat
tctgagaatc aaatcggaaa ggtagaagaa tcgagtcgga aaaatggaaa cgacgaaaag

60
120

taacagcagc	gagtcgatg	tcaacgccaa	atgggacgct	tgtctcgatc	tcactgctcg	180
tcgctttgtc	tactcttccc	tcggcggcgc	tttcgccggt	cttctcttct	tcaggagtcc	240
ggttacgaga	tgggcgtcga	ttgcttttgg	tgctggaatt	ggatttggtt	ctgcatacac	300
agattgttct	cgtgtttttg	atgcgtcttc	ttcaacttca	gctactttat	tagcagctcc	360
caagagtaca	gagacttctg	tatctcaggc	agcagaagag	tgaagacaac	gaggaagctt	420
ggaggtaaaa	aaccaaacad	tgataggggt	acattacgaa	atggtaattg	atcttgagg	480
acaaggcttt	tgagataacg	ccattgttaa	aaaaaaaaactt	ttgcttctca	gtgtgggttt	540
gtacactgat	gtcaaaattg	ttaatgaccc	actcattttt	ttttgttttg	aaaaatctta	600
tgctctttta	cttgagaaat	aattcctccg	ttgatttggt	tgctctact	gttccttcat	660
tc						

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Met	Glu	Thr	Thr	Lys	Ser	Asn	Ser	Ser	Glu	Ser	Asp	Val	Asn	Ala	Lys	
1				5					10					15		
Trp	Asp	Ala	Cys	Leu	Asp	Leu	Thr	Ala	Arg	Arg	Phe	Val	Tyr	Ser	Ser	
			20					25					30			
Leu	Gly	Gly	Ala	Phe	Ala	Gly	Leu	Leu	Phe	Phe	Arg	Ser	Pro	Val	Thr	
			35				40					45				
Arg	Trp	Ala	Ser	Ile	Ala	Phe	Gly	Ala	Gly	Ile	Gly	Ile	Gly	Ser	Ala	
			50			55					60					
Tyr	Thr	Asp	Cys	Ser	Arg	Val	Phe	Asp	Ala	Ser	Ser	Ser	Thr	Ser	Ala	
			65			70				75				80		
Thr	Leu	Leu	Ala	Ala	Pro	Lys	Ser	Thr	Glu	Thr	Ser	Val	Ser	Gln	Ala	
				85					90					95		
Ala	Glu	Glu														

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Met	Ser	Thr	Pro	Asn	Gly	Thr	Leu	Val	Ser	Ile	Ser	Leu	Leu	Val	Ala	
1				5				10					15			
Leu	Ser	Thr	Leu	Pro	Ser	Ala	Ala	Leu	Ser	Pro	Val	Phe	Ser	Ser	Ser	
			20					25				30				
Gly	Val	Arg	Leu	Arg	Asp	Gly	Arg	Arg	Leu	Leu	Leu	Val	Leu	Glu	Leu	
			35				40					45				
Val	Leu	Val	Leu	His	Thr	Gln	Ile	Val	Leu	Val	Phe	Leu	Met	Arg	Leu	
			50			55					60					
Leu	Gln	Leu	Gln	Leu	Leu	Tyr										
						70										

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

Met	Gly	Arg	Leu	Ser	Arg	Ser	His	Cys	Ser	Ser	Leu	Cys	Leu	Leu	Phe
1			5					10				15			
Pro	Arg	Arg	Arg	Phe	Arg	Arg	Ser	Ser	Leu	Leu	Gln	Glu	Ser	Gly	Tyr
		20					25				30				
Glu	Met	Gly	Val	Asp	Cys	Phe	Trp	Cys	Trp	Asn	Trp	Tyr	Trp	Phe	Cys
		35					40				45				
Ile	His	Arg	Leu	Phe	Ser	Cys	Phe								
	50					55									

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 853 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..853
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

ccattaccwa	kaacatccta	atcgaaaagt	aatcggagtt	caggcttcag	cattctctct	60
tcttctctct	cgcagccgta	gtttttgatc	ttctcttcaa	ttctctctcc	tgatggccac	120
gtccgcggtc	ctctccggtg	ccagatcgat	gcttcgagct	gcttcctcac	gcagcgccgc	180
tgcttctact	ggccgcttcg	cctctcaagc	gaaatccgct	ccaccattgt	ttagagccac	240
tgccagaaga	agcccactgc	tttctcctct	ccgaaatcct	gtggaactga	gcttctgtgt	300
ggagtcattg	ttaccatata	actcggctac	agcttcagcg	ctaatagact	caaagctttc	360
tatctctggc	caaacctatg	gctggctctc	tgacggctga	cacaagtgtg	gatgaagaca	420
acgaagccaa	gatctgggta	taaacgatta	gaacgggttt	caggcaataa	gataggcttt	480
agatacacat	caagcaatgg	ttgatgctgc	atttgtgttt	aaaagaactg	gttctttacat	540
atcttcttaa	aaaaaataca	tgtaccggga	aaagtgcctt	cttttcttgd	tggttatagc	600
atttgagtta	ttactgattg	gtcttatact	cccagcttgc	aatgatgatg	tgtgatgagt	660
tagccagagg	aacaatgaag	ctacagttta	tgtacaaaac	tctacctttt	aaagcctttc	720
ttcttaaaaa	acttaggaac	gaaaaccctc	ttaattttgt	ttctgagttt	cttggagagc	780
ttttgtttgt	tttcagccta	ttaagtaaga	catgttgtat	tggttggacg	agtaactgat	840
gtttggtata	att					

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met Ala Thr Ser Ala Val Leu Ser Gly Ala Arg Ser Met Leu Arg Ala

1	5	10	15												
Ala	Ser	Ser	Arg	Ser	Ala	Ala	Ala	Ser	Thr	Gly	Arg	Phe	Ala	Ser	Gln
	20							25					30		
Ala	Lys	Ser	Ala	Pro	Pro	Leu	Phe	Arg	Ala	Thr	Ala	Arg	Arg	Ser	Pro
	35						40					45			
Leu	Leu	Ser	Pro	Leu	Arg	Asn	Pro	Val	Glu	Leu	Ser	Phe	Cys	Val	Glu
	50					55					60				
Ser	Leu	Leu	Pro	Tyr	His	Ser	Ala	Thr	Ala	Ser	Ala	Leu	Met	Thr	Ser
65				70						75					80
Lys	Leu	Ser	Ile	Ser	Gly	Gln	Thr	Tyr	Gly	Trp	Leu	Ser	Asp	Gly	
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Met	Leu	Arg	Ala	Ala	Ser	Ser	Arg	Ser	Ala	Ala	Ala	Ser	Thr	Gly	Arg
1					5				10					15	
Phe	Ala	Ser	Gln	Ala	Lys	Ser	Ala	Pro	Pro	Leu	Phe	Arg	Ala	Thr	Ala
			20					25					30		
Arg	Arg	Ser	Pro	Leu	Leu	Ser	Pro	Leu	Arg	Asn	Pro	Val	Glu	Leu	Ser
		35				40						45			
Phe	Cys	Val	Glu	Ser	Leu	Leu	Pro	Tyr	His	Ser	Ala	Thr	Ala	Ser	Ala
	50					55				60					
Leu	Met	Thr	Ser	Lys	Leu	Ser	Ile	Ser	Gly	Gln	Thr	Tyr	Gly	Trp	Leu
65				70					75					80	
Ser	Asp	Gly													

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

Met	Met	Met	Cys	Asp	Glu	Leu	Ala	Arg	Gly	Thr	Met	Lys	Leu	Gln	Phe
1			5						10					15	
Met	Tyr	Lys	Thr	Leu	Pro	Phe	Lys	Ala	Phe	Leu	Leu	Lys	Lys	Leu	Arg
		20					25						30		
Asn	Glu	Asn	Pro	Leu	Asn	Phe	Val	Ser	Glu	Phe	Leu	Gly	Glu	Leu	Leu
	35				40							45			
Phe	Val	Phe	Ser	Leu	Leu	Ser	Lys	Thr	Cys	Cys	Ile	Gly	Trp	Thr	Ser
	50					55					60				
Asn															
65															

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1139

(D) OTHER INFORMATION: / Ceres Seq. ID 1482508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

caatcatctg atctttccct ctctcagcaa tgcattgatct tgcattttct atcagtgttc	60
aaagctgaaa aaaatcgaaac tgggtctgtt gatttcttca ggtctaaaat cagattagat	120
tagagaagaa gaagaagaat gctggaagct gtagatagct caggagtggg gaatggagga	180
ttcccgagaa ttacagagctt ttacggcgat tgcagttagt aagaagagtt atcgggtattg	240
ccacgtcata caaaagtggg ggtcaccgga aacaaccgga cgaatcggt gcttgttggg	300
cttcaaggtg ttgtcaaaaa agctgtcggt ctcggtgggt ggcattgggt ggttttgaca	360
aatggaatag aagtaaagtt gcagaggaat gcgcttagtg tccttgaacc tcctactgga	420
aacgaagaag acgatgatct tgatttcgaa aacacacaga ggaatggctc tgatatgatt	480
gtttcttttc cagcatctga ggacacactg aagcctcata agtcgaagct aagagggcag	540
agatcatctc ggtcatctca caagcagatg agcagggtct tatcatctga ctgcgaatca	600
aaaagtctcg gttttactcc tcctgaaaaac atgaagggtg atcttagcaa attggaaatg	660
cctgctttac tgaattattg gcgacatttt aaccttggg atgcaattcc aaatccatca	720
aaggagcaac taattgacat tgttcaaagg cacttcatgt ctacgcaaatt ggatgagctt	780
caggttattg tggggtttgt ccaagctgca aagagaatga agaaggcttg caagtttcaa	840
tccaaagaat ccagaaacac tgatcttaac tgcattcagct aaagaaaagc cctgactctt	900
aacaaatcct gtatgtacgg tacatcaact tgtttaacca tttgtggctt gctaagttta	960
gttcttctag tgatgtttgg ctaaagggtg gatgttgttt cttctttgct tctgttgttt	1020
agccaatgta agtaccatca aaaaacccaa ataactctct aaagctccct attggaaact	1080
atcttgtctg atacgatctg gagtgaccgg tatgttggtt gaatgtaaat atgtttggg	

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1482509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

Met	Leu	Glu	Ala	Val	Asp	Ser	Ser	Gly	Val	Val	Asn	Gly	Gly	Phe	Pro
1			5					10						15	
Gln	Ile	Gln	Ser	Phe	Tyr	Gly	Asp	Cys	Ser	Ser	Glu	Glu	Glu	Leu	Ser
			20					25						30	
Val	Leu	Pro	Arg	His	Thr	Lys	Val	Val	Val	Thr	Gly	Asn	Asn	Arg	Thr
			35					40						45	
Lys	Ser	Val	Leu	Val	Gly	Leu	Gln	Gly	Val	Val	Lys	Lys	Ala	Val	Gly
			50					55						60	
Leu	Gly	Gly	Trp	His	Trp	Leu	Val	Leu	Thr	Asn	Gly	Ile	Glu	Val	Lys
65								70						80	
Leu	Gln	Arg	Asn	Ala	Leu	Ser	Val	Leu	Glu	Pro	Pro	Thr	Gly	Asn	Glu
			85					90						95	
Glu	Asp	Asp	Asp	Leu	Asp	Phe	Glu	Asn	Thr	Gln	Arg	Asn	Gly	Ser	Asp
			100					105						110	
Met	Ile	Val	Ser	Phe	Pro	Ala	Ser	Glu	Asp	Thr	Leu	Lys	Pro	His	Lys
			115					120						125	
Ser	Lys	Leu	Arg	Gly	Gln	Arg	Ser	Ser	Arg	Ser	Ser	His	Lys	Thr	Met
			130					135						140	

Ser Arg Ser Leu Ser Ser Asp Ser Gln Ser Lys Ser Ser Gly Phe Thr
145 150 155 160
Pro Pro Glu Asn Met Lys Val Asp Leu Ser Lys Leu Glu Met Pro Ala
165 170 175
Leu Leu Asn Tyr Trp Arg His Phe Asn Leu Val Asp Ala Ile Pro Asn
180 185 190
Pro Ser Lys Glu Gln Leu Ile Asp Ile Val Gln Arg His Phe Met Ser
195 200 205
Gln Gln Met Asp Glu Leu Gln Val Ile Val Gly Phe Val Gln Ala Ala
210 215 220
Lys Arg Met Lys Lys Ala Cys Lys Phe Gln Ser Lys Glu Ser Arg Asn
225 230 235 240
Thr Asp Leu Asn Cys Ile Ser
245

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1482510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met Ile Val Ser Phe Pro Ala Ser Glu Asp Thr Leu Lys Pro His Lys
1 5 10 15
Ser Lys Leu Arg Gly Gln Arg Ser Ser Arg Ser Ser His Lys Thr Met
20 25 30
Ser Arg Ser Leu Ser Ser Asp Ser Gln Ser Lys Ser Ser Gly Phe Thr
35 40 45
Pro Pro Glu Asn Met Lys Val Asp Leu Ser Lys Leu Glu Met Pro Ala
50 55 60
Leu Leu Asn Tyr Trp Arg His Phe Asn Leu Val Asp Ala Ile Pro Asn
65 70 75 80
Pro Ser Lys Glu Gln Leu Ile Asp Ile Val Gln Arg His Phe Met Ser
85 90 95
Gln Gln Met Asp Glu Leu Gln Val Ile Val Gly Phe Val Gln Ala Ala
100 105 110
Lys Arg Met Lys Lys Ala Cys Lys Phe Gln Ser Lys Glu Ser Arg Asn
115 120 125
Thr Asp Leu Asn Cys Ile Ser
130 135

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1323

(D) OTHER INFORMATION: / Ceres Seq. ID 1482514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

ccattaccta gaacatccta atcaaaaaat tgatgttgat gataaagtct tatctgtttc 60
aattgatgca ggatgatgga gattgggctg ctattggtgt gaaagatggt caaaaattga 120
tgatgatggg aactgctgat gagatagtga aagctcctga gaaggccatt gtttttgcag 180

```
agaatctacc tgaagaagcg ctagccacta atctggggtta cagtgcgtggc cttgtcaatc 240
ttggcaacac gtgttacatg aactccacgg tgcagtgctt aaaatctgtc ccagagttga 300
aatctgcatt atccaattac tcacttgctg cccgaagcaa tgatgttgac cagacttctc 360
acatgctcac agttgccaca cgtgagttat ttgggtgagct tgatagaagt gtcaatgctg 420
tttcgccttc acagttcttg atggtattac gaaaaaagta tcctcagttt agtcagttgc 480
agaatggaat gcacatgcag caggatgctg aagaatggtg gacacaactg ttatacacc 540
tttctcagtc cctaaaagca ccaacttcca gcgaaggtgc tgatgctgtg aaagctctat 600
ttggtgtcaa tctccagagc aggttgctt gtcaagaaag tggcgaagaa agctcagaga 660
cagaatctgt atattctcta aaatgtcata tatcacatga agtgaaccac ttgcatgaag 720
gattaaaaca tggactgaaa ggggaacttg aaaaaacatc tcctgctctt ggccgtactg 780
cactctacgt caaggagtca cttatagatt ccttgccaag gtacttgact gttcagttcg 840
tgcggttttt ctggaagagg gagagtaatc agaaagcaaa gatcctcagg aaagtggatt 900
acccgctggg gttggatata tttagccttt gctctgagga tcttcggaag aaactggaag 960
ctcctcgcca gaaacttaga gaggaggaag gtaaaaagct tgggtcttcaa actagtgcta 1020
agagtggctc aaaggacagt gatgtgaaaa tgactgatgc agaggcgtct gcaaatggaa 1080
gtggagaatc atccacagta aaccacaggg aagggtactt gagccactct tagcactagt 1140
ttgaagacca agcctaaaca atgcttccac cttgtgttct ttttggatta taayccttca 1200
tgagttaatt ttggttgaac ctttggtagt atatgttgct ggattgtgca ctttctgttt 1260
tcctctctc ttccaaacta ctttattttt gcttatagat cttaatgttc tagttttgct 1320
ttt
```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..366
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```
Met Leu Met Ile Lys Ser Tyr Leu Phe Leu Leu Met Gln Asp Asp Gly
1          5          10          15
Asp Trp Ala Ala Ile Gly Val Lys Asp Gly Gln Lys Leu Met Met Met
          20          25          30
Gly Thr Ala Asp Glu Ile Val Lys Ala Pro Glu Lys Ala Ile Val Phe
          35          40          45
Ala Glu Asn Leu Pro Glu Glu Ala Leu Ala Thr Asn Leu Gly Tyr Ser
          50          55          60
Ala Gly Leu Val Asn Leu Gly Asn Thr Cys Tyr Met Asn Ser Thr Val
65          70          75          80
Gln Cys Leu Lys Ser Val Pro Glu Leu Lys Ser Ala Leu Ser Asn Tyr
          85          90          95
Ser Leu Ala Ala Arg Ser Asn Asp Val Asp Gln Thr Ser His Met Leu
          100          105          110
Thr Val Ala Thr Arg Glu Leu Phe Gly Glu Leu Asp Arg Ser Val Asn
          115          120          125
Ala Val Ser Pro Ser Gln Phe Trp Met Val Leu Arg Lys Lys Tyr Pro
          130          135          140
Gln Phe Ser Gln Leu Gln Asn Gly Met His Met Gln Gln Asp Ala Glu
145          150          155          160
Glu Cys Trp Thr Gln Leu Leu Tyr Thr Leu Ser Gln Ser Leu Lys Ala
          165          170          175
Pro Thr Ser Ser Glu Gly Ala Asp Ala Val Lys Ala Leu Phe Gly Val
          180          185          190
Asn Leu Gln Ser Arg Leu His Cys Gln Glu Ser Gly Glu Glu Ser Ser
195          200          205
Glu Thr Glu Ser Val Tyr Ser Leu Lys Cys His Ile Ser His Glu Val
```

210	215	220
Asn His Leu His Glu Gly	Leu Lys His Gly Leu Lys Gly Glu Leu Glu	
225	230	235
Lys Thr Ser Pro Ala Leu Gly Arg Thr Ala Leu Tyr Val Lys Glu Ser		240
	245	250
Leu Ile Asp Ser Leu Pro Arg Tyr Leu Thr Val Gln Phe Val Arg Phe		255
	260	265
Phe Trp Lys Arg Glu Ser Asn Gln Lys Ala Lys Ile Leu Arg Lys Val		270
	275	280
Asp Tyr Pro Leu Val Leu Asp Ile Phe Asp Leu Cys Ser Glu Asp Leu		285
	290	295
Arg Lys Lys Leu Glu Ala Pro Arg Gln Lys Leu Arg Glu Glu Glu Gly		300
305	310	315
Lys Lys Leu Gly Leu Gln Thr Ser Ala Lys Ser Gly Ser Lys Asp Ser		320
	325	330
Asp Val Lys Met Thr Asp Ala Glu Ala Ser Ala Asn Gly Ser Gly Glu		335
	340	345
Ser Ser Thr Val Asn Pro Gln Glu Gly Thr Leu Ser His Ser		350
	355	360
		365

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Met Ile Lys Ser Tyr Leu Phe Gln Leu Met Gln Asp Asp Gly Asp Trp	
1	5
Ala Ala Ile Gly Val Lys Asp Gly Gln Lys Leu Met Met Met Gly Thr	10
	20
Ala Asp Glu Ile Val Lys Ala Pro Glu Lys Ala Ile Val Phe Ala Glu	25
	35
Asn Leu Pro Glu Glu Ala Leu Ala Thr Asn Leu Gly Tyr Ser Ala Gly	40
	50
Leu Val Asn Leu Gly Asn Thr Cys Tyr Met Asn Ser Thr Val Gln Cys	55
65	70
Leu Lys Ser Val Pro Glu Leu Lys Ser Ala Leu Ser Asn Tyr Ser Leu	75
	85
Ala Ala Arg Ser Asn Asp Val Asp Gln Thr Ser His Met Leu Thr Val	90
	100
Ala Thr Arg Glu Leu Phe Gly Glu Leu Asp Arg Ser Val Asn Ala Val	105
	115
Ser Pro Ser Gln Phe Trp Met Val Leu Arg Lys Lys Tyr Pro Gln Phe	120
	130
Ser Gln Leu Gln Asn Gly Met His Met Gln Gln Asp Ala Glu Glu Cys	135
145	150
Trp Thr Gln Leu Leu Tyr Thr Leu Ser Gln Ser Leu Lys Ala Pro Thr	155
	165
Ser Ser Glu Gly Ala Asp Ala Val Lys Ala Leu Phe Gly Val Asn Leu	170
	180
Gln Ser Arg Leu His Cys Gln Glu Ser Gly Glu Glu Ser Ser Glu Thr	185
	195
Glu Ser Val Tyr Ser Leu Lys Cys His Ile Ser His Glu Val Asn His	200
	210
	215
	220

Leu His Glu Gly Leu Lys His Gly Leu Lys Gly Glu Leu Glu Lys Thr
225 230 235 240
Ser Pro Ala Leu Gly Arg Thr Ala Leu Tyr Val Lys Glu Ser Leu Ile
245 250 255
Asp Ser Leu Pro Arg Tyr Leu Thr Val Gln Phe Val Arg Phe Phe Trp
260 265 270
Lys Arg Glu Ser Asn Gln Lys Ala Lys Ile Leu Arg Lys Val Asp Tyr
275 280 285
Pro Leu Val Leu Asp Ile Phe Asp Leu Cys Ser Glu Asp Leu Arg Lys
290 295 300
Lys Leu Glu Ala Pro Arg Gln Lys Leu Arg Glu Glu Glu Gly Lys Lys
305 310 315 320
Leu Gly Leu Gln Thr Ser Ala Lys Ser Gly Ser Lys Asp Ser Asp Val
325 330 335
Lys Met Thr Asp Ala Glu Ala Ser Ala Asn Gly Ser Gly Glu Ser Ser
340 345 350
Thr Val Asn Pro Gln Glu Gly Thr Leu Ser His Ser
355 360

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met Gln Asp Asp Gly Asp Trp Ala Ala Ile Gly Val Lys Asp Gly Gln
1 5 10 15
Lys Leu Met Met Met Gly Thr Ala Asp Glu Ile Val Lys Ala Pro Glu
20 25 30
Lys Ala Ile Val Phe Ala Glu Asn Leu Pro Glu Glu Ala Leu Ala Thr
35 40 45
Asn Leu Gly Tyr Ser Ala Gly Leu Val Asn Leu Gly Asn Thr Cys Tyr
50 55 60
Met Asn Ser Thr Val Gln Cys Leu Lys Ser Val Pro Glu Leu Lys Ser
65 70 75 80
Ala Leu Ser Asn Tyr Ser Leu Ala Ala Arg Ser Asn Asp Val Asp Gln
85 90 95
Thr Ser His Met Leu Thr Val Ala Thr Arg Glu Leu Phe Gly Glu Leu
100 105 110
Asp Arg Ser Val Asn Ala Val Ser Pro Ser Gln Phe Trp Met Val Leu
115 120 125
Arg Lys Lys Tyr Pro Gln Phe Ser Gln Leu Gln Asn Gly Met His Met
130 135 140
Gln Gln Asp Ala Glu Glu Cys Trp Thr Gln Leu Leu Tyr Thr Leu Ser
145 150 155 160
Gln Ser Leu Lys Ala Pro Thr Ser Ser Glu Gly Ala Asp Ala Val Lys
165 170 175
Ala Leu Phe Gly Val Asn Leu Gln Ser Arg Leu His Cys Gln Glu Ser
180 185 190
Gly Glu Glu Ser Ser Glu Thr Glu Ser Val Tyr Ser Leu Lys Cys His
195 200 205
Ile Ser His Glu Val Asn His Leu His Glu Gly Leu Lys His Gly Leu
210 215 220
Lys Gly Glu Leu Glu Lys Thr Ser Pro Ala Leu Gly Arg Thr Ala Leu

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (1) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..630
(D) OTHER INFORMATION: / Ceres Seq. ID 1482525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605.						
aaccttcgca	gctagatctg	gacgcttttt	actgactaga	ctcctgacaa	tatcttcac	60
acaaatagca	ttacattgat	gagccatgca	tcyaatcctt	ttgctctgac	cttcatttat	120
ctgcacagta	aaatgctccg	tccaacaatt	attgcaaaag	caatggccac	agwccattct	180
tgtcatgtga	tcacctggta	aatcctccat	gcaaacatca	caactcatct	gtgaagactg	240
aggaaaggaa	gagttgccat	attgataatc	gaagacagtg	acaccagctc	cagaaaacaa	300
rcatatmtttt	mctttctmaa	caaacacagc	aaacaacttc	tccacatccc	actggtaatg	360
aataagaaga	gtccgtgcat	ggtgctcctt	tattgataac	aattscatca	cccttagcaa	420
atctttctctc	tgtgctgcta	gaagcgattc	ctgagtgatg	acctgagttg	tttgawcytt	480
tagaggacaa	gaggctgcaa	ttcaagactc	ttcawtatca	attccatcga	aaagaatctt	540
catcggagga	gtaataggca	agccctcttc	ctccgcgccta	aaataatcat	ccatcgatca	600
caattctggt	tttcgattag	gatgttctag				

(2) INFORMATION FOR SEQ ID NO:604:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1482526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:															
Met	Ser	His	Ala	Xaa	Asn	Pro	Phe	Ala	Leu	Thr	Phe	Ile	Tyr	Leu	His
1			5						10					15	
Ser	Lys	Met	Leu	Arg	Pro	Thr	Ile	Ile	Ala	Lys	Ala	Met	Ala	Thr	Xaa
			20					25					30		
His	Ser	Cys	His	Val	Ile	Thr	Trp								
		35				40									

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..657
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

attacctaga acatcctaata caaaaagtat caatggcttc cttcacctgt tcttctccat	60
cttcgatttt acctattatt gatacgagaa gtgggaattt gcgatgcaca ttccagtctc	120
aggtttcttg tgggattcag agagatgata atggacgccg tggttgccgg aggagaacat	180
tgacgaagaa ggacgatatg ttgcgttaca aaatgcaaag agttccattt gtggaagagc	240
aagtgaggaa gataagagra gttgggaaag taatgacaat ggacatagag cagcttcttt	300
tgagggaaga caatcggttt gaatttgtca atagcgtagc agctgaagca acagagtacg	360
tggaacaaga cagagacgaa tatggagggtt ccaaaaaagc tatctttcat gttctaagca	420
accgtgtgaa cgatctcggc tttgaccgcc ctgaggctta tgtagaagct gatccttaca	480
aaccgggtcc tggctatttg ttggagtact acacttgata tattataaca aaaagtgtca	540
atgtacttta cagcttttgt tcttgtatta ccaaaaccaa atcaatgcgt ttcacagctt	600
tgttgttttc ttggccagat ttcattttat ttatttagat ttactagatg aagacgg	

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..171
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Tyr	Leu	Glu	His	Pro	Asn	Gln	Lys	Val	Ser	Met	Ala	Ser	Phe	Thr	Cys	
1			5						10					15		
Ser	Ser	Pro	Ser	Ser	Ile	Leu	Pro	Ile	Ile	Asp	Thr	Arg	Ser	Gly	Asn	
			20					25					30			
Leu	Arg	Cys	Thr	Phe	Gln	Ser	Gln	Val	Ser	Cys	Gly	Ile	Gln	Arg	Asp	
			35				40					45				
Asp	Asn	Gly	Arg	Arg	Val	Trp	Arg	Arg	Arg	Thr	Leu	Thr	Lys	Lys	Asp	
			50			55				60						
Asp	Met	Leu	Arg	Tyr	Lys	Met	Gln	Arg	Val	Pro	Phe	Val	Glu	Glu	Gln	
			65		70				75				80			
Val	Arg	Lys	Ile	Arg	Xaa	Val	Gly	Lys	Val	Met	Thr	Met	Asp	Ile	Glu	
			85				90						95			
Gln	Leu	Leu	Leu	Arg	Glu	Asp	Asn	Arg	Phe	Glu	Phe	Val	Asn	Ser	Val	
			100				105						110			
Ala	Ala	Glu	Ala	Thr	Glu	Tyr	Val	Asp	Lys	Asn	Arg	Asp	Glu	Tyr	Gly	
			115			120						125				
Gly	Ser	Lys	Lys	Ala	Ile	Phe	His	Val	Leu	Ser	Asn	Arg	Val	Asn	Asp	
			130		135					140						
Leu	Gly	Phe	Asp	Arg	Pro	Glu	Ala	Tyr	Val	Glu	Ala	Asp	Pro	Tyr	Lys	
			145		150					155				160		
Pro	Gly	Pro	Gly	Tyr	Leu	Leu	Glu	Tyr	Tyr	Thr						
			165							170						

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

Met	Ala	Ser	Phe	Thr	Cys	Ser	Ser	Pro	Ser	Ser	Ile	Leu	Pro	Ile	Ile	
1				5				10					15			
Asp	Thr	Arg	Ser	Gly	Asn	Leu	Arg	Cys	Thr	Phe	Gln	Ser	Gln	Val	Ser	
			20					25					30			
Cys	Gly	Ile	Gln	Arg	Asp	Asp	Asn	Gly	Arg	Arg	Val	Trp	Arg	Arg	Arg	
			35				40					45				
Thr	Leu	Thr	Lys	Lys	Asp	Asp	Met	Leu	Arg	Tyr	Lys	Met	Gln	Arg	Val	
	50					55					60					
Pro	Phe	Val	Glu	Glu	Gln	Val	Arg	Lys	Ile	Arg	Xaa	Val	Gly	Lys	Val	
65					70					75				80		
Met	Thr	Met	Asp	Ile	Glu	Gln	Leu	Leu	Leu	Arg	Glu	Asp	Asn	Arg	Phe	
				85					90					95		
Glu	Phe	Val	Asn	Ser	Val	Ala	Ala	Glu	Ala	Thr	Glu	Tyr	Val	Asp	Lys	
			100					105					110			
Asn	Arg	Asp	Glu	Tyr	Gly	Gly	Ser	Lys	Lys	Ala	Ile	Phe	His	Val	Leu	
		115					120						125			
Ser	Asn	Arg	Val	Asn	Asp	Leu	Gly	Phe	Asp	Arg	Pro	Glu	Ala	Tyr	Val	
	130					135				140						
Glu	Ala	Asp	Pro	Tyr	Lys	Pro	Gly	Pro	Gly	Tyr	Leu	Leu	Glu	Tyr	Tyr	
145					150					155					160	
Thr																

(2) INFORMATION FOR SEQ ID NO:608:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met	Leu	Arg	Tyr	Lys	Met	Gln	Arg	Val	Pro	Phe	Val	Glu	Glu	Gln	Val	
1				5					10					15		
Arg	Lys	Ile	Arg	Xaa	Val	Gly	Lys	Val	Met	Thr	Met	Asp	Ile	Glu	Gln	
			20					25					30			
Leu	Leu	Leu	Arg	Glu	Asp	Asn	Arg	Phe	Glu	Phe	Val	Asn	Ser	Val	Ala	
		35				40						45				
Ala	Glu	Ala	Thr	Glu	Tyr	Val	Asp	Lys	Asn	Arg	Asp	Glu	Tyr	Gly	Gly	
	50					55					60					
Ser	Lys	Lys	Ala	Ile	Phe	His	Val	Leu	Ser	Asn	Arg	Val	Asn	Asp	Leu	
65				70						75				80		
Gly	Phe	Asp	Arg	Pro	Glu	Ala	Tyr	Val	Glu	Ala	Asp	Pro	Tyr	Lys	Pro	
			85						90					95		
Gly	Pro	Gly	Tyr	Leu	Leu	Glu	Tyr	Tyr	Thr							
		100						105								

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..814

(D) OTHER INFORMATION: / Ceres Seq. ID 1482542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

agcaccggac	cacacaatct	tcccccaaat	ctcgcttcca	tcgctctctt	ccacggaaat	60
ctcagcacac	caatcatggg	acttatctct	ctttactttc	aatattttct	cactttctaa	120
tcctatcctt	ctaattttat	ttagatgtca	atcattgtga	ataggattat	gagcctgctt	180
agttgcattg	gactccaatt	gggtgaattg	gctaagaaat	ttcgacatgg	tgcgttcata	240
taattcgact	gcaacctcta	caaagctgga	aaacatgaat	gaacatacgc	ctctgtggat	300
tgcacagatc	tctatctgct	tctttttgga	tgaacggagg	gagaaagacc	taggcatact	360
cagtgtatccc	atgaattttg	tgctcctagg	tacatcattt	ggggctcgta	cagtgtagtt	420
gtgaatctca	ctaagatgcc	aacgagacct	tccaagaaat	cagttgcata	cctgcttggt	480
cgtgctccac	ttcttttgaa	cagatggatt	gcatgcagaa	tttcagacac	tatgctctcg	540
ttgaccagt	ctaaatttaag	agtcagattt	tgatgaggaa	gttttagcaag	taacttggct	600
gaaacagcat	gcttttctgt	tatttgattt	gcttctactg	ggcactggat	aagattctct	660
ggctgacctc	tagttttaca	tagtctctct	gatagcgtgt	gaccgatgta	gggggtaagg	720
gatatcagaa	gttttaatgc	tccaaccctt	aattcgtcac	gaggattggt	gatgagttct	780
atcatggcaa	agcttgctgc	ggtttctttg	atcg			

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1482543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Ala	Pro	Asp	His	Thr	Ile	Phe	Pro	Gln	Ile	Ser	Pro	Pro	Ser	Pro	Leu
1				5					10					15	
Ser	Thr	Glu	Ile	Ser	Ala	His	Gln	Ser	Trp	Asp	Leu	Ser	Leu	Phe	Thr
		20					25						30		
Phe	Asn	Ile	Phe	Ser	Leu	Ser	Asn	Pro	Ile	Leu	Leu	Ile	Leu	Phe	Arg
		35					40						45		
Cys	Gln	Ser	Leu												

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1482544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met	Val	Arg	Ser	Tyr	Asn	Ser	Thr	Ala	Thr	Ser	Thr	Lys	Leu	Glu	Asn
1				5					10					15	
Met	Asn	Glu	His	Thr	Pro	Leu	Trp	Ile	Ala	Gln	Ile	Ser	Ile	Cys	Phe

20 25 30
Phe Leu Asp Glu Arg Arg Glu Lys Asp Leu Gly Ile Leu Ser Asp Pro
35 40 45
Met Asn Phe Val Leu Leu Gly Thr Ser Phe Gly Ala Arg Thr Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Asn Glu His Thr Pro Leu Trp Ile Ala Gln Ile Ser Ile Cys Phe
1 5 10 15
Phe Leu Asp Glu Arg Arg Glu Lys Asp Leu Gly Ile Leu Ser Asp Pro
20 25 30
Met Asn Phe Val Leu Leu Gly Thr Ser Phe Gly Ala Arg Thr Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

gataccttgct acaaaatgtc gcgtaattct tctactgatt tcagctcaat cgctcaaatt 60
cgagtttgctg tttagaaatt gaagttgact cttctgttct tgaatctatc tccgatcggt 120
gaactatctc tcagtagcag gagattgac actccttcga cattgctctt tgaattcgctc 180
ctcaagggtta ttaatgagct cgtagaagct accagaaatg gcgtccatga gctctgggtga 240
tgaaagcctt cgacttttgc tgtttgattt gaggagaggt tttagacttc tcgacgcagt tatcagtgat 300
agagaaaatt ttgttctttt atcctgcccga tttagacttc tctccggagg cggcttgtga 360
cgggctcagt gaagggtcta ttacttttac tagacttttc tctccggagg cggcttgtga 420
agtgatcgaa gcagaaagac attcccatgt tttctatgag gctgaacctg atatctggat 480
ggttatgggt gtggagaaaa ataaggagac aggagcgata tggaggatcg atgcattaag 540
gaggggtgctt aaagaagtgc actcactctt tgtgatgttt cacgggtcaa ttagggcatt 600
aatcgaaaaa gaaccaacag gagggcttac ccgatcacta ttgtaccctg tcatcacaga 660
ttatttaagc acatttcaaa tatggtctct ctcggaagac tgctgctgtg aattttttgt 720
tggaagaaaa cttcagctac caactttccg tgaaactttg agagagcgtg gaactgttca 780
aatgcttact ttagcaaggg acactgcagt tgaagttcag tctcttgctc aagtactaga 840
ttcatgtgct gggagcttac gatgtcactc tatgatctta tttcaagatc ttttggtttc 900
aacaaccctc tcagctgatg ataccgtcga cttgtttaca tttgcggtaa tgaggttgac 960
atctgaaatc tcttctagat ctaatctggc acccgttggc tcaattgatt ccctacactc 1020
aagaaacggg aataacatgc atcatgttat taggccacta caaaatgata agtggacaaa 1080
agggaaagat gggtttctaa taaccgatat ttggggctct gagactggcg gctcccctga 1140
ttctgccatc cctacaattt ggcttcagca gacacaagaa agaattgtatc tccttgccct 1200
tcagcataaa agtctcacct tacttcttct gatgcctaca aatgccattg tcaatggaga 1260
tttaagcatc tcagccgtga aacagcaagt tattgaagat gcatcactga gaattttgaa 1320
aattgaagag aatattttcaa gaggggtggg cggtgagaat gcttaccata ttaagggtta 1380
1440

ccgttactta	gtagttgata	atgacacgaa	agtatccaga	tcttctcctt	caggaaaagt	1500
aacaacactt	gcaaaggagt	ctctacttgc	actaaacaag	cttagagaag	aagtggattc	1560
agaaaaaagc	cgtgcaaaaag	gacaggagaa	agacatggaa	atatgcatca	gagctaagaa	1620
caatgtgtgg	gtgatcgccc	gtgtgaccag	aggcaaagag	ctttacatgg	ctttggagaa	1680
aggcagcgac	actcttcttg	ataccacaga	cgctgttgga	agattcagca	acagggtattg	1740
cagcggagca	ttcttgatgg	actaagtttt	cgtgttcttt	cttctgggtt	tgggaagagg	1800
gttcttctag	tttcaagtac	gaagtgaaaa	gctcagaaga	agtaatgagc	acttctctct	1860
cagccattaa	ttttgttttg	tgagaaattg	cagagaggaa	aacgattgtg	ttcttagttg	1920
gcctgtagat	atgtaacaat	gatattccac	gttggatcag	tgcaaacaaa	tccttttttg	1980

tg

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1482547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Met	Ala	Ser	Met	Ser	Ser	Gly	Asp	Glu	Ser	Leu	Arg	Leu	Cys	Met	Phe
1			5					10						15	
Asp	Leu	Arg	Arg	Gly	Gln	Thr	Glu	Gly	Gln	Glu	Leu	Glu	Lys	Ile	Leu
			20					25					30		
Phe	Phe	Tyr	Pro	Ala	Asp	Leu	Asp	Phe	Ser	Thr	Gln	Leu	Ser	Val	Ile
		35					40					45			
Gly	Leu	Ser	Glu	Gly	Leu	Ile	Thr	Phe	Thr	Arg	Leu	Phe	Ser	Pro	Glu
		50				55					60				
Ala	Ala	Cys	Glu	Val	Ile	Glu	Ala	Glu	Arg	His	Ser	His	Val	Phe	Tyr
65					70				75					80	
Glu	Ala	Glu	Pro	Asp	Ile	Trp	Met	Val	Met	Val	Val	Glu	Lys	Asn	Lys
			85						90					95	
Glu	Thr	Gly	Ala	Ile	Trp	Arg	Ile	Asp	Ala	Leu	Arg	Arg	Val	Leu	Lys
			100					105					110		
Glu	Val	His	Ser	Leu	Phe	Val	Met	Phe	His	Gly	Ser	Ile	Arg	Ala	Leu
		115					120					125			
Ile	Glu	Lys	Glu	Pro	Thr	Gly	Gly	Leu	Thr	Arg	Ser	Leu	Leu	Tyr	Pro
		130				135					140				
Phe	Ile	Thr	Asp	Tyr	Leu	Ser	Thr	Phe	Gln	Ile	Trp	Ser	Leu	Ser	Glu
145				150					155					160	
Asp	Cys	Cys	Cys	Glu	Phe	Phe	Val	Gly	Lys	Lys	Leu	Gln	Leu	Pro	Thr
			165						170					175	
Phe	Arg	Glu	Thr	Leu	Arg	Glu	Arg	Gly	Thr	Val	Gln	Met	Leu	Thr	Leu
			180					185					190		
Ala	Arg	Asp	Thr	Ala	Val	Glu	Val	Gln	Ser	Leu	Val	Gln	Val	Leu	Asp
		195				200						205			
Ser	Cys	Ala	Gly	Ser	Leu	Arg	Cys	His	Ser	Met	Ile	Leu	Phe	Gln	Asp
		210				215					220				
Leu	Leu	Val	Ser	Thr	Thr	Leu	Ser	Ala	Asp	Asp	Thr	Val	Asp	Leu	Phe
225				230					235					240	
Thr	Phe	Ala	Val	Met	Arg	Leu	Thr	Ser	Lys	Ala	Phe	Ser	Ser	Asp	Thr
			245						250					255	
Ser	Ser	Trp	Ser	Tyr	Leu	Arg	Lys	Gly	Pro	Gly	Ser	Ser	Glu	Ile	Ser
		260						265					270		
Ser	Arg	Ser	Asn	Leu	Ala	Pro	Val	Gly	Ser	Ile	Asp	Ser	Leu	His	Ser
		275				280						285			
Arg	Asn	Gly	Asn	Asn	Met	His	His	Val	Ile	Arg	Pro	Leu	Gln	Asn	Asp

290						295						300							
Lys	Trp	Thr	Lys	Gly	Lys	Asp	Gly	Phe	Leu	Ile	Thr	Asp	Ile	Trp	Gly				
305					310					315					320				
Leu	Glu	Thr	Gly	Gly	Ser	Pro	Asp	Ser	Ala	Ile	Pro	Thr	Ile	Trp	Leu				
				325					330						335				
Gln	Gln	Thr	Gln	Glu	Arg	Met	Tyr	Leu	Leu	Ala	Tyr	Gln	His	Lys	Ser				
			340					345					350						
Leu	Thr	Leu	Leu	Leu	Met	Pro	Thr	Asn	Ala	Ile	Val	Asn	Gly	Asp					
			355				360				365								
Leu	Ser	Ile	Ser	Ala	Val	Lys	Gln	Gln	Val	Ile	Glu	Asp	Ala	Ser	Leu				
	370					375				380									
Arg	Ile	Leu	Lys	Ile	Glu	Glu	Asn	Ile	Ser	Arg	Gly	Trp	Gly	Gly	Glu				
385					390					395					400				
Asn	Ala	Tyr	His	Ile	Lys	Gly	Tyr	Arg	Tyr	Leu	Val	Val	Asp	Asn	Asp				
			405					410						415					
Thr	Lys	Val	Ser	Arg	Ser	Ser	Pro	Ser	Gly	Lys	Val	Thr	Thr	Leu	Ala				
			420					425					430						
Lys	Glu	Ser	Leu	Leu	Ala	Leu	Asn	Lys	Leu	Arg	Glu	Glu	Val	Asp	Ser				
		435				440					445								
Glu	Lys	Ser	Arg	Ala	Lys	Gly	Gln	Glu	Lys	Asp	Met	Glu	Ile	Cys	Ile				
	450					455				460									
Arg	Ala	Lys	Asn	Asn	Val	Trp	Val	Ile	Ala	Arg	Val	Thr	Arg	Gly	Lys				
465					470					475					480				
Glu	Leu	Tyr	Met	Ala	Leu	Glu	Lys	Gly	Ser	Asp	Thr	Leu	Leu	Asp	Thr				
			485					490						495					
Thr	Asp	Ala	Val	Gly	Arg	Phe	Ser	Asn	Arg	Tyr	Cys	Ser	Gly	Ala	Phe				
			500					505					510						
Leu	Met	Asp																	
		515																	

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 512 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1482548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

Met	Ser	Ser	Gly	Asp	Glu	Ser	Leu	Arg	Leu	Cys	Met	Phe	Asp	Leu	Arg				
1			5				10							15					
Arg	Gly	Gln	Thr	Glu	Gly	Gln	Glu	Leu	Glu	Lys	Ile	Leu	Phe	Phe	Tyr				
		20					25					30							
Pro	Ala	Asp	Leu	Asp	Phe	Ser	Thr	Gln	Leu	Ser	Val	Ile	Gly	Leu	Ser				
		35					40					45							
Glu	Gly	Leu	Ile	Thr	Phe	Thr	Arg	Leu	Phe	Ser	Pro	Glu	Ala	Ala	Cys				
	50					55				60									
Glu	Val	Ile	Glu	Ala	Glu	Arg	His	Ser	His	Val	Phe	Tyr	Glu	Ala	Glu				
65			70				75							80					
Pro	Asp	Ile	Trp	Met	Val	Met	Val	Val	Glu	Lys	Asn	Lys	Glu	Thr	Gly				
			85				90							95					
Ala	Ile	Trp	Arg	Ile	Asp	Ala	Leu	Arg	Arg	Val	Leu	Lys	Glu	Val	His				
		100					105						110						
Ser	Leu	Phe	Val	Met	Phe	His	Gly	Ser	Ile	Arg	Ala	Leu	Ile	Glu	Lys				
	115					120						125							
Glu	Pro	Thr	Gly	Gly	Leu	Thr	Arg	Ser	Leu	Leu	Tyr	Pro	Phe	Ile	Thr				
	130					135						140							

Asp	Tyr	Leu	Ser	Thr	Phe	Gln	Ile	Trp	Ser	Leu	Ser	Glu	Asp	Cys	Cys	
145					150					155					160	
Cys	Glu	Phe	Phe	Val	Gly	Lys	Lys	Leu	Gln	Leu	Pro	Thr	Phe	Arg	Glu	
				165					170					175		
Thr	Leu	Arg	Glu	Arg	Gly	Thr	Val	Gln	Met	Leu	Thr	Leu	Ala	Arg	Asp	
			180					185						190		
Thr	Ala	Val	Glu	Val	Gln	Ser	Leu	Val	Gln	Val	Leu	Asp	Ser	Cys	Ala	
		195					200					205				
Gly	Ser	Leu	Arg	Cys	His	Ser	Met	Ile	Leu	Phe	Gln	Asp	Leu	Leu	Val	
	210					215					220					
Ser	Thr	Thr	Leu	Ser	Ala	Asp	Asp	Thr	Val	Asp	Leu	Phe	Thr	Phe	Ala	
225					230					235					240	
Val	Met	Arg	Leu	Thr	Ser	Lys	Ala	Phe	Ser	Ser	Asp	Thr	Ser	Ser	Trp	
				245					250					255		
Ser	Tyr	Leu	Arg	Lys	Gly	Pro	Gly	Ser	Ser	Glu	Ile	Ser	Ser	Arg	Ser	
		260					265							270		
Asn	Leu	Ala	Pro	Val	Gly	Ser	Ile	Asp	Ser	Leu	His	Ser	Arg	Asn	Gly	
	275						280					285				
Asn	Asn	Met	His	His	Val	Ile	Arg	Pro	Leu	Gln	Asn	Asp	Lys	Trp	Thr	
	290					295					300					
Lys	Gly	Lys	Asp	Gly	Phe	Leu	Ile	Thr	Asp	Ile	Trp	Gly	Leu	Glu	Thr	
305					310					315					320	
Gly	Gly	Ser	Pro	Asp	Ser	Ala	Ile	Pro	Thr	Ile	Trp	Leu	Gln	Gln	Thr	
				325					330					335		
Gln	Glu	Arg	Met	Tyr	Leu	Leu	Ala	Tyr	Gln	His	Lys	Ser	Leu	Thr	Leu	
			340					345					350			
Leu	Leu	Leu	Met	Pro	Thr	Asn	Ala	Ile	Val	Asn	Gly	Asp	Leu	Ser	Ile	
		355					360					365				
Ser	Ala	Val	Lys	Gln	Gln	Val	Ile	Glu	Asp	Ala	Ser	Leu	Arg	Ile	Leu	
	370					375				380						
Lys	Ile	Glu	Glu	Asn	Ile	Ser	Arg	Gly	Trp	Gly	Gly	Glu	Asn	Ala	Tyr	
385					390					395					400	
His	Ile	Lys	Gly	Tyr	Arg	Tyr	Leu	Val	Val	Asp	Asn	Asp	Thr	Lys	Val	
				405					410					415		
Ser	Arg	Ser	Ser	Pro	Ser	Gly	Lys	Val	Thr	Thr	Leu	Ala	Lys	Glu	Ser	
			420					425					430			
Leu	Leu	Ala	Leu	Asn	Lys	Leu	Arg	Glu	Glu	Val	Asp	Ser	Glu	Lys	Ser	
		435					440					445				
Arg	Ala	Lys	Gly	Gln	Glu	Lys	Asp	Met	Glu	Ile	Cys	Ile	Arg	Ala	Lys	
	450					455					460					
Asn	Asn	Val	Trp	Val	Ile	Ala	Arg	Val	Thr	Arg	Gly	Lys	Glu	Leu	Tyr	
465					470					475					480	
Met	Ala	Leu	Glu	Lys	Gly	Ser	Asp	Thr	Leu	Leu	Asp	Thr	Thr	Asp	Ala	
				485					490					495		
Val	Gly	Arg	Phe	Ser	Asn	Arg	Tyr	Cys	Ser	Gly	Ala	Phe	Leu	Met	Asp	
			500					505					510			

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

Met	Phe	Asp	Leu	Arg	Arg	Gly	Gln	Thr	Glu	Gly	Gln	Glu	Leu	Glu	Lys
1				5					10					15	
Ile	Leu	Phe	Phe	Tyr	Pro	Ala	Asp	Leu	Asp	Phe	Ser	Thr	Gln	Leu	Ser
			20					25					30		
Val	Ile	Gly	Leu	Ser	Glu	Gly	Leu	Ile	Thr	Phe	Thr	Arg	Leu	Phe	Ser
		35					40					45			
Pro	Glu	Ala	Ala	Cys	Glu	Val	Ile	Glu	Ala	Glu	Arg	His	Ser	His	Val
	50						55				60				
Phe	Tyr	Glu	Ala	Glu	Pro	Asp	Ile	Trp	Met	Val	Met	Val	Val	Glu	Lys
65					70					75				80	
Asn	Lys	Glu	Thr	Gly	Ala	Ile	Trp	Arg	Ile	Asp	Ala	Leu	Arg	Arg	Val
				85					90					95	
Leu	Lys	Glu	Val	His	Ser	Leu	Phe	Val	Met	Phe	His	Gly	Ser	Ile	Arg
			100					105					110		
Ala	Leu	Ile	Glu	Lys	Glu	Pro	Thr	Gly	Gly	Leu	Thr	Arg	Ser	Leu	Leu
		115						120					125		
Tyr	Pro	Phe	Ile	Thr	Asp	Tyr	Leu	Ser	Thr	Phe	Gln	Ile	Trp	Ser	Leu
	130					135					140				
Ser	Glu	Asp	Cys	Cys	Cys	Glu	Phe	Phe	Val	Gly	Lys	Lys	Leu	Gln	Leu
145					150					155				160	
Pro	Thr	Phe	Arg	Glu	Thr	Leu	Arg	Glu	Arg	Gly	Thr	Val	Gln	Met	Leu
				165					170					175	
Thr	Leu	Ala	Arg	Asp	Thr	Ala	Val	Glu	Val	Gln	Ser	Leu	Val	Gln	Val
			180					185					190		
Leu	Asp	Ser	Cys	Ala	Gly	Ser	Leu	Arg	Cys	His	Ser	Met	Ile	Leu	Phe
		195					200					205			
Gln	Asp	Leu	Leu	Val	Ser	Thr	Thr	Leu	Ser	Ala	Asp	Asp	Thr	Val	Asp
	210					215					220				
Leu	Phe	Thr	Phe	Ala	Val	Met	Arg	Leu	Thr	Ser	Lys	Ala	Phe	Ser	Ser
225					230					235				240	
Asp	Thr	Ser	Ser	Trp	Ser	Tyr	Leu	Arg	Lys	Gly	Pro	Gly	Ser	Ser	Glu
				245					250					255	
Ile	Ser	Ser	Arg	Ser	Asn	Leu	Ala	Pro	Val	Gly	Ser	Ile	Asp	Ser	Leu
			260					265					270		
His	Ser	Arg	Asn	Gly	Asn	Asn	Met	His	His	Val	Ile	Arg	Pro	Leu	Gln
		275					280					285			
Asn	Asp	Lys	Trp	Thr	Lys	Gly	Lys	Asp	Gly	Phe	Leu	Ile	Thr	Asp	Ile
	290					295					300				
Trp	Gly	Leu	Glu	Thr	Gly	Gly	Ser	Pro	Asp	Ser	Ala	Ile	Pro	Thr	Ile
305					310					315				320	
Trp	Leu	Gln	Gln	Thr	Gln	Glu	Arg	Met	Tyr	Leu	Leu	Ala	Tyr	Gln	His
				325					330					335	
Lys	Ser	Leu	Thr	Leu	Leu	Leu	Leu	Met	Pro	Thr	Asn	Ala	Ile	Val	Asn
			340					345					350		
Gly	Asp	Leu	Ser	Ile	Ser	Ala	Val	Lys	Gln	Gln	Val	Ile	Glu	Asp	Ala
	355						360					365			
Ser	Leu	Arg	Ile	Leu	Lys	Ile	Glu	Glu	Asn	Ile	Ser	Arg	Gly	Trp	Gly
	370					375					380				
Gly	Glu	Asn	Ala	Tyr	His	Ile	Lys	Gly	Tyr	Arg	Tyr	Leu	Val	Val	Asp
385					390					395				400	
Asn	Asp	Thr	Lys	Val	Ser	Arg	Ser	Ser	Pro	Ser	Gly	Lys	Val	Thr	Thr
			405						410					415	
Leu	Ala	Lys	Glu	Ser	Leu	Leu	Ala	Leu	Asn	Lys	Leu	Arg	Glu	Glu	Val
			420					425					430		
Asp	Ser	Glu	Lys	Ser	Arg	Ala	Lys	Gly	Gln	Glu	Lys	Asp	Met	Glu	Ile
		435					440					445			
Cys	Ile	Arg	Ala	Lys	Asn	Asn	Val	Trp	Val	Ile	Ala	Arg	Val	Thr	Arg
	450					455						460			

0.2

[illegible]